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TO: Patricia Duffy
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Tuesday, July 11, 2006
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Location: Biotech-Chem Library
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Technical Information Specialist
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residues 1-51 of SEQ ID NO:1
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Patricia A. Duffy, Ph.D.
Primary Patent Examiner
571-272-0855,
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OM protein - protein search, using sw model

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
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SUMMARIES

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| 163 | 50 | 24.9 | 167 | 1 | US-08-465-982-2 | Sequence 2, Appl | 236 | 50 | 24.9 | 455 | 2 | US-09-004-838-101 | Sequence 101, App |
| 164 | 50 | 24.9 | 167 | 1 | US-08-465-982-2 | Sequence 2, Appl | 237 | 50 | 24.9 | 455 | 2 | US-09-004-838-101 | Sequence 101, App |
| 165 | 50 | 24.9 | 167 | 1 | US-08-465-982-57 | Sequence 57, Appl | 238 | 50 | 24.9 | 455 | 2 | US-09-252-991A-18110 | Sequence 18110, A |
| 166 | 50 | 24.9 | 197 | 1 | US-08-468-347-24 | Sequence 24, Appl | 239 | 50 | 24.9 | 455 | 2 | US-09-747-371-3 | Sequence 3, Appl |
| 167 | 50 | 24.9 | 197 | 1 | US-08-467-388-24 | Sequence 24, Appl | 240 | 50 | 24.9 | 455 | 2 | US-09-640-211A-975 | Sequence 975, App |
| 168 | 50 | 24.9 | 197 | 1 | US-08-469-219-24 | Sequence 24, Appl | 241 | 50 | 24.9 | 455 | 2 | US-10-046-433-61 | Sequence 61, Appl |
| 169 | 50 | 24.9 | 197 | 1 | US-08-469-219-24 | Sequence 24, Appl | 242 | 50 | 24.9 | 455 | 2 | US-08-804-166-6 | Sequence 6, Appl |
| 170 | 50 | 24.9 | 197 | 2 | US-09-228-152-24 | Sequence 21, Appl | 243 | 50 | 24.9 | 455 | 2 | US-08-910-991-6 | Sequence 6, Appl |
| 171 | 50 | 24.9 | 197 | 2 | US-08-828-683A-21 | Sequence 21, Appl | 244 | 50 | 24.9 | 455 | 2 | US-09-756-186-6 | Sequence 6, Appl |
| 172 | 50 | 24.9 | 197 | 2 | US-09-902-540-10551 | Sequence 10551, A | 245 | 50 | 24.9 | 455 | 2 | US-09-756-186-6 | Sequence 6, Appl |

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|-----|------|------|------|---|----------------------|--------------------|-----|------|------|-----|---|--------------------|--------------------|
| 246 | 49 | 24.4 | 297 | 2 | US-09-548-130-6 | Sequence 6, Appl1 | 319 | 46.5 | 23.1 | 75 | 1 | US-08-461-965-57 | Sequence 57, Appl1 |
| 247 | 49 | 24.4 | 297 | 2 | US-09-949-016-7016 | Sequence 7016, Ap | 320 | 46.5 | 23.1 | 75 | 1 | US-08-634-641-57 | Sequence 57, Appl1 |
| 248 | 49 | 24.4 | 297 | 2 | US-09-949-016-11181 | Sequence 11181, A | 321 | 46.5 | 23.1 | 75 | 2 | US-09-249-471-57 | Sequence 57, Appl1 |
| 249 | 49 | 24.4 | 299 | 2 | US-09-548-130-3 | Sequence 3, Appl1 | 322 | 46.5 | 23.1 | 75 | 2 | US-09-249-472-57 | Sequence 57, Appl1 |
| 250 | 49 | 24.4 | 299 | 2 | US-10-119-466-12 | Sequence 12, Appl1 | 323 | 46.5 | 23.1 | 75 | 2 | US-09-249-451-57 | Sequence 57, Appl1 |
| 251 | 49 | 24.4 | 310 | 2 | US-10-094-749-3057 | Sequence 3057, Ap | 324 | 46.5 | 23.1 | 75 | 2 | US-08-809-455-57 | Sequence 57, Appl1 |
| 252 | 49 | 24.4 | 310 | 2 | US-09-949-016-6700 | Sequence 6700, Ap | 325 | 46.5 | 23.1 | 75 | 2 | US-09-249-461-57 | Sequence 57, Appl1 |
| 253 | 49 | 24.4 | 406 | 2 | US-09-949-016-10006 | Sequence 10006, A | 326 | 46.5 | 23.1 | 75 | 2 | US-09-249-448-57 | Sequence 57, Appl1 |
| 254 | 49 | 24.4 | 1089 | 2 | US-09-902-540-14239 | Sequence 14239, A | 327 | 46.5 | 23.1 | 75 | 2 | US-09-249-447-57 | Sequence 57, Appl1 |
| 255 | 49 | 24.4 | 3635 | 2 | US-09-845-583A-2 | Sequence 2, Appl1 | 328 | 46.5 | 23.1 | 75 | 2 | US-09-498-556-57 | Sequence 57, Appl1 |
| 256 | 49 | 24.4 | 3635 | 2 | US-10-037-417-47 | Sequence 47, Appl1 | 329 | 46.5 | 23.1 | 88 | 1 | US-08-469-202-20 | Sequence 50, Appl1 |
| 257 | 49 | 24.4 | 3635 | 2 | US-10-037-182-4 | Sequence 4, Appl1 | 330 | 46.5 | 23.1 | 94 | 1 | US-08-465-380-22 | Sequence 22, Appl1 |
| 258 | 48.5 | 24.1 | 348 | 2 | US-10-188-495-69 | Sequence 69, Appl1 | 331 | 46.5 | 23.1 | 94 | 1 | US-08-480-478-51 | Sequence 51, Appl1 |
| 259 | 48.5 | 24.1 | 530 | 1 | US-08-448-196A-9 | Sequence 9, Appl1 | 332 | 46.5 | 23.1 | 94 | 1 | US-08-486-397-22 | Sequence 22, Appl1 |
| 260 | 48 | 23.9 | 56 | 2 | US-09-177-249-273 | Sequence 151, App | 333 | 46.5 | 23.1 | 94 | 1 | US-08-486-399-22 | Sequence 22, Appl1 |
| 261 | 48 | 23.9 | 95 | 2 | US-09-177-249-273 | Sequence 273, App | 334 | 46.5 | 23.1 | 94 | 1 | US-08-461-966-22 | Sequence 22, Appl1 |
| 262 | 48 | 23.9 | 95 | 3 | US-09-071-838A-273 | Sequence 273, App | 335 | 46.5 | 23.1 | 94 | 1 | US-08-326-110A-51 | Sequence 51, Appl1 |
| 263 | 48 | 23.9 | 95 | 3 | US-09-950-933A-64 | Sequence 273, App | 336 | 46.5 | 23.1 | 94 | 1 | US-08-634-641-22 | Sequence 22, Appl1 |
| 264 | 48 | 23.9 | 99 | 2 | US-09-570-767-39208 | Sequence 39208, A | 337 | 46.5 | 23.1 | 94 | 2 | US-09-249-471-22 | Sequence 22, Appl1 |
| 265 | 48 | 23.9 | 116 | 2 | US-09-270-767-54425 | Sequence 54425, A | 338 | 46.5 | 23.1 | 94 | 2 | US-09-249-472-22 | Sequence 22, Appl1 |
| 266 | 48 | 23.9 | 127 | 2 | US-09-489-039A-11660 | Sequence 11660, A | 339 | 46.5 | 23.1 | 94 | 2 | US-09-249-451-22 | Sequence 22, Appl1 |
| 267 | 48 | 23.9 | 276 | 2 | US-09-270-767-32903 | Sequence 32903, A | 340 | 46.5 | 23.1 | 94 | 2 | US-09-809-455-22 | Sequence 22, Appl1 |
| 268 | 48 | 23.9 | 276 | 2 | US-09-342-681C-17 | Sequence 48120, A | 341 | 46.5 | 23.1 | 94 | 2 | US-09-249-461-22 | Sequence 22, Appl1 |
| 269 | 48 | 23.9 | 448 | 2 | US-09-342-681C-17 | Sequence 17, Appl1 | 342 | 46.5 | 23.1 | 94 | 2 | US-09-249-448-22 | Sequence 22, Appl1 |
| 270 | 48 | 23.9 | 448 | 2 | US-09-342-681C-19 | Sequence 19, Appl1 | 343 | 46.5 | 23.1 | 94 | 2 | US-09-249-471-22 | Sequence 22, Appl1 |
| 271 | 48 | 23.9 | 500 | 1 | US-08-896-005-1 | Sequence 1, Appl1 | 344 | 46.5 | 23.1 | 192 | 1 | US-08-086-428B-84 | Sequence 84, Appl1 |
| 272 | 48 | 23.9 | 689 | 2 | US-09-177-249-2 | Sequence 2, Appl1 | 345 | 46.5 | 23.1 | 192 | 1 | US-08-468-570-84 | Sequence 84, Appl1 |
| 273 | 48 | 23.9 | 689 | 2 | US-09-061-769A-2 | Sequence 2, Appl1 | 346 | 46.5 | 23.1 | 192 | 1 | US-08-290-665A-84 | Sequence 84, Appl1 |
| 274 | 48 | 23.9 | 689 | 2 | US-09-812-283-2 | Sequence 2, Appl1 | 347 | 46.5 | 23.1 | 192 | 1 | US-08-466-601A-84 | Sequence 84, Appl1 |
| 275 | 48 | 23.9 | 689 | 2 | US-10-176-884-14 | Sequence 14, Appl1 | 348 | 46.5 | 23.1 | 192 | 5 | PCT-US95-10398-84 | Sequence 84, Appl1 |
| 276 | 48 | 23.9 | 689 | 3 | US-09-071-838A-2 | Sequence 2, Appl1 | 349 | 46.5 | 23.1 | 319 | 2 | US-09-851-138C-232 | Sequence 232, App |
| 277 | 48 | 23.9 | 764 | 2 | US-09-949-016-9367 | Sequence 9367, Ap | 350 | 46.5 | 23.1 | 350 | 1 | US-08-999-811-4 | Sequence 4, Appl1 |
| 278 | 48 | 23.9 | 932 | 2 | US-10-176-884-15 | Sequence 15, Appl1 | 351 | 46.5 | 23.1 | 350 | 1 | US-08-824-96E-2 | Sequence 2, Appl1 |
| 279 | 48 | 23.9 | 969 | 1 | US-08-284-941-2 | Sequence 2, Appl1 | 352 | 46.5 | 23.1 | 350 | 2 | US-09-042-105-4 | Sequence 4, Appl1 |
| 280 | 48 | 23.9 | 969 | 1 | US-08-447-642-2 | Sequence 2, Appl1 | 353 | 46.5 | 23.1 | 350 | 2 | US-08-510-133A-33 | Sequence 33, Appl1 |
| 281 | 48 | 23.9 | 969 | 2 | US-09-366-503-2 | Sequence 2, Appl1 | 354 | 46.5 | 23.1 | 350 | 2 | US-08-585-89S-33 | Sequence 33, Appl1 |
| 282 | 48 | 23.9 | 969 | 2 | US-09-961-403-6 | Sequence 6, Appl1 | 355 | 46.5 | 23.1 | 350 | 2 | US-10-084-486-4 | Sequence 4, Appl1 |
| 283 | 48 | 23.9 | 969 | 2 | US-09-949-016-6240 | Sequence 6240, Ap | 356 | 46.5 | 23.1 | 350 | 2 | US-09-499-468-4 | Sequence 4, Appl1 |
| 284 | 48 | 23.9 | 969 | 5 | PCT-US93-02147A-2 | Sequence 2, Appl1 | 357 | 46.5 | 23.1 | 350 | 2 | US-09-219-444-4 | Sequence 4, Appl1 |
| 285 | 48 | 23.9 | 969 | 5 | US-09-513-999C-7856 | Sequence 7856, Ap | 358 | 46.5 | 23.1 | 415 | 2 | US-08-795-430-11 | Sequence 11, Appl1 |
| 286 | 47.5 | 23.6 | 122 | 2 | US-09-370-838C-206 | Sequence 206, App | 359 | 46.5 | 23.1 | 415 | 2 | US-08-355-700-11 | Sequence 11, Appl1 |
| 287 | 47.5 | 23.6 | 197 | 2 | US-09-854-133-206 | Sequence 206, App | 360 | 46.5 | 23.1 | 415 | 2 | US-08-601-133-41 | Sequence 41, Appl1 |
| 288 | 47.5 | 23.6 | 197 | 2 | US-09-902-540-10416 | Sequence 10416, A | 361 | 46.5 | 23.1 | 415 | 2 | US-08-671-572B-41 | Sequence 41, Appl1 |
| 289 | 47.5 | 23.6 | 198 | 2 | US-09-561-709B-11 | Sequence 11, Appl1 | 362 | 46.5 | 23.1 | 415 | 2 | US-09-534-376A-11 | Sequence 11, Appl1 |
| 290 | 47.5 | 23.6 | 1798 | 2 | US-09-917-254-87 | Sequence 87, Appl1 | 363 | 46.5 | 23.1 | 415 | 1 | US-08-999-811-2 | Sequence 2, Appl1 |
| 291 | 47.5 | 23.6 | 1798 | 2 | US-09-949-016-11625 | Sequence 11625, A | 364 | 46.5 | 23.1 | 419 | 2 | US-09-042-105-2 | Sequence 2, Appl1 |
| 292 | 47.5 | 23.6 | 3597 | 2 | US-10-037-417-6 | Sequence 6, Appl1 | 365 | 46.5 | 23.1 | 419 | 2 | US-08-795-430-8 | Sequence 8, Appl1 |
| 293 | 47.5 | 23.6 | 3600 | 2 | US-10-104-047-3105 | Sequence 3105, Ap | 366 | 46.5 | 23.1 | 419 | 2 | US-09-355-700-8 | Sequence 8, Appl1 |
| 294 | 47.5 | 23.6 | 137 | 2 | US-09-330-230A-676 | Sequence 676, App | 367 | 46.5 | 23.1 | 419 | 2 | US-09-375-248-4 | Sequence 4, Appl1 |
| 295 | 47.5 | 23.6 | 137 | 2 | US-09-328-352-5960 | Sequence 5960, Ap | 368 | 46.5 | 23.1 | 419 | 2 | US-09-465-966-2 | Sequence 2, Appl1 |
| 296 | 47 | 23.4 | 137 | 2 | US-09-830-230A-675 | Sequence 675, App | 369 | 46.5 | 23.1 | 419 | 2 | US-09-631-092B-13 | Sequence 13, Appl1 |
| 297 | 47 | 23.4 | 137 | 2 | US-09-830-230A-675 | Sequence 675, App | 370 | 46.5 | 23.1 | 419 | 2 | US-09-631-092B-13 | Sequence 13, Appl1 |
| 298 | 47 | 23.4 | 137 | 2 | US-09-830-230A-675 | Sequence 675, App | 371 | 46.5 | 23.1 | 419 | 2 | US-09-631-092B-13 | Sequence 13, Appl1 |
| 299 | 47 | 23.4 | 137 | 2 | US-09-830-230A-675 | Sequence 675, App | 372 | 46.5 | 23.1 | 419 | 2 | US-09-631-092B-13 | Sequence 13, Appl1 |
| 300 | 47 | 23.4 | 137 | 2 | US-09-830-230A-675 | Sequence 675, App | 373 | 46.5 | 23.1 | 419 | 2 | US-09-631-092B-13 | Sequence 13, Appl1 |
| 301 | 47 | 23.4 | 137 | 2 | US-09-830-230A-675 | Sequence 675, App | 374 | 46.5 | 23.1 | 419 | 2 | US-09-631-092B-13 | Sequence 13, Appl1 |
| 302 | 47 | 23.4 | 137 | 2 | US-09-830-230A-675 | Sequence 675, App | 375 | 46.5 | 23.1 | 419 | 2 | US-09-631-092B-13 | Sequence 13, Appl1 |
| 303 | 47 | 23.4 | 137 | 2 | US-09-830-230A-675 | Sequence 675, App | 376 | 46.5 | 23.1 | 419 | 2 | US-09-631-092B-13 | Sequence 13, Appl1 |
| 304 | 47 | 23.4 | 137 | 2 | US-09-830-230A-675 | Sequence 675, App | 377 | 46.5 | 23.1 | 419 | 2 | US-09-631-092B-13 | Sequence 13, Appl1 |
| 305 | 47 | 23.4 | 137 | 2 | US-09-830-230A-675 | Sequence 675, App | 378 | 46.5 | 23.1 | 419 | 2 | US-09-631-092B-13 | Sequence 13, Appl1 |
| 306 | 47 | 23.4 | 137 | 2 | US-09-830-230A-675 | Sequence 675, App | 379 | 46.5 | 23.1 | 419 | 2 | US-09-631-092B-13 | Sequence 13, Appl1 |
| 307 | 47 | 23.4 | 137 | 2 | US-09-830-230A-675 | Sequence 675, App | 380 | 46.5 | 23.1 | 419 | 2 | US-09-631-092B-13 | Sequence 13, Appl1 |
| 308 | 47 | 23.4 | 137 | 2 | US-09-830-230A-675 | Sequence 675, App | 381 | 46.5 | 23.1 | 419 | 2 | US-09-631-092B-13 | Sequence 13, Appl1 |
| 309 | 47 | 23.4 | 137 | 2 | US-09-830-230A-675 | Sequence 675, App | 382 | 46.5 | 23.1 | 419 | 2 | US-09-631-092B-13 | Sequence 13, Appl1 |
| 310 | 47 | 23.4 | 137 | 2 | US-09-830-230A-675 | Sequence 675, App | 383 | 46.5 | 23.1 | 419 | 2 | US-09-631-092B-13 | Sequence 13, Appl1 |
| 311 | 47 | 23.4 | 137 | 2 | US-09-830-230A-675 | Sequence 675, App | 384 | 46.5 | 23.1 | 419 | 2 | US-09-631-092B-13 | Sequence 13, Appl1 |
| 312 | 47 | 23.4 | 137 | 2 | US-09-830-230A-675 | Sequence 675, App | 385 | 46.5 | 23.1 | 419 | 2 | US-09-631-092B-13 | Sequence 13, Appl1 |
| 313 | 47 | 23.4 | 137 | 2 | US-09-830-230A-675 | Sequence 675, App | 386 | 46.5 | 23.1 | 419 | 2 | US-09-631-092B-13 | Sequence 13, Appl1 |
| 314 | 47 | 23.4 | 137 | 2 | US-09-830-230A-675 | Sequence 675, App | 387 | 46.5 | 23.1 | 419 | 2 | US-09-631-092B-13 | Sequence 13, Appl1 |
| 315 | 47 | 23.4 | 137 | 2 | US-09-830-230A-675 | Sequence 675, App | 388 | 46.5 | 23.1 | 419 | 2 | US-09-631-092B-13 | Sequence 13, Appl1 |
| 316 | 46.5 | 23.1 | 75 | 1 | US-08-465-380-57 | Sequence 57, Appl1 | 389 | 46.5 | 23.1 | 419 | 2 | US-08-743-868-2 | Sequence 2, Appl1 |
| 317 | 46.5 | 23.1 | 75 | 1 | US-08-486-397-57 | Sequence 57, Appl1 | 390 | 46.5 | 23.1 | 419 | 2 | US-09-499-468-2 | Sequence 2, Appl1 |
| 318 | 46.5 | 23.1 | 75 | 1 | US-08-486-399-57 | Sequence 57, Appl1 | 391 | 46.5 | 23.1 | 419 | 2 | US-09-219-442-2 | Sequence 2, Appl1 |

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| 392 | 46.5 | 23.1 | 419 | 3 | US-09-765-534B-21 | Sequence 21, Appl | 465 | 46 | 1257 | 2 | US-09-195-524-8 | Sequence 8, Appl | |
| 393 | 46.5 | 23.1 | 419 | 5 | PCT-US96-09001-2 | Sequence 2, Appl | 466 | 46 | 1257 | 2 | US-09-310-685-6 | Sequence 6, Appl | |
| 394 | 46.5 | 23.1 | 450 | 2 | US-08-635-886C-201 | Sequence 201, App | 467 | 46 | 1257 | 2 | US-08-477-451-12 | Sequence 12, Appl | |
| 395 | 46.5 | 23.1 | 450 | 2 | US-08-974-690C-201 | Sequence 201, Appl | 468 | 46 | 1257 | 1 | US-08-262-037-118 | Sequence 118, Appl | |
| 396 | 46.5 | 23.1 | 574 | 2 | US-09-352-990-14 | Sequence 14, Appl | 469 | 45.5 | 109 | 55 | 1 | US-09-585-173B-14 | Sequence 14, Appl |
| 397 | 46.5 | 23.1 | 704 | 2 | US-09-590-656-2 | Sequence 2, Appl | 470 | 45.5 | 22.6 | 232 | 2 | US-09-252-991A-27052 | Sequence 27052, A |
| 398 | 46.5 | 23.1 | 704 | 2 | US-09-733-764-2 | Sequence 2, Appl | 471 | 45.5 | 22.6 | 232 | 2 | US-09-248-796A-18748 | Sequence 18748, A |
| 399 | 46.5 | 23.1 | 883 | 2 | US-09-964-956-37 | Sequence 37, Appl | 472 | 45.5 | 22.6 | 272 | 2 | US-09-744-639-167 | Sequence 167, App |
| 400 | 46.5 | 23.1 | 940 | 2 | US-09-964-956-39 | Sequence 39, Appl | 473 | 45.5 | 22.6 | 702 | 2 | US-09-949-016-7288 | Sequence 7288, App |
| 401 | 46.5 | 23.1 | 977 | 2 | US-09-590-656-1 | Sequence 1, Appl | 474 | 45.5 | 1157 | 2 | US-09-538-092-1328 | Sequence 1328, App | |
| 402 | 46.5 | 23.1 | 977 | 2 | US-09-733-764-1 | Sequence 1, Appl | 475 | 45 | 56 | 2 | US-08-469-260A-419 | Sequence 419, App | |
| 403 | 46.5 | 23.1 | 999 | 2 | US-09-747-371-2 | Sequence 2, Appl | 476 | 45 | 56 | 2 | US-08-468-446-419 | Sequence 419, App | |
| 404 | 46.5 | 23.1 | 1124 | 1 | US-08-323-474-2 | Sequence 2, Appl | 477 | 45 | 56 | 2 | US-08-467-344A-419 | Sequence 419, App | |
| 405 | 46.5 | 23.1 | 1124 | 2 | US-09-949-016-5946 | Sequence 5946, Ap | 478 | 45 | 69 | 2 | US-08-424-550B-419 | Sequence 419, App | |
| 406 | 46.5 | 23.1 | 1124 | 5 | PCT-US93-06093-2 | Sequence 2, Appl | 479 | 45 | 22.4 | 91 | 2 | US-09-950-933A-87 | Sequence 87, Appl |
| 407 | 46.5 | 23.1 | 1157 | 2 | US-09-949-016-9568 | Sequence 9568, Ap | 480 | 45 | 22.4 | 91 | 2 | US-09-270-767-40990 | Sequence 40990, A |
| 408 | 46.5 | 23.1 | 1286 | 2 | US-09-964-956-38 | Sequence 38, Appl | 481 | 45 | 22.4 | 109 | 2 | US-09-270-767-56206 | Sequence 56206, A |
| 409 | 46.5 | 23.1 | 1286 | 2 | US-10-017-216-7 | Sequence 7, Appl | 482 | 45 | 22.4 | 109 | 2 | US-09-270-767-39585 | Sequence 39585, A |
| 410 | 46.5 | 23.1 | 1597 | 2 | US-09-964-956-41 | Sequence 41, Appl | 483 | 45 | 22.4 | 129 | 2 | US-09-270-767-54802 | Sequence 54802, A |
| 411 | 46.5 | 23.1 | 1597 | 2 | US-10-017-216-6 | Sequence 6, Appl | 484 | 45 | 22.4 | 139 | 2 | US-09-422-869-14 | Sequence 14, Appl |
| 412 | 46.5 | 23.1 | 1641 | 2 | US-09-964-956-40 | Sequence 40, Appl | 485 | 45 | 22.4 | 142 | 2 | US-09-252-991A-22334 | Sequence 22334, A |
| 413 | 46.5 | 23.1 | 1641 | 2 | US-10-017-216-5 | Sequence 5, Appl | 486 | 45 | 22.4 | 145 | 2 | US-09-513-007-4 | Sequence 4, Appl |
| 414 | 46.5 | 23.1 | 1958 | 2 | US-10-028-946-4 | Sequence 4, Appl | 487 | 45 | 22.4 | 181 | 2 | US-09-970-532-4 | Sequence 4, Appl |
| 415 | 46.5 | 23.1 | 2053 | 2 | US-09-964-956-11 | Sequence 11, Appl | 488 | 45 | 22.4 | 181 | 2 | US-09-970-532-4 | Sequence 4, Appl |
| 416 | 46.5 | 23.1 | 2053 | 2 | US-10-017-216-2 | Sequence 2, Appl | 489 | 45 | 22.4 | 181 | 2 | US-09-970-532-4 | Sequence 4, Appl |
| 417 | 46.5 | 23.1 | 2054 | 2 | US-10-028-946-2 | Sequence 2, Appl | 490 | 45 | 22.4 | 188 | 2 | US-09-252-991A-19720 | Sequence 19720, A |
| 418 | 46.5 | 23.1 | 2056 | 2 | US-10-017-216-4 | Sequence 4, Appl | 491 | 45 | 22.4 | 194 | 2 | US-09-252-991A-24154 | Sequence 24154, A |
| 419 | 46.5 | 23.1 | 2056 | 2 | US-09-964-956-9 | Sequence 9, Appl | 492 | 45 | 22.4 | 196 | 2 | US-09-949-016-8932 | Sequence 8932, Ap |
| 420 | 46.5 | 23.1 | 2594 | 2 | US-08-718-388-7 | Sequence 7, Appl | 493 | 45 | 22.4 | 196 | 2 | US-09-949-016-8933 | Sequence 8933, Ap |
| 421 | 46.5 | 23.1 | 3033 | 1 | US-07-925-695-8 | Sequence 8, Appl | 494 | 45 | 22.4 | 196 | 2 | US-09-949-016-8935 | Sequence 8935, Ap |
| 422 | 46.5 | 23.1 | 67 | 2 | US-09-910-009A-291 | Sequence 291, App | 495 | 45 | 22.4 | 196 | 2 | US-09-949-016-8936 | Sequence 8936, Ap |
| 423 | 46.5 | 23.1 | 94 | 2 | US-09-950-933A-44 | Sequence 44, Appl | 496 | 45 | 22.4 | 196 | 2 | US-09-949-016-8937 | Sequence 8937, Ap |
| 424 | 46.5 | 23.1 | 94 | 2 | US-09-950-933A-82 | Sequence 82, Appl | 497 | 45 | 22.4 | 196 | 2 | US-09-949-016-8938 | Sequence 8938, Ap |
| 425 | 46.5 | 23.1 | 158 | 2 | US-09-902-540-16690 | Sequence 16690, A | 498 | 45 | 22.4 | 250 | 3 | US-09-936-271C-23 | Sequence 22, Appl |
| 426 | 46.5 | 23.1 | 192 | 1 | US-08-086-428B-71 | Sequence 71, Appl | 499 | 45 | 22.4 | 295 | 3 | US-09-936-271C-22 | Sequence 22, Appl |
| 427 | 46.5 | 23.1 | 192 | 1 | US-08-468-570-71 | Sequence 71, Appl | 500 | 45 | 22.4 | 298 | 2 | US-08-889-108-4 | Sequence 4, Appl |
| 428 | 46.5 | 23.1 | 192 | 1 | US-08-290-665A-71 | Sequence 71, Appl | 501 | 45 | 22.4 | 298 | 2 | US-08-120-601B-4 | Sequence 4, Appl |
| 429 | 46.5 | 23.1 | 192 | 2 | US-08-466-601A-71 | Sequence 71, Appl | 502 | 45 | 22.4 | 298 | 5 | PCT-US94-10358-4 | Sequence 4, Appl |
| 430 | 46.5 | 23.1 | 192 | 5 | PCT-US95-10398-71 | Sequence 71, Appl | 503 | 45 | 22.4 | 392 | 2 | US-09-270-767-11714 | Sequence 11714, A |
| 431 | 46.5 | 23.1 | 193 | 2 | US-08-836-075A-16 | Sequence 16, Appl | 504 | 45 | 22.4 | 468 | 2 | US-09-147-955-12 | Sequence 12, Appl |
| 432 | 46.5 | 23.1 | 193 | 2 | US-09-851-138C-16 | Sequence 16, Appl | 505 | 45 | 22.4 | 471 | 2 | US-09-513-007-2 | Sequence 2, Appl |
| 433 | 46.5 | 23.1 | 214 | 2 | US-09-214-278-1 | Sequence 1, Appl | 506 | 45 | 22.4 | 471 | 2 | US-09-513-007-2 | Sequence 2, Appl |
| 434 | 46.5 | 23.1 | 214 | 2 | US-09-855-722-1 | Sequence 1, Appl | 507 | 45 | 22.4 | 474 | 2 | US-09-434-708-2 | Sequence 2, Appl |
| 435 | 46.5 | 23.1 | 254 | 2 | US-09-252-991A-19771 | Sequence 19771, A | 508 | 45 | 22.4 | 534 | 4 | US-09-252-991A-28232 | Sequence 28232, A |
| 436 | 46.5 | 23.1 | 277 | 2 | US-08-635-886C-205 | Sequence 205, App | 509 | 45 | 22.4 | 597 | 2 | US-09-949-016-7931 | Sequence 7931, Ap |
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| 444 | 46.5 | 23.1 | 355 | 2 | US-09-573-986-14 | Sequence 14, Appl | 517 | 45 | 22.4 | 2548 | 4 | US-09-172-422-1 | Sequence 1, Appl |
| 445 | 46.5 | 23.1 | 359 | 2 | US-09-699-266A-11 | Sequence 11, Appl | 518 | 45 | 22.4 | 4544 | 1 | US-08-469-486-52 | Sequence 52, Appl |
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| 453 | 46.5 | 23.1 | 1055 | 2 | US-09-214-278-2 | Sequence 4, Appl | 526 | 44.5 | 22.1 | 75 | 1 | US-08-480-478-35 | Sequence 35, Appl |
| 454 | 46.5 | 23.1 | 1055 | 2 | US-09-855-722-2 | Sequence 2, Appl | 527 | 44.5 | 22.1 | 75 | 1 | US-08-486-337-6 | Sequence 6, Appl |
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| 460 | 46.5 | 23.1 | 1238 | 2 | US-09-214-278-5 | Sequence 5, Appl | 533 | 44.5 | 22.1 | 75 | 1 | US-08-326-110A-35 | Sequence 35, Appl |
| 461 | 46.5 | 23.1 | 1338 | 2 | US-09-855-722-5 | Sequence 5, Appl | 534 | 44.5 | 22.1 | 75 | 1 | US-08-634-641-6 | Sequence 6, Appl |
| 462 | 46.5 | 23.1 | 1348 | 2 | US-08-882-046-6 | Sequence 6, Appl | 535 | 44.5 | 22.1 | 75 | 1 | US-08-634-641-6 | Sequence 6, Appl |
| 463 | 46.5 | 23.1 | 1248 | 2 | US-09-566-047-6 | Sequence 6, Appl | 536 | 44.5 | 22.1 | 75 | 2 | US-09-249-471-6 | Sequence 6, Appl |
| 464 | 46.5 | 23.1 | 1257 | 2 | US-08-611-729A-8 | Sequence 8, Appl | 537 | 44.5 | 22.1 | 75 | 2 | US-09-249-471-6 | Sequence 6, Appl |

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| 540 | 44.5 | 22.1 | 75 | 2 | US-09-249-451-6 | Sequence 6, Appl | 613 | 44.5 | 22.1 | 1063 | 2 | US-09-695-481-6 | Sequence 8, Appl |
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| 543 | 44.5 | 22.1 | 75 | 2 | US-08-809-455-41 | Sequence 41, Appl | 616 | 44.5 | 22.1 | 1180 | 2 | US-08-367-264-8 | Sequence 2, Appl |
| 544 | 44.5 | 22.1 | 75 | 2 | US-09-249-461-6 | Sequence 6, Appl | 617 | 44.5 | 22.1 | 1180 | 2 | US-08-660-148-2 | Sequence 8, Appl |
| 545 | 44.5 | 22.1 | 75 | 2 | US-09-249-461-41 | Sequence 41, Appl | 618 | 44.5 | 22.1 | 1180 | 2 | US-09-153-757-8 | Sequence 8, Appl |
| 546 | 44.5 | 22.1 | 75 | 2 | US-09-249-448-6 | Sequence 6, Appl | 619 | 44.5 | 22.1 | 1180 | 2 | US-09-459-715-8 | Sequence 8, Appl |
| 547 | 44.5 | 22.1 | 75 | 2 | US-09-249-448-11 | Sequence 41, Appl | 620 | 44.5 | 22.1 | 1212 | 1 | US-08-072-574-10 | Sequence 10, Appl |
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| 549 | 44.5 | 22.1 | 75 | 2 | US-09-249-473-41 | Sequence 41, Appl | 622 | 44.5 | 22.1 | 1212 | 2 | US-08-367-264-10 | Sequence 10, Appl |
| 550 | 44.5 | 22.1 | 75 | 2 | US-09-498-556-6 | Sequence 6, Appl | 623 | 44.5 | 22.1 | 1212 | 2 | US-08-660-148-5 | Sequence 10, Appl |
| 551 | 44.5 | 22.1 | 75 | 2 | US-09-498-556-6 | Sequence 41, Appl | 624 | 44.5 | 22.1 | 1212 | 2 | US-09-153-757-10 | Sequence 10, Appl |
| 552 | 44.5 | 22.1 | 79 | 1 | US-08-465-380-8 | Sequence 8, Appl | 625 | 44.5 | 22.1 | 1212 | 2 | US-09-459-715-10 | Sequence 10, Appl |
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| 559 | 44.5 | 22.1 | 79 | 2 | US-09-249-471-8 | Sequence 8, Appl | 632 | 44 | 21.9 | 51 | 1 | US-08-345-175-5 | Sequence 5, Appl |
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| 562 | 44.5 | 22.1 | 79 | 2 | US-08-809-451-8 | Sequence 8, Appl | 635 | 44 | 21.9 | 51 | 2 | US-09-827-948-6 | Sequence 6, Appl |
| 563 | 44.5 | 22.1 | 79 | 2 | US-09-249-461-8 | Sequence 8, Appl | 636 | 44 | 21.9 | 51 | 2 | US-09-741-106-5 | Sequence 6, Appl |
| 564 | 44.5 | 22.1 | 79 | 2 | US-09-249-448-8 | Sequence 8, Appl | 637 | 44 | 21.9 | 51 | 2 | US-10-176-071-6 | Sequence 6, Appl |
| 565 | 44.5 | 22.1 | 79 | 2 | US-09-249-473-8 | Sequence 8, Appl | 638 | 44 | 21.9 | 51 | 2 | PCT-US95-09464-5 | Sequence 5, Appl |
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| 570 | 44.5 | 22.1 | 98 | 1 | US-08-480-397-21 | Sequence 21, Appl | 643 | 44 | 21.9 | 58 | 1 | US-08-463-432B-37 | Sequence 37, Appl |
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| 572 | 44.5 | 22.1 | 98 | 1 | US-08-461-965-21 | Sequence 21, Appl | 645 | 44 | 21.9 | 58 | 1 | US-08-206-310A-37 | Sequence 37, Appl |
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| 575 | 44.5 | 22.1 | 98 | 2 | US-09-249-471-21 | Sequence 21, Appl | 648 | 44 | 21.9 | 58 | 1 | US-08-399-115A-37 | Sequence 37, Appl |
| 576 | 44.5 | 22.1 | 98 | 2 | US-09-249-472-21 | Sequence 21, Appl | 649 | 44 | 21.9 | 58 | 1 | US-09-136-012A-35 | Sequence 35, Appl |
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| 578 | 44.5 | 22.1 | 98 | 2 | US-09-249-461-21 | Sequence 21, Appl | 651 | 44 | 21.9 | 58 | 2 | US-09-414-878-66 | Sequence 66, Appl |
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| 587 | 44.5 | 22.1 | 180 | 2 | US-09-878-281A-28 | Sequence 28, Appl | 660 | 44 | 21.9 | 63 | 2 | US-09-950-933A-74 | Sequence 74, Appl |
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| 607 | 44.5 | 22.1 | 877 | 1 | US-09-153-757-12 | Sequence 12, Appl | 680 | 44 | 21.9 | 192 | 5 | PCT-US95-10398-72 | Sequence 72, Appl |
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|-----|----|------|-----|---|----------------------|--------------------|-----|----|------|------|---|----------------------|-------------------|
| 684 | 44 | 21.9 | 213 | 7 | 5466783-25 | Patent No. 5466783 | 757 | 44 | 21.9 | 575 | 2 | US-09-949-016-11266 | Sequence 11266, A |
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| 691 | 44 | 21.9 | 276 | 1 | US-08-286-521-9 | Sequence 9, Appl | 764 | 44 | 21.9 | 645 | 2 | US-09-602-812A-13 | Sequence 11, Appl |
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| 704 | 44 | 21.9 | 291 | 2 | US-10-000-489-52 | Sequence 52, Appl | 777 | 44 | 21.9 | 782 | 2 | US-09-644-600-10 | Sequence 10, Appl |
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| 722 | 44 | 21.9 | 304 | 2 | US-09-054-272-16 | Sequence 16, Appl | 795 | 44 | 21.9 | 1255 | 2 | US-09-806-703A-7517 | Sequence 7517, Ap |
| 723 | 44 | 21.9 | 304 | 2 | US-10-377-817-2 | Sequence 2, Appl | 796 | 44 | 21.9 | 1255 | 2 | US-09-949-016-7517 | Sequence 8955, Ap |
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ALIGNMENTS

RESULT 1
US-09-854-864-7

Sequence 7, Application US/09854864

Patent No. 6774106

GENERAL INFORMATION:

APPLICANT: THEILL, LARS EYDE

FILE REFERENCE: A-686B

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

TITLE OF INVENTION: BLYS/AGP-3, AND TACI

FILE REFERENCE: A-686B

CURRENT APPLICATION NUMBER: US/09/854,864

PRIOR FILING DATE: 2001-09-11

PRIOR APPLICATION NUMBER: US 60/204,039

PRIOR FILING DATE: 2000-05-12

PRIOR APPLICATION NUMBER: US 60/214,591

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn version 3.1

SEQ ID NO 7

LENGTH: 34

TYPE: PRT

ORGANISM: Homo sapiens

US-09-854-864-7

Query Match 100.0%; Score 201, DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.3e-17;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSONEYFDSLHACIPCOLRCSSNTPLTCORYC 34
Db 1 CSONEYFDSLHACIPCOLRCSSNTPLTCORYC 34

RESULT 2

US-09-854-864-6

Sequence 6, Application US/09854864

Patent No. 6774106

GENERAL INFORMATION:

APPLICANT: THEILL, LARS EYDE

FILE REFERENCE: A-686B

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

TITLE OF INVENTION: BLYS/AGP-3, AND TACI

FILE REFERENCE: A-686B

CURRENT APPLICATION NUMBER: US/09/854,864

PRIOR FILING DATE: 2001-09-11

PRIOR APPLICATION NUMBER: US 60/204,039

PRIOR FILING DATE: 2000-05-12

PRIOR APPLICATION NUMBER: US 60/214,591

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn version 3.1

SEQ ID NO 6

LENGTH: 51

TYPE: PRT

ORGANISM: Homo sapiens

US-09-854-864-6

Query Match 100.0%; Score 201, DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 4.9e-17;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSONEYFDSLHACIPCOLRCSSNTPLTCORYC 34
Db 5 CSONEYFDSLHACIPCOLRCSSNTPLTCORYC 38

RESULT 3
US-09-854-864-21

Sequence 21, Application US/09854864

Patent No. 6774106

GENERAL INFORMATION:

APPLICANT: THEILL, LARS EYDE

FILE REFERENCE: A-686B

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

TITLE OF INVENTION: BLYS/AGP-3, AND TACI

FILE REFERENCE: A-686B

CURRENT APPLICATION NUMBER: US/09/854,864

PRIOR FILING DATE: 2001-09-11

PRIOR APPLICATION NUMBER: US 60/204,039

PRIOR FILING DATE: 2000-05-12

PRIOR APPLICATION NUMBER: US 60/214,591

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn version 3.1

SEQ ID NO 21

LENGTH: 58

TYPE: PRT

ORGANISM: Homo sapiens

US-09-854-864-21

Query Match 100.0%; Score 201, DB 2; Length 58;
Best Local Similarity 100.0%; Pred. No. 5.5e-17;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSONEYFDSLHACIPCOLRCSSNTPLTCORYC 34
Db 1 CSONEYFDSLHACIPCOLRCSSNTPLTCORYC 34

RESULT 4
US-09-854-864-13

Sequence 13, Application US/09854864

Patent No. 6774106

GENERAL INFORMATION:

APPLICANT: THEILL, LARS EYDE

FILE REFERENCE: A-686B

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

TITLE OF INVENTION: BLYS/AGP-3, AND TACI

FILE REFERENCE: A-686B

CURRENT APPLICATION NUMBER: US/09/854,864

PRIOR FILING DATE: 2001-09-11

PRIOR APPLICATION NUMBER: US 60/204,039

PRIOR FILING DATE: 2000-05-12

PRIOR APPLICATION NUMBER: US 60/214,591

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31

SOFTWARE: Patentin version 3.1
SEQ ID NO 13
LENGTH: 81
TYPE: PRT
ORGANISM: Consensus
US-09-854-864-13

Query Match 100.0%; Score 201; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 7.6e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEFYDSLHACIPCOLRCSSNTPPLTCORYC 34
DB 1 CSQNEFYDSLHACIPCOLRCSSNTPPLTCORYC 34

RESULT 5
US-09-854-864-5
Sequence 5, Application US/09854864
Patent No. 6774106
GENERAL INFORMATION:
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
PRIOR FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 181
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-864-5

Query Match 100.0%; Score 201; DB 2; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEFYDSLHACIPCOLRCSSNTPPLTCORYC 34
DB 5 CSQNEFYDSLHACIPCOLRCSSNTPPLTCORYC 38

RESULT 6
US-09-565-423-11
Sequence 11, Application US/09565423
Patent No. 6475987
GENERAL INFORMATION:
APPLICANT: Shu, Hong-Bing
TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
FILE REFERENCE: 2879-72
CURRENT APPLICATION NUMBER: US/09/565,423
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: UNKNOWN
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/132,892
PRIOR FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 184
TYPE: PRT
ORGANISM: Homo sapiens
US-09-565-423-11

Query Match 100.0%; Score 201; DB 2; Length 184;

Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEFYDSLHACIPCOLRCSSNTPPLTCORYC 34
DB 8 CSQNEFYDSLHACIPCOLRCSSNTPPLTCORYC 41

RESULT 7
US-09-949-016-11115
Sequence 11115, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11115
LENGTH: 192
TYPE: PRT
ORGANISM: Human
US-09-949-016-11115

Query Match 100.0%; Score 201; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.8e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEFYDSLHACIPCOLRCSSNTPPLTCORYC 34
DB 16 CSQNEFYDSLHACIPCOLRCSSNTPPLTCORYC 49

RESULT 8
US-09-854-864-9
Sequence 9, Application US/09854864
Patent No. 6774106
GENERAL INFORMATION:
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
PRIOR FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-864-9

Query Match 100.0%; Score 201; DB 2; Length 283;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEFYDSLHACIPCOLRCSSNTPPLTCORYC 34
DB 5 CSQNEFYDSLHACIPCOLRCSSNTPPLTCORYC 38

```
RESULT 9
US-09-565-423-17
; Sequence 17, Application US/09565423
; Patent No. 6475987
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-565-423-17

Query Match      67.7%; Score 136; DB 2; Length 185;
Best Local Similarity 70.6%; Pred. No. 8,4e-09;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY      1 CSONEYFDSLHACIPCOLRGSSNTPPLTCORYC 34
      :|||||:|||||:|||||:|||||:|||||:
Db      5 CFHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36

RESULT 10
US-09-854-864-11
; Sequence 11, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Murine
US-09-854-864-11

Query Match      67.7%; Score 136; DB 2; Length 185;
Best Local Similarity 70.6%; Pred. No. 8,4e-09;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY      1 CSONEYFDSLHACIPCOLRGSSNTPPLTCORYC 34
      :|||||:|||||:|||||:|||||:|||||:
Db      5 CFHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36

RESULT 11
US-09-854-864-10
; Sequence 10, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
```

```
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-854-864-10

Query Match      67.7%; Score 136; DB 2; Length 281;
Best Local Similarity 70.6%; Pred. No. 1,3e-08;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY      1 CSONEYFDSLHACIPCOLRGSSNTPPLTCORYC 34
      :|||||:|||||:|||||:|||||:|||||:
Db      5 CFHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36

RESULT 12
US-09-854-864-12
; Sequence 12, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: human-murine Consensus
US-09-854-864-12

Query Match      46.5%; Score 93.5; DB 2; Length 117;
Best Local Similarity 69.7%; Pred. No. 0.00057;
Matches 23; Conservative 1; Mismatches 2; Indels 7; Gaps 4;

QY      2 SONEYFDSLHACIPCOLRGSSNTPPLTCORYC 34
      :|||||:|||||:|||||:|||||:|||||:
Db      2 AQCEYFDSLHAC-PC-LRCS----PPTCQ-YC 27

RESULT 13
US-09-854-864-20
; Sequence 20, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
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PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
SEQ ID NO 20
LENGTH: 59
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-864-20

Query Match 33.1%; Score 66.5; DB 2; Length 59;
Best Local Similarity 32.4%; Pred. No. 0.46;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSONEYFDSLHACIPCOLRGSSNTPPLTCORXC 34
DB 1 CPEEQYWDPLGTGCMCKTICNHQS-QRTCAAF 33

RESULT 14

US-09-854-864-16
Sequence 16, Application US/09854864
Patent No. 6774106
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
FILE REFERENCE: BLYS/AGP-3, AND TACT
CURRENT APPLICATION NUMBER: US/09/854,864
PRIOR FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
SEQ ID NO 16
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-864-16

Query Match 33.1%; Score 66.5; DB 2; Length 67;
Best Local Similarity 32.4%; Pred. No. 0.52; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSONEYFDSLHACIPCOLRGSSNTPPLTCORXC 34
DB 1 CPEEQYWDPLGTGCMCKTICNHQS-QRTCAAF 33

RESULT 15

US-08-810-572A-6
Sequence 6, Application US/08810572A
Patent No. 5969102
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
APPLICANT: von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,572A
FILING DATE: 28-FEB-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-810-572A-6

Query Match 33.1%; Score 66.5; DB 1; Length 166;
Best Local Similarity 32.4%; Pred. No. 1.3;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSONEYFDSLHACIPCOLRGSSNTPPLTCORXC 34
DB 34 CPEEQYWDPLGTGCMCKTICNHQS-QRTCAAF 66

RESULT 16

US-09-290-333-6
Sequence 6, Application US/09290333
Patent No. 6316222
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
APPLICANT: von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/290,333
FILING DATE: 12-APR-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 6:


```

? REGISTRATION NUMBER: 26,742
? REFERENCE/DOCKET NUMBER: 1340-I-007
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 201-487-5800
? TELEFAX: 201-343-1684
? INFORMATION FOR SEO ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 293 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? HYPOTHETICAL: NO
? FRAGMENT TYPE: N-terminal
? ORIGINAL SOURCE:
? ORGANISM: Homo sapiens
? OS-08-810-572A-2

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| | | | | | | | |
|-----------------------|-------|--------------|------|------------|----|--------|-----|
| Query Match | 33.1% | Score | 66.5 | DB | 1 | length | 293 |
| Best Local Similarity | 32.4% | Pred. No. | 2.2 | | | | |
| Matches | 11 | Conservative | 8 | Mismatches | 14 | Indels | 1 |
| | | | | | | Gaps | 1 |

QY 1 CSQNEYFDLSLHACIPQCLRCSSNTPPLTQRCYC 34
Db 34 CPREQYMDPLLTGTCMSCKTICNHQS-QRTCAFAFC 66

RESULT 20
US-09-290-333-2

APPLICANT: Bram, Richard J.

TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF

NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th fl.
:

```

;
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA

```

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;      COMPUTER READABLE FORM:
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;      MEDIUM TYPE: Floppy disk
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;      COMPUTER: IBM PC compatible
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/290,333

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SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-290-333-2

| | | | | | | | |
|-----------------------|-------|--------------|-------|------------|----|--------|-----|
| Query Match | 33.1% | Score | 66.5 | DB | 2 | Length | 293 |
| Best Local Similarity | 32.4% | Pred. | No. 2 | 2 | | | |
| Matches | 11 | Conservative | 8 | Mismatches | 14 | Indels | 1 |
| | | | | | | Gaps | 1 |

QY 1 CSQNEYFDLSLHACIPQQLRCSNTPLPLCQRYC 34
 Db 34 CPKEQYMDPLLTGTCMSCKTICNHQS-QRTCAFC 66

RESULT 21
US-09-782-857A-2
; Sequence 2, Application US/09782857A

APPLICANT: Bram, Richard J.

TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF

NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hockensack Ave, Continental Plaza, 4th
FLOOR

```
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA
```

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;
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: floppy disk
;      COMPUTER: IBM PC compatible
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/782,857A
;

```

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; ; CLASSIFICATION: <Unknown>
; ; PRIOR APPLICATION DATA:
; ; APPLICATION NUMBER: 08/810,572
; ;

```

ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742

TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684

SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acid


```
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kitchell, Barbara S.
/ REGISTRATION NUMBER: 33,928
/ REFERENCE/DOCKET NUMBER: UTSD:418\KIT
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 713-787-1400
/ TELEFAX: 713-789-2679
/ TELEX: 79-0924
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2476 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-276-967-2

Query Match 27.9%; Score 56; DB 1; Length 2476;
Best Local Similarity 31.6%; Pred. No. 3e+02;
Matches 12; Conservative 8; Mismatches 14; Indels 4; Gaps 2;

Oy 1 CSONEYFDSLHACIP-CO---LRSSNTPLTCQRYC 34
Db 1851 CSAHSVYTSVPSCLPSCDPEGCTGAGAPSTCEGC 1888

RESULT 31
US-10-094-749-2652
/ Sequence 2652, Application US/10094749
/ Patent No. 6979557
/ GENERAL INFORMATION:
/ APPLICANT: ISOGAI, TAKAO
/ APPLICANT: SUGIYAMA, TOMOYASU
/ APPLICANT: OTSUKI, TETSUJI
/ APPLICANT: MAKAMATSU, AI
/ APPLICANT: SATO, HIROYUKI
/ APPLICANT: ISHII, SHIZUKO
/ APPLICANT: YAMAMOTO, JUN-ICHI
/ APPLICANT: ISONO, YUUKO
/ APPLICANT: HIO, YURI
/ APPLICANT: OTSUKA, KAORU
/ APPLICANT: NAGAI, KEIICHI
/ APPLICANT: IRIE, RYOTARO
/ APPLICANT: TAMECHIKA, ICHIRO
/ APPLICANT: SEKI, NAOHICO
/ APPLICANT: YOSHIKAWA, TSUTOMU
/ APPLICANT: OTSUKA, MOTOMYUKI
/ APPLICANT: NAGAHARI, KENJI
/ APPLICANT: MASUHO, YASUHIKO
/ TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
/ FILE REFERENCE: 084335/0160
/ CURRENT APPLICATION NUMBER: US/10/094,749
/ CURRENT FILING DATE: 2002-03-12
/ PRIOR APPLICATION NUMBER: 60/350,435
/ PRIOR FILING DATE: 2002-01-24
/ PRIOR APPLICATION NUMBER: JP 2001-328381
/ PRIOR FILING DATE: 2001-09-14
/ NUMBER OF SEQ ID NOS: 3381
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2652
/ LENGTH: 955
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-094-749-2652

Query Match 27.6%; Score 55.5; DB 2; Length 955;
Best Local Similarity 37.5%; Pred. No. 1.4e+02;
Matches 12; Conservative 4; Mismatches 11; Indels 5; Gaps 1;
```

```
RESULT 32
US-10-094-749-2573
/ Sequence 2573, Application US/10094749
/ Patent No. 6979557
/ GENERAL INFORMATION:
/ APPLICANT: ISOGAI, TAKAO
/ APPLICANT: SUGIYAMA, TOMOYASU
/ APPLICANT: OTSUKI, TETSUJI
/ APPLICANT: MAKAMATSU, AI
/ APPLICANT: SATO, HIROYUKI
/ APPLICANT: ISHII, SHIZUKO
/ APPLICANT: YAMAMOTO, JUN-ICHI
/ APPLICANT: ISONO, YUUKO
/ APPLICANT: HIO, YURI
/ APPLICANT: OTSUKA, KAORU
/ APPLICANT: NAGAI, KEIICHI
/ APPLICANT: IRIE, RYOTARO
/ APPLICANT: TAMECHIKA, ICHIRO
/ APPLICANT: SEKI, NAOHICO
/ APPLICANT: YOSHIKAWA, TSUTOMU
/ APPLICANT: OTSUKA, MOTOMYUKI
/ APPLICANT: NAGAHARI, KENJI
/ APPLICANT: MASUHO, YASUHIKO
/ TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
/ FILE REFERENCE: 084335/0160
/ CURRENT APPLICATION NUMBER: US/10/094,749
/ CURRENT FILING DATE: 2002-03-12
/ PRIOR APPLICATION NUMBER: 60/350,435
/ PRIOR FILING DATE: 2002-01-24
/ PRIOR APPLICATION NUMBER: JP 2001-328381
/ PRIOR FILING DATE: 2001-09-14
/ NUMBER OF SEQ ID NOS: 3381
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2573
/ LENGTH: 824
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-094-749-2573

Query Match 27.4%; Score 55; DB 2; Length 824;
Best Local Similarity 38.2%; Pred. No. 1.4e+02;
Matches 13; Conservative 5; Mismatches 14; Indels 2; Gaps 1;

Oy 1 CSONEYFDSLHACIPCOLRCSNTPLTCQRYC 34
Db 393 CGKSNVYSLURECV--KLKPSDPTVPLMAKVC 424

RESULT 33
US-09-621-976-6330
/ Sequence 6330, Application US/09621976
/ Patent No. 6639063
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Giordano, J.Y.
/ APPLICANT: Joberlt, S.
/ TITLE OF INVENTION: ESTs and Encoded Human Proteins.
/ FILE REFERENCE: GENSET.054PR2
/ CURRENT APPLICATION NUMBER: US/09/621,976
/ CURRENT FILING DATE: 2000-07-21
/ NUMBER OF SEQ ID NOS: 19335
/ SOFTWARE: Patent.pm
/ SEQ ID NO 6330
/ LENGTH: 98
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-621-976-6330

Query Match 26.9%; Score 54; DB 2; Length 98;
Best Local Similarity 38.1%; Pred. No. 23;
Matches 8; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
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Oy 14 CIPCOLRCSSNTPPLTCORC 34
Db 58 CIPCPSPSSSCPPOCTKPC 78

RESULT 34
US-09-471-276-1590
; Sequence 1590, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6822072
; FILE REFERENCE: GENSET 025CPI
; CURRENT APPLICATION NUMBER: US/09/471,276
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 09/057,719
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/069,047
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: PCT/IB99/00712
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 1590
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-471-276-1590

Query Match 26.9%; Score 54; DB 2; Length 98;
Best Local Similarity 38.1%; Pred. No. 23;
Matches 8; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Oy 14 CIPCOLRCSSNTPPLTCORC 34
Db 58 CIPCPSPSSSCPPOCTKPC 78

RESULT 35
US-09-252-991A-25721
; Sequence 25721, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.116
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25721
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25721

Query Match 26.9%; Score 54; DB 2; Length 431;
Best Local Similarity 50.0%; Pred. No. 96;
Matches 10; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

Oy 13 ACIPCOLRCSSNTPPLTCOR 32
Db 242 AC--CRACSNAMPPTACRR 259

RESULT 36
US-09-257-580-2
; Sequence 2, Application US/09257580
; Patent No. 6307036
; GENERAL INFORMATION:
; APPLICANT: Yorkshire Cancer Research
; TITLE OF INVENTION: Tumour Suppressor Gene
; FILE REFERENCE: Canine p53
; CURRENT APPLICATION NUMBER: US/09/257,580
; CURRENT FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: 9804178.3
; PRIOR FILING DATE: 1998-02-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Canis
US-09-257-580-2

Query Match 26.6%; Score 53.5; DB 2; Length 381;
Best Local Similarity 48.3%; Pred. No. 97;
Matches 14; Conservative 1; Mismatches 13; Indels 1; Gaps 1;

Oy 4 NEYFDLHACIPCOLRCSSNTPPLTCOR 32
Db 118 NKLFCQLAKTC-PVQLWVSPPTVCR 145

RESULT 37
US-08-718-388-9
; Sequence 9, Application US/08718388
; Patent No. 6271362
; GENERAL INFORMATION:
; APPLICANT: MORIKAWA, MINORU
; APPLICANT: HARADA, NAOKI
; TITLE OF INVENTION: GENE ENCODING IGG Fc REGION-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/718,388
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 0230-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5405 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-718-388-9

Query Match 26.6%; Score 53.5; DB 2; Length 5405;
Best Local Similarity 34.3%; Pred. No. 1.3e+03;
Matches 12; Conservative 5; Mismatches 13; Indels 5; Gaps 2;

```
Oy      1 CSQNEYPDSLHACIPCOLRCSNTPTTCORYC 34
Db      2733 CPONSHVE---LCADTCSLGCSSALSAFLQCPDGC 2763

RESULT 38
US-09-950-933A-61
; Sequence 61, Application US/09950933A
; Patent No. 6875907
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro, Pedro
; TITLE OF INVENTION: Antimicrobial Peptides and Methods of
; FILE OF INVENTION: Use
; FILE REFERENCE: 35718/238472
; CURRENT APPLICATION NUMBER: US/09/950,933A
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/232,569
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Glycine max
US-09-950-933A-61

Query Match      26.4%; Score 53; DB 2; Length 108;
Best Local Similarity 44.4%; Pred. No. 33;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Oy      17 COLRCSNTPTTCORYC 34
Db      53 CTRCSAHSRPRVNCRRAC 70

RESULT 39
US-09-848-295-2
; Sequence 2, Application US/09848295
; Patent No. 6623941
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Tumor Necrosis Factor TR20 and Methods Based
; FILE OF INVENTION: Theoreon
; FILE REFERENCE: PF527
; CURRENT APPLICATION NUMBER: US/09/848,295
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/202,193
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-848-295-2

Query Match      26.1%; Score 52.5; DB 2; Length 142;
Best Local Similarity 29.4%; Pred. No. 49;
Matches 10; Conservative 8; Mismatches 15; Indels 1; Gaps 1;

Oy      1 CSQNEYPDSLHACIPCOLRCSNTPTTCORYC 34
Db      4 CPBEOYMAALLGTCMFCRKAICMHS-QRTCAASC 36

RESULT 40
US-09-950-933A-65
; Sequence 65, Application US/09950933A
; Patent No. 6875907
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro, Pedro
; TITLE OF INVENTION: Antimicrobial Peptides and Methods of
; FILE OF INVENTION: Use
; FILE REFERENCE: 35718/238472
; CURRENT APPLICATION NUMBER: US/09/950,933A
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/232,569
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Glycine max
US-09-950-933A-65

Query Match      25.9%; Score 52; DB 2; Length 115;
Best Local Similarity 44.4%; Pred. No. 46;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Oy      17 COLRCSNTPTTCORYC 34
Db      60 CRVACSLHSRPRKICRRAC 77

RESULT 41
US-09-877-730-26
; Sequence 26, Application US/09877730
; Patent No. 6465632
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6465632e1 Human Phosphatases and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0189-USA
; CURRENT APPLICATION NUMBER: US/09/877,730
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,607
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 547
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-877-730-26

Query Match      25.9%; Score 52; DB 2; Length 547;
Best Local Similarity 33.3%; Pred. No. 2.1e+02;
Matches 10; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Oy      4 NEYFDSLHACIPCOLRCSNTPTTCORYC 33
Db      503 NSFIDAKVLSGICISRSISIPPCVCKMY 532

RESULT 42
US-09-877-730-24
; Sequence 24, Application US/09877730
; Patent No. 6465632
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
```

```

; TITLE OF INVENTION: No. 6465632e1 Human Phosphatases and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0189-USA
; CURRENT APPLICATION NUMBER: US/09/877,730
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,607
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 624
; TYPE: PRT
; ORGANISM: homo sapiens
; US-09-877-730-24

Query Match
Best Local Similarity 25.9%; Score 52; DB 2; Length 624;
Matches 10; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 4 NEYPSLHACIPQCRSSNTPPLTCQRY 33
Db 580 NSFIDAKVSCGICISRSISPPCVCKMY 609

RESULT 43
US-09-877-730-22
; Sequence 22, Application US/09877730
; Patent No. 6465632
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6465632e1 Human Phosphatases and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0189-USA
; CURRENT APPLICATION NUMBER: US/09/877,730
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,607
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 712
; TYPE: PRT
; ORGANISM: homo sapiens
; US-09-877-730-22

Query Match
Best Local Similarity 25.9%; Score 52; DB 2; Length 712;
Matches 10; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 4 NEYPSLHACIPQCRSSNTPPLTCQRY 33
Db 668 NSFIDAKVSCGICISRSISPPCVCKMY 697

RESULT 44
US-09-877-730-16
; Sequence 16, Application US/09877730
; Patent No. 6465632
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6465632e1 Human Phosphatases and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0189-USA
; CURRENT APPLICATION NUMBER: US/09/877,730

```

```

; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,607
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 826
; TYPE: PRT
; ORGANISM: homo sapiens
; US-09-877-730-16

Query Match
Best Local Similarity 25.9%; Score 52; DB 2; Length 826;
Matches 10; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 4 NEYPSLHACIPQCRSSNTPPLTCQRY 33
Db 782 NSFIDAKVSCGICISRSISPPCVCKMY 811

RESULT 45
US-09-877-730-6
; Sequence 6, Application US/09877730
; Patent No. 6465632
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6465632e1 Human Phosphatases and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0189-USA
; CURRENT APPLICATION NUMBER: US/09/877,730
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,607
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 904
; TYPE: PRT
; ORGANISM: homo sapiens
; US-09-877-730-6

Query Match
Best Local Similarity 25.9%; Score 52; DB 2; Length 904;
Matches 10; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 4 NEYPSLHACIPQCRSSNTPPLTCQRY 33
Db 860 NSFIDAKVSCGICISRSISPPCVCKMY 889

RESULT 46
US-09-877-730-12
; Sequence 12, Application US/09877730
; Patent No. 6465632
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6465632e1 Human Phosphatases and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0189-USA
; CURRENT APPLICATION NUMBER: US/09/877,730
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,607

```

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; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 991
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-877-730-12

Query Match          25.9%; Score 52; DB 2; Length 991;
Best Local Similarity 33.3%; Pred. No. 3.7e+02;
Matches 10; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

OY 4 NEYFDSLHACIPQQLRCSSNTPPLTCORY 33
Db 1025 NSFIDAKVLSCGICISRSISPPPCVCKMY 1054

RESULT 47
US-09-877-730-2
; Sequence 2, Application US/09877730
; Patent No. 6465632
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abulin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6465632e1 Human Phosphatases and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0189-USA
; CURRENT APPLICATION NUMBER: US/09/877,730
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,607
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1069
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-877-730-2

Query Match          25.9%; Score 52; DB 2; Length 1069;
Best Local Similarity 33.3%; Pred. No. 4e+02;
Matches 10; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

OY 4 NEYFDSLHACIPQQLRCSSNTPPLTCORY 33
Db 1025 NSFIDAKVLSCGICISRSISPPPCVCKMY 1054

RESULT 48
US-08-117-080-12
; Sequence 12, Application US/08117080
; Patent No. 5482928
; GENERAL INFORMATION:
; APPLICANT: DE BOLLÉ, MIGUEL
; APPLICANT: BROEKAERT, WILLEM F
; APPLICANT: CAMMUE, BRUNO PA
; APPLICANT: VANDERLEYDEN, JOZEF
; APPLICANT: REES, SARAH B
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, NW; NINTH FLOOR, EAST
; STREET: TOWER
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; 
```

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,080
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00423
; FILING DATE: 10-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9105052.6
; FILING DATE: 11-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9105684.6
; FILING DATE: 19-MAR-1991
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861 3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: FIGURE 7 AMINO ACID SEQUENCE MJ-AMP2
US-08-117-080-12

Query Match          25.6%; Score 51.5; DB 1; Length 63;
Best Local Similarity 38.5%; Pred. No. 29;
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

OY 10 LHHACIPQQLRCSSNT-PPLTCORYC 34
Db 24 MIEACIGNGRCNENVGPPYCCSGFC 49

RESULT 49
US-08-471-329-12
; Sequence 12, Application US/08471329
; Patent No. 5689048
; GENERAL INFORMATION:
; APPLICANT: DE BOLLÉ, MIGUEL
; APPLICANT: BROEKAERT, WILLEM F
; APPLICANT: CAMMUE, BRUNO PA
; APPLICANT: VANDERLEYDEN, JOZEF
; APPLICANT: REES, SARAH B
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, NW; NINTH FLOOR, EAST
; STREET: TOWER
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,329
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117,080
; FILING DATE: 20-DEC-1993
; 
```

APPLICATION NUMBER: PCT/GB92/00423
FILING DATE: 10-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9105052.6
FILING DATE: 11-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9105684.6
FILING DATE: 19-MAR-1991
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861 3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: FIGURE 7 AMINO ACID SEQUENCE MJ-AMP2
US-08-471-329-12

Query Match 25.6%; Score 51.5; DB 1; Length 63;
Best Local Similarity 38.5%; Pred. No. 29;
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY 10 LHACIPCOLRCSNT-PPLTCORYC 34
DB 24 MIEACIGNGRCNENVGPPYCCSGFC 49

RESULT 50
US-08-915-142-12
Sequence 12, Application US/08915142
Patent No. 5942663
GENERAL INFORMATION:
APPLICANT: DE BOLLE, MIGUEL
APPLICANT: BROEKERT, WILLEM F
APPLICANT: CAMMUE, BRUNO PA
APPLICANT: VANDERLEYDEN, JOZEP
APPLICANT: REES, SARAH B
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DABRY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, NW; NINTH FLOOR, EAST
STREET: TOWER
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,142
FILING DATE: 20-AUG-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/471,329
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 08/117,080
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: PCT/GB92/00423
FILING DATE: 10-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9105052.6
FILING DATE: 11-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9105684.6

FILING DATE: 19-MAR-1991
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861 3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: FIGURE 7 AMINO ACID SEQUENCE MJ-AMP2
US-08-915-142-12

Query Match 25.6%; Score 51.5; DB 1; Length 63;
Best Local Similarity 38.5%; Pred. No. 29;
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY 10 LHACIPCOLRCSNT-PPLTCORYC 34
DB 24 MIEACIGNGRCNENVGPPYCCSGFC 49

RESULT 51
US-08-465-380-4
Sequence 4, Application US/08465380
Patent No. 5863894
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H. L. Mensens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Gansseman, Matthew Moyle,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,380
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

ORIGINAL SOURCE:
ORGANISM: Ancylostoma caninum
US-08-465-380-4

Query Match 25.6%; Score 51.5; DB 1; Length 77;
Best Local Similarity 29.3%; Pred. No. 36;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

Qy 1 CSONEYFDSLHAC---IPCQLRCSNTP---PLTCGRYC 34
Db 6 CGENEWLMD---CGTQKPCAKCNBEPPEEDPICRSRG 42

RESULT 52

US-08-465-380-40
Sequence 40, Application US/08465380
Patent No. 5863894

GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,380
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma caninum
US-08-465-380-40

Query Match 25.6%; Score 51.5; DB 1; Length 77;
Best Local Similarity 29.3%; Pred. No. 36;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

Qy 1 CSONEYFDSLHAC---IPCQLRCSNTP---PLTCGRYC 34
Db 6 CGENEWLMD---CGTQKPCAKCNBEPPEEDPICRSRG 42

RESULT 53
US-08-480-478-33
Sequence 33, Application US/08480478
Patent No. 5864009

GENERAL INFORMATION:
APPLICANT: GEORGE P. VLASUK, PATRICK ERIC
APPLICANT: HUGO STANSENS, JORIS HILDA
APPLICANT: LIEVEN MESSENS, MARC JOZEF
APPLICANT: LAUWERYS, YVES RENE LAROCHE;
APPLICANT: LAURENT STEPHANE JESPERS, and
APPLICANT: YANNICK GEORGES JOZEF
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTI-
TITLE OF INVENTION: COAGULANT PROTEIN
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,478
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: 18 OCTOBER 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 208/290
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-480-478-33

Query Match 25.6%; Score 51.5; DB 1; Length 77;
Best Local Similarity 29.3%; Pred. No. 36;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

Qy 1 CSONEYFDSLHAC---IPCQLRCSNTP---PLTCGRYC 34
Db 6 CGENEWLMD---CGTQKPCAKCNBEPPEEDPICRSRG 42

RESULT 54
US-08-486-397-4
Sequence 4, Application US/08486397
Patent No. 586542

GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN

NUMBER OF SEQUENCES: 357
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,397
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/269
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma caninum
US-08-486-397-4

Query Match 25.6%; Score 51.5; DB 1; Length 77;
Best Local Similarity 29.3%; Pred. No. 36;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;
QY 1 CSONEYFDSLHAC--IPCOLRCSSNTP---PLTCORYC 34
DB 6 CGENEWLDD---CGTQKPCFAKCNBPPEEDPICRSKGC 42

RESULT 55
US-08-486-397-40
Sequence 40, Application US/08486397
Patent No. 5866542
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
NUMBER OF SEQUENCES: 357
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,397
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/269
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma caninum
US-08-486-397-40

Query Match 25.6%; Score 51.5; DB 1; Length 77;
Best Local Similarity 29.3%; Pred. No. 36;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;
QY 1 CSONEYFDSLHAC--IPCOLRCSSNTP---PLTCORYC 34
DB 6 CGENEWLDD---CGTQKPCFAKCNBPPEEDPICRSKGC 42

RESULT 56
US-08-486-399-4
Sequence 4, Application US/08486399
Patent No. 5866543
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,399
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.

CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,471
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,455
FILING DATE: April 17, 1997
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma caninum
US-09-249-471-4

Query Match 25.6%; Score 51.5; DB 2; Length 77;
Best Local Similarity 29.3%; Pred. No. 36;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

Qy 1 CSONEYFDSLHAC---IPCQLRCSSNTP---PLTCORYC 34
Db 6 CGENEWLDD---CGTQKPCCKAKCNBEPPEEDPICRSRG 42

RESULT 64
US-09-249-471-40
Sequence 40, Application US/09249471
Patent No. 6040441
GENERAL INFORMATION:
APPLICANT: Viasuk, George Phillip
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Ganssemans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,471
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,455
FILING DATE: April 17, 1997
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma caninum
US-09-249-471-40

Query Match 25.6%; Score 51.5; DB 2; Length 77;
Best Local Similarity 29.3%; Pred. No. 36;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

Qy 1 CSONEYFDSLHAC---IPCQLRCSSNTP---PLTCORYC 34
Db 6 CGENEWLDD---CGTQKPCCKAKCNBEPPEEDPICRSRG 42

RESULT 65
US-09-249-472-4
Sequence 4, Application US/09249472
Patent No. 6046318
GENERAL INFORMATION:
APPLICANT: Viasuk, George Phillip
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Ganssemans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W.

```

; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C., DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/249,472
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/809,455
; FILING DATE: April 17, 1997
; APPLICATION NUMBER: PCT/US96/12231
; FILING DATE: October 17, 1995
; APPLICATION NUMBER: 08/486,399
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/486,397
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/465,380
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/461,965
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 216/270
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO.: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum
; US-09-249-472-4

Query Match      25.6%; Score 51.5; DB 2; Length 77;
Best Local Similarity    29.3%; Pred.No. 36;
Matches   12; Conservative        6; Mismatches   12; Indels       11; Gaps         3,

Cy              1 CSONEYPSLHAAC--IPQQLRGSSNTP----PLTCQRVC 34
               :|::||:                |:::||:            |: 
Db             6 CGENEMWLD-----CGTGRPCEAKCNBPPEEHPICRSRGC 42
               ||::||:                  ||::||||:          || 

RESULT 66
US-09-249-472-40
; Sequence 40, Application US/09249472
; Patent No. 6046318
; GENERAL INFORMATION:
; APPLICANT: Vlasuk, George Phillip
; APPLICANT: Stanssens, Patrick Eric Hugo
; APPLICANT: Messens, Joris Hilda Lieven
; APPLICANT: Lauwereys, Marc Josef
; APPLICANT: Laroche, Yves Rene
```

```

1 APPLICANT: Jespers, Laurent Stephane
2 APPLICANT: Gansemans, Yannick Georges Jozef
3 APPLICANT: Moyle, Matthew
4 APPLICANT: Bergum, Peter W.
5 TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
6 TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
7 TITLE OF INVENTION: PROTEIN
8 NUMBER OF SEQUENCES: 356
9 CORRESPONDENCE ADDRESS:
10 ADDRESSEE: Lyon & Lyon
11 STREET: 633 West Filth Street
12 STREET: Suite 4700
13 CITY: Los Angeles
14 STATE: California
15 COUNTRY: U.S.A.
16 ZIP: 90071
17
18 COMPUTER READABLE FORM:
19 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
20 MEDIUM TYPE: storage
21 COMPUTER: IBM Compatible
22 OPERATING SYSTEM: IBM P.C. DOS 5.0
23 SOFTWARE: Word Perfect 5.1
24 CURRENT APPLICATION DATA:
25 APPLICATION NUMBER: US/09/249,472
26 FILING DATE:
27
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: 08/809,455
30 FILING DATE: April 17, 1997
31 APPLICATION NUMBER: PCT/US95/13231
32 FILING DATE: October 17, 1995
33 APPLICATION NUMBER: 08/486,399
34 FILING DATE: June 5, 1995
35 APPLICATION NUMBER: 08/486,397
36 FILING DATE: June 5, 1995
37 APPLICATION NUMBER: 08/465,380
38 FILING DATE: June 5, 1995
39 APPLICATION NUMBER: 08/461,965
40 FILING DATE: June 5, 1995
41 APPLICATION NUMBER: 08/326,110
42 FILING DATE: October 18, 1994
43 ATTORNEY/AGENT INFORMATION:
44 NAME: BIGGS, SUZANNE L.
45 REGISTRATION NUMBER: 30,158
46 REFERENCE/DOCKET NUMBER: 216/270
47 TELECOMMUNICATION INFORMATION:
48 TELEPHONE: (213) 489-1600
49 TELEFAX: (213) 955-0440
50 TELEX: 67-3510
51 INFORMATION FOR SEQ ID NO: 40:
52 SEQUENCE CHARACTERISTICS:
53 LENGTH: 77 amino acids
54 TYPE: amino acid
55 TOPOLOGY: linear
56 MOLECULE TYPE: peptide
57 ORIGINAL SOURCE:
58 ORGANISM: Ancylostoma caninum
59
60 US-09-249-472-40
61
62 Query Match 25.6%; Score 51.5; DB 2; Length 77;
63 Best Local Similarity 29.3%; Pred. NO. 36;
64 Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;
65
66 1 CSONEYFDSLHAC--IPCOLRCSNTP---PLTCORYC 34
67 |:::|:::|:::|:::|:::|:::|:::|
68 Db 6 CGENEMIDD----CGTQKPCAKCNBPPEHEDPICRSRC 42
69
70 RESULT 67
71 US-09-249-451-4
72 : Sequence 4, Application US/09249451
73 : Parent No. 6087487
74 : GENERAL INFORMATION:
75 : APPLICANT: Vlaauk, George Phillip

```


RESULT 69
US-08-809-455-4
; Sequence 4, Application US/08809455
; Patent No. 6090916
; GENERAL INFORMATION:
; APPLICANT: Vlasuk, George Phillip
; APPLICANT: Stanssens, Patrick Eric Hugo
; APPLICANT: Messens, Joris Hilda Lieven
; APPLICANT: Lauwereys, Marc Josef
; APPLICANT: Laroche, Yves Rene
; APPLICANT: Jespers, Laurent Stephane
; APPLICANT: Ganssemans, Yannick Georges Jozef
; APPLICANT: Moyle, Matthew
; APPLICANT: Bergum, Peter W.
; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,455
; FILING DATE: April 17, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13231
; FILING DATE: October 17, 1995
; APPLICATION NUMBER: 08/486,399
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/486,397
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/465,380
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/461,965
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 216/270
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum
; US-08-809-455-4
Query Match 25.6%; Score 51.5; DB 2; Length 77;
Best Local Similarity 29.3%; Pred. No. 36;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

DB 6 CGENEMBLD-----CCTGKPCAKCKNEPPEEDPICRSRC 42
RESULT 70
US-08-809-455-40
; Sequence 40, Application US/08809455
; Patent No. 6090916
; GENERAL INFORMATION:
; APPLICANT: Vlasuk, George Phillip
; APPLICANT: Stanssens, Patrick Eric Hugo
; APPLICANT: Messens, Joris Hilda Lieven
; APPLICANT: Lauwereys, Marc Josef
; APPLICANT: Laroche, Yves Rene
; APPLICANT: Jespers, Laurent Stephane
; APPLICANT: Ganssemans, Yannick Georges Jozef
; APPLICANT: Moyle, Matthew
; APPLICANT: Bergum, Peter W.
; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,455
; FILING DATE: April 17, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13231
; FILING DATE: October 17, 1995
; APPLICATION NUMBER: 08/486,399
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/486,397
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/465,380
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/461,965
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 216/270
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum
; US-08-809-455-40
Query Match 25.6%; Score 51.5; DB 2; Length 77;
Best Local Similarity 29.3%; Pred. No. 36;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

QY 1 CSONEYFDSLHAC---IPCQLRCSSNTP-----PLTCORYC 34
Db 6 CGENEMULD-----CGTOKPCEAKCNEBPPEEDPICRSKGC 42

RESULT 71

US-09-249-461-4
; Sequence 4, Application US/09249461
; Patent No. 6096877

GENERAL INFORMATION:

APPLICANT: Vlasuk, George Phillip
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Ganssemans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,461

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/809,455
FILING DATE: April 17, 1997
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE: Ancylostoma caninum

US-09-249-461-4

Query Match 25.6%; Score 51.5; DB 2; Length 77;
Best Local Similarity 29.3%; Pred. No. 36;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

QY 1 CSONEYFDSLHAC---IPCQLRCSSNTP-----PLTCORYC 34
Db 6 CGENEMULD-----CGTOKPCEAKCNEBPPEEDPICRSKGC 42

RESULT 72

US-09-249-461-40
; Sequence 40, Application US/09249461
; Patent No. 6096877

GENERAL INFORMATION:

APPLICANT: Vlasuk, George Phillip
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Ganssemans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,461

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/809,455
FILING DATE: April 17, 1997
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-09-249-461-4

MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma caninum
US-09-249-461-40

Query Match 25.6%; Score 51.5; DB 2; Length 77;
Best Local Similarity 29.3%; Pred. No. 36;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

Oy 1 CSONEYFSLHAC---IPCQRCSSNTP---PLTCQRYC 34
Db 6 CGENEWLDD---CGTQKPCAKCNBEPPEEDPICRSRG 42

RESULT 73

US-09-249-448-4
Sequence 4, Application US/09249448

PATENT INFORMATION:
PATENT NO. 6121435
APPLICANT: Vlasuk, George Phillip
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Gansemans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,448
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,455
FILING DATE: April 17, 1997
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma caninum
US-09-249-448-4

Query Match 25.6%; Score 51.5; DB 2; Length 77;
Best Local Similarity 29.3%; Pred. No. 36;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

Oy 1 CSONEYFSLHAC---IPCQRCSSNTP---PLTCQRYC 34
Db 6 CGENEWLDD---CGTQKPCAKCNBEPPEEDPICRSRG 42

RESULT 74

US-09-249-448-40
Sequence 40, Application US/09249448

PATENT INFORMATION:
PATENT NO. 6121435
APPLICANT: Vlasuk, George Phillip
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Gansemans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,448
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,455
FILING DATE: April 17, 1997
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:

FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma caninum
US-09-249-473-40

Query Match 25.6%; Score 51.5; DB 2; Length 77;
Best Local Similarity 29.3%; Pred. No. 36;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

Oy 1 CSONEYFDSLHAC---IPCQLRCSSNTP---PLTCQRYC 34
Db 6 CGENEWLDD---CGTQKPCAKCNEPPEBEDPICRSRC 42

RESULT 77
US-09-498-556-4
Sequence 4, Application US/09498556
Patent No. 6872808
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Llieven
Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
Ganssemans, Yannick Georges Jozef
Moyle, Matthew
Bergum, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
INHIBITORS AND ANTICOAGULANT
PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,556
FILING DATE: 04-Feb-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,455
FILING DATE: April 17, 1997
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397

FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma caninum
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-498-556-4

Query Match 25.6%; Score 51.5; DB 2; Length 77;
Best Local Similarity 29.3%; Pred. No. 36;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

Oy 1 CSONEYFDSLHAC---IPCQLRCSSNTP---PLTCQRYC 34
Db 6 CGENEWLDD---CGTQKPCAKCNEPPEBEDPICRSRC 42

RESULT 78
US-09-498-556-40
Sequence 40, Application US/09498556
Patent No. 6872808
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Llieven
Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
Ganssemans, Yannick Georges Jozef
Moyle, Matthew
Bergum, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
INHIBITORS AND ANTICOAGULANT
PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,556
FILING DATE: 04-Feb-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,455
FILING DATE: April 17, 1997

APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma caninum
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-498-556-40

Query Match 25.6%; Score 51.5; DB 2; Length 77;
Best Local Similarity 29.3%; Pred. No. 36;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

QY 1 CSQNEFYDSLHAC---IPCQLRCSSNTP---PLTCQRYC 34
Db 6 CGENEWLDD---CGTQKPCCAKCNPEPPEEDPICRSRGC 42

RESULT 79
US-08-465-380-7
Sequence 7, Application US/08465380
Patent No. 5863894
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Strassens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,380
FILING DATE: June 5, 1995
CLASSIFICATION: 530
Prior Application Data:
APPLICATION NUMBER: 08/326,110

FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 81 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma caninum
US-08-465-380-7

Query Match 25.6%; Score 51.5; DB 1; Length 81;
Best Local Similarity 29.3%; Pred. No. 37;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

QY 1 CSQNEFYDSLHAC---IPCQLRCSSNTP---PLTCQRYC 34
Db 10 CGENEWLDD---CGTQKPCCAKCNPEPPEEDPICRSRGC 46

RESULT 80
US-08-480-478-36
Sequence 36, Application US/08480478
Patent No. 5864009
GENERAL INFORMATION:
APPLICANT: GEORGE P. VLASUK, PATRICK ERIC
APPLICANT: HUGO STRASSENS, JORIS HILDA
APPLICANT: LIEVEN MESSENS, MARC JOZEF
APPLICANT: LAURENTS, YVES RENE LAROCHE,
APPLICANT: LAURENT STEPHANE JESPEERS, and
APPLICANT: YANNICK GEORGES JOZEF
APPLICANT: GANSEMANS
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTI-
TITLE OF INVENTION: COAGULANT PROTEIN
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,478
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
Prior Application Data:
APPLICATION NUMBER: 08/326,110
FILING DATE: 18 OCTOBER 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 208/290
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 36:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 81 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-480-478-36

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| | | | | | | | |
|-----------------------|-------|--------------|------|------------|----|--------|----|
| Query Match | 25.6% | Score | 51.5 | DB | 1 | Length | 81 |
| Best Local Similarity | 29.3% | Pred. No. | 37 | | | | |
| Matches | 12 | Conservative | 6 | Mismatches | 12 | Indels | 11 |
| | | | | | | Gaps | 3 |

OY 1 CSQNEYFDSLTHAC---IPCQLRCSSNTP-----PLTCQRVC 34
 | : | : | : | : | : | : | : | : | : |
DB 10 CGENEWLDD----CGTQKPCEAKCNEDPEEEDPICRSRGC 46

RESULT 81
US-08-486-397-7

GENERAL INFORMATION:
APPLICANT: George P. Vlasak, Patric H. Stranssens,
APPLICANT: Joris H.J. Mensens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Ganssemaans, Matthew Moyle,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATOIDE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 357
CORRESPONDENCE ADDRESS:

| | | | | |
|-----------------------|----------------|------------------|------------------|-------------|
| Query Match | 25.6% | Score 51.5 | DB 1 | Length 81 |
| Best Local Similarity | 29.3% | Pred. No. 37 | | |
| Matches 12 | Conservative 6 | Mismatches 12 | Indels 11 | Gaps 3 |
| QY | 1 | CSQNEYFDSLHAC--- | IPQQLRCSNRP----- | PLTCRCYC 34 |
| | : : : | : : : : | : : | : |

Db 10 CGENWLLD---CGTQKPCBAKNEEPPEEDPICRSRC 46

RESULT 82
US-08-486-399-7
; Sequence 7, Application US/08486399

1 GENERAL INFORMATION:
2 APPLICANT: George P. Vlasuk, Patric H. Stanssens,
3 APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
4 APPLICANT: Yves R. Laroche, Laurent S. Jespers,
5 APPLICANT: Yvanick G.J. Gansmeaux, Matthew Moyle,
6 APPLICANT: Peter W. Beegum
7 TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
8 TITLE OF INVENTION: PROTEIN
9 NUMBER OF SEQUENCES: 356
10
11 CORRESPONDENCE ADDRESS: 1

```

Query Match          25.6%; Score 51.5; DB 1; Length 81;
Best Local Similarity 29.3%; Pred. No. 37;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

Oy      1 CSQNEYFDSLHAC---IPCOLRCSSTP----PLTCQRRC 34
        |::|||::|::|::|::|::|::|::|::|::|::|::|::|
Db       10 CGENEMWDD---CGTQKPCEARKNRPPEEDPFICRSQC 46

RESULT 83
US-08-461-965-7
: Sequence 7, Application US/08461965
: Patent No. 5872098
: GENERAL INFORMATION:
: APPLICANT: George P. Vlausk, Patric H. Stranssens,
: APPLICANT: Joris H.L. Mensens, Marc U. Lauwereys,
: APPLICANT: Yves R. Larocche, Laurent S. Jespers,
: APPLICANT: Yannick G.-J. Gansemaens, Matthew Moyle,
```

APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,965
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 210/243
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 81 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma caninum
US-08-461-965-7

Query Match 25.6%; Score 51.5; DB 1; Length 81;
Best Local Similarity 29.3%; Pred. No. 37;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

QY 1 CSONEYFDSLHAC---IPCQLRCSNTP---PLTCQRYC 34
DB 10 CGENEWLDD---CGTQKPCBEAKCNEPPEEDDPICRSRC 46

RESULT 84
US-08-326-110A-36
Sequence 36, Application US/08326110A
Patent No. 5945275
GENERAL INFORMATION:
APPLICANT: GEORGE P. VLASUK; PATRICK ERIC
APPLICANT: HUGO STANGSENS; JORIS HILDA
APPLICANT: LIEVEN MESSENS; MARC JOZER
APPLICANT: LAUWEREYS; YVES RENE LAROCHE;
APPLICANT: LAURENT STEPHANE JESPEERS; and
APPLICANT: YANNICK GEORGES JOZEF
APPLICANT: GANSEMAN
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTI-
TITLE OF INVENTION: COAGULANT PROTEIN
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California

COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/326,110A
FILING DATE: 18 OCTOBER 1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 208/290
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 81 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-326-110A-36

Query Match 25.6%; Score 51.5; DB 1; Length 81;
Best Local Similarity 29.3%; Pred. No. 37;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

QY 1 CSONEYFDSLHAC---IPCQLRCSNTP---PLTCQRYC 34
DB 10 CGENEWLDD---CGTQKPCBEAKCNEPPEEDDPICRSRC 46

RESULT 85
US-08-634-641-7
Sequence 7, Application US/08634641
Patent No. 5955294
GENERAL INFORMATION:
APPLICANT: Vlasuk, George P. Vlasuk
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Menssens, Joris Hilda Lieven
APPLICANT: Lauweres, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Gansmans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,641
FILING DATE: April 19, 1996

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13231
; FILING DATE: October 17, 1995
; APPLICATION NUMBER: 08/486,399
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/486,397
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/465,380
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/461,965
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 219/136
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 81 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum
; US-08-634-641-7

Query Match      25.6%; Score 51.5; DB 1; Length 81;
Best Local Similarity 29.3%; Pred. No. 37;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

Qy      1  CSONEYFDSLHAC---IPCQLRCSNTP---PLTCORYC 34
Db      10 CGENEMWLD---CGTQKPCBAKCNBPBEPEDPICRSRC 46

RESULT 86
US-09-249-471-7
; Sequence 7, Application US/09249471
; Patent No. 6040441
; GENERAL INFORMATION:
; APPLICANT: Vlausk, George Phillip
; APPLICANT: Stanssens, Patrick Eric Hugo
; APPLICANT: Messens, Joris Hilda Lieven
; APPLICANT: Lauwereys, Marc Josef
; APPLICANT: Laroche, Yves Rene
; APPLICANT: Jespers, Laurent Stephane
; APPLICANT: Ganssemans, Yannick Georges Jozef
; APPLICANT: Moyle, Matthew
; APPLICANT: Bergum, Peter W.
; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/249,471
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/809,455
; FILING DATE: April 17, 1997
; APPLICATION NUMBER: PCT/US95/13231
; FILING DATE: October 17, 1995
; APPLICATION NUMBER: 08/486,399
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/486,397
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/465,380
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/461,965
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 216/270
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 81 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum
; US-09-249-471-7

Query Match      25.6%; Score 51.5; DB 2; Length 81;
Best Local Similarity 29.3%; Pred. No. 37;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

Qy      1  CSONEYFDSLHAC---IPCQLRCSNTP---PLTCORYC 34
Db      10 CGENEMWLD---CGTQKPCBAKCNBPBEPEDPICRSRC 46

RESULT 87
US-09-249-472-7
; Sequence 7, Application US/09249472
; Patent No. 6046318
; GENERAL INFORMATION:
; APPLICANT: Vlausk, George Phillip
; APPLICANT: Stanssens, Patrick Eric Hugo
; APPLICANT: Messens, Joris Hilda Lieven
; APPLICANT: Lauwereys, Marc Josef
; APPLICANT: Laroche, Yves Rene
; APPLICANT: Jespers, Laurent Stephane
; APPLICANT: Ganssemans, Yannick Georges Jozef
; APPLICANT: Moyle, Matthew
; APPLICANT: Bergum, Peter W.
; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage

```


STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,455
FILING DATE: April 17, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 81 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma caninum
US-08-809-455-7

Query Match 25.6%; Score 51.5; DB 2; Length 81;
Best Local Similarity 29.3%; Pred. No. 37;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

QY 1 CSONEYFDSLHAC--IPCOLRCSNTP---PLTCORYC 34
Db 10 CGENWMLD---CGTQKPCRAKCNBPPEEDPICSRGC 46

RESULT 90
US-09-249-461-7
Sequence 7, Application US/09249461
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Ganssemans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,461
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,455
FILING DATE: April 17, 1997
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 81 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma caninum
US-09-249-461-7

Query Match 25.6%; Score 51.5; DB 2; Length 81;
Best Local Similarity 29.3%; Pred. No. 37;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

QY 1 CSONEYFDSLHAC--IPCOLRCSNTP---PLTCORYC 34
Db 10 CGENWMLD---CGTQKPCRAKCNBPPEEDPICSRGC 46

RESULT 91
US-09-249-448-7
Sequence 7, Application US/09249448
Patent No. 6121435
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Ganssemans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE

TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,448
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,455
FILING DATE: April 17, 1997
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 81 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma caninum
US-09-249-448-7

Query Match 25.6%; Score 51.5; DB 2; Length 81;
Best Local Similarity 29.3%; Pred. No. 37;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

Qy 1 CSONEYFDSLHAC--IPQQLRCSSNTP---PLTCQRYC 34
Db 10 CGENEMLDD---CGTQKPCCAKCNBEPPEEDPICRSRG 46

RESULT 92
US-09-249-473-7
Sequence 7, Application US/09249473
Patent No. 6534629
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Stephane

APPLICANT: Gansemans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,473
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,455
FILING DATE: April 17, 1997
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 81 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma caninum
US-09-249-473-7

Query Match 25.6%; Score 51.5; DB 2; Length 81;
Best Local Similarity 29.3%; Pred. No. 37;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

Qy 1 CSONEYFDSLHAC--IPQQLRCSSNTP---PLTCQRYC 34
Db 10 CGENEMLDD---CGTQKPCCAKCNBEPPEEDPICRSRG 46

RESULT 93
US-09-498-556-7
Sequence 7, Application US/09498556
Patent No. 6872808
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
APPLICANT: Stanssens, Patrick Eric Hugo

Messens, Joris Hilda Lieven
 Lauwerey, Marc Josef
 Laroche, Yves Rene
 Jespers, Laurent Stephane
 Ganssemans, Yannick Georges Jozef
 Moyle, Mathew
 Bergum, Peter W.
 TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
 INHIBITORS AND ANTICOAGULANT
 PROTEIN
 NUMBER OF SEQUENCES: 356
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/498,556
 FILING DATE: 04-Feb-2000
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/809,455
 FILING DATE: April 17, 1997
 APPLICATION NUMBER: PCT/US95/13231
 FILING DATE: October 17, 1995
 APPLICATION NUMBER: 08/486,399
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/486,397
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/465,380
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/461,965
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/326,110
 FILING DATE: October 18, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: BIGGS, SUZANNE L.
 REGISTRATION NUMBER: 30,158
 REFERENCE/DOCKET NUMBER: 216/270
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 81 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 ORIGINAL SOURCE:
 ORGANISM: Ancylostoma caninum
 SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 DS-09-498-556-7

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Query Match      25.6% Score 51.5; DB 2; Length 81,  
Best Local Similarity   29.3%; Pged No. 37;  
Matches    12; Conservative     6; Mismatches    12; Indels    11; Gaps    3  
  
Qy          1 CSONEFVPSLHAC--IPQLRGCSNTP----PLTQRVC 34  
              ::::|::|::|::|::|:  
Db         10 CGENEMLPD---CGTKPCFEAKNEEPPEEDPTCRSGC 46
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RESULT 94
.US-08-465-380-20

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? Sequence 20, Application US/08465380
? Patent No. 5863894
? GENERAL INFORMATION:
? APPLICANT: George P. Vlasak, Patric H. Stanssens,
? APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
? APPLICANT: Yves R. Laroche, Laurent S. Jespers,
? APPLICANT: Yvanck G.J. Ganssemaers, Matthew Moyle,
? APPLICANT: Peter W. Bergum
? TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
? TITLE OF INVENTION: PROTEIN
? NUMBER OF SEQUENCES: 356
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Lyon & Lyon
? STREET: 633 West Fifth Street
? STREET: Suite 4700
? City: Los Angeles
? STATE: California
? COUNTRY: U.S.A.
? ZIP: 90071
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
? MEDIUM TYPE: storage
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: IBM P.C. DOS 5.0
? SOFTWARE: Word Perfect 5.1
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/465,380
? FILING DATE: June 5, 1995
? CLASSIFICATION: 530
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/326,110
? FILING DATE: October 18, 1994
? ATTORNEY/AGENT INFORMATION:
? NAME: BIGGS, SUZANNE L.
? REGISTRATION NUMBER: 30,158
? REFERENCE/DOCKET NUMBER: 213/268
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (213) 489-1600
? TELEFAX: (213) 955-0440
? TELEX: 67-3510
? INFORMATION FOR SEQ ID NO: 20:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 100 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? ORIGINAL SOURCE:
? ORGANISM: Ancylostoma caninum
? US-08-465-380-20

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Query Match      25.6%; Score 51.5; DB 1; Length 100;
Best Local Similarity 29.3%; Pred. No. 46;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

Oy          1 CSQNEYFDSLHAC---IPCOLRCSSNTP---PLTCORYC 34
           |||::|||::|||
Db          29 CGENEWLDD----CGTQKPCCAKCNBEPPEEDPDCRSRGC 65

RESULT 95
US-08-480-478-48
Sequence 48: Application US/08480478
Patent No. 5864009
GENERAL INFORMATION:
APPLICANT: GEORGE P. VLASUK; PATRICK ERIC
APPLICANT: HUGO STANSSENS; JORIS HILDA
APPLICANT: LIEVEN MESSENS; MARC JOZER
APPLICANT: LAURERYS; YVES RENE LAROCHÉ;
APPLICANT: LAURENT STEPHANE JESSEERS; and
APPLICANT: YANNICK GEORGES JOZER
APPLICANT: GANSEWANS
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTI-
COAGULANT PROTEIN
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Query Match          25.6%; Score 51.5; DB 1; Length 100;
Best Local Similarity 29.3%; Pred. No. 46;
Matches      12; Conservative    6; Mismatches     12; Indels    11; Gaps      3.

Qy              1 CSQNEVDFSLHAC---IPCOLRSSNTP-----PLTCORYC 34
                |::|::|::|::|::|::|::|::|::|::|::|::|::|
Db              29 CGENEWLDD----CGTQKPCAKKNKEEPDEEDPICRGRGC 65

RESULT 96
US-08-486-397-20
; Sequence 20, Application US/08486397
; Patent No. 5866542
;
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc U. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.V. Gansemans, Matthew Moyle,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
PROTEIN
NUMBER OF SEQUENCES: 357
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1

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RESULT 97
US-08-486-399--20
Sequence 20, Application US/08486399
Patent No. 5866543
GENERAL INFORMATION:
APPLICANT: George P. Vlaauk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Ganssemans, Matthew Moyle,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,399
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/270
TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma caninum
US-08-486-399-20

Query Match 25.6%; Score 51.5; DB 1; Length 100;
Best Local Similarity 29.3%; Pred. No. 46;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;
OY 1 CSQNEYFDSLHAC---IPCQLRCSSNTP---PLTCQRYC 34
DB 29 CGENEWLDD---CGTQKPCAKCNKEPPEEDPICRSRGC 65

RESULT 96
US-08-461-965-20
Sequence 20, Application US/08461965
Patent No. 5872098
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H. L. Mensens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461.965
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326.110
ATTORNEY/AGENT INFORMATION:
FILING DATE: October 18, 1994
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 210/243
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma caninum
US-08-461-965-20

Query Match 25.6%; Score 51.5; DB 1; Length 100;
Best Local Similarity 29.3%; Pred. No. 46;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;
OY 1 CSQNEYFDSLHAC---IPCQLRCSSNTP---PLTCQRYC 34
DB 29 CGENEWLDD---CGTQKPCAKCNKEPPEEDPICRSRGC 65

RESULT 99
US-08-326-110A-48
Sequence 48, Application US/08326110A
Patent No. 5945275
GENERAL INFORMATION:
APPLICANT: GEORGE P. VLASUK; PATRICK ERIC
APPLICANT: HUGO STANSENS; JORIS HILDA
APPLICANT: LIEVEN MESSENS; MARC JOZEF
APPLICANT: LAUWEREYS; YVES RENE LAROCHE;
APPLICANT: LAURENT STEPHANE JESPEERS; and
APPLICANT: YANNICK GEORGES JOZEF
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTI-
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/326.110A
FILING DATE: 18 OCTOBER 1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 208/290
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-326-110A-48

Query Match 25.6%; Score 51.5; DB 1; Length 100;
Best Local Similarity 29.3%; Pred. No. 46;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;
OY 1 CSQNEYFDSLHAC---IPCQLRCSSNTP---PLTCQRYC 34
DB 29 CGENEWLDD---CGTQKPCAKCNKEPPEEDPICRSRGC 65

RESULT 100
US-08-634-641-20
Sequence 20, Application US/08634641

Patent No. 5955294
GENERAL INFORMATION:
APPLICANT: Vlasuk, George P. Vlasuk
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Mensens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Gansemans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,641
FILING DATE: April 19, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 219/136
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ. ID NO. 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma caninum
US-08-634-641-20

Query Match 25.6%; Score 51.5; DB 1; Length 100;
Best Local Similarity 29.3%; Pred. No. 46;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

QY 1 CSQNEYFDSLHAC---IPQILRCSSNTP---PLTCQRYC 34
DB 29 CGENETLDD---CGTQKPEAKCKNEPPEEDPILCRSGC 65

Search completed: July 10, 2006, 16:42:59
JOB time : 22 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:40:42 ; Search time 66.8 Seconds
(without alignments)

470.816 Million cell updates/sec

Title: US-10-077-137a-1_COPY_8_41

Perfect score: 201
Sequence: 1 CSQNEYPDLHACIPQQLRCSNTPLTCQRYC 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database :

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------|
| 1 | 201 | 100.0 | 135 | 2 | Q2TQ40_HUMAN |
| 2 | 201 | 100.0 | 184 | 1 | TRN17_HUMAN |
| 3 | 201 | 100.0 | 184 | 2 | Q6P846_HUMAN |
| 4 | 136 | 67.7 | 185 | 1 | TRN17_MOUSE |
| 5 | 72.5 | 36.1 | 499 | 2 | O88714_MOUSE |
| 6 | 72.5 | 36.1 | 1674 | 2 | O80Z18_MOUSE |
| 7 | 72.5 | 36.1 | 2850 | 2 | O80T03_MOUSE |
| 8 | 71.5 | 35.6 | 74 | 2 | O5S084_MOUSE |
| 9 | 71.5 | 35.6 | 140 | 2 | O5S083_MOUSE |
| 10 | 71.5 | 35.6 | 249 | 1 | TR13B_MOUSE |
| 11 | 71.5 | 35.6 | 249 | 2 | O5S082_MOUSE |
| 12 | 68.5 | 34.1 | 1569 | 2 | O6W4X9_HUMAN |
| 13 | 67.5 | 33.6 | 1877 | 1 | PCSK5_MOUSE |
| 14 | 66.5 | 33.1 | 293 | 1 | TR13B_HUMAN |
| 15 | 66.5 | 33.1 | 293 | 2 | Q4ACK1_HUMAN |
| 16 | 65.5 | 33.1 | 1023 | 2 | O53F36_HUMAN |
| 17 | 65.5 | 32.6 | 1025 | 2 | Q7R6J7_GIALA |
| 18 | 64.5 | 32.1 | 5374 | 2 | O99ND0_MOUSE |
| 19 | 64.5 | 32.1 | 5376 | 1 | ZAN_MOUSE |
| 20 | 64 | 31.8 | 762 | 2 | O410Y5_GIBZE |
| 21 | 63.5 | 31.6 | 799 | 2 | O501Y7_ENTHI |
| 22 | 63.5 | 31.6 | 802 | 2 | O50Y51_ENTHI |
| 23 | 63 | 31.3 | 1150 | 2 | O50PT4_ENTHI |
| 24 | 62.5 | 31.1 | 442 | 2 | O2UIG2_ASPOR |
| 25 | 62.5 | 31.1 | 1294 | 2 | O7QGV0_ANOGA |
| 26 | 61.5 | 30.6 | 3005 | 2 | O6BRG4_PARTE |
| 27 | 61 | 30.3 | 192 | 2 | O3W613_PACTO |
| 28 | 61 | 30.3 | 966 | 2 | O22378_CAEBL |
| 29 | 61 | 30.3 | 1560 | 2 | O5JSG7_HUMAN |
| 30 | 60 | 29.9 | 830 | 2 | O4RTY8_TETNG |
| 31 | 60 | 29.9 | 867 | 1 | SSPO_BOVIN |

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| 32 | 60 | 29.9 | 5146 | 2 | O8SPM4_BOVIN |
| 33 | 59.5 | 29.6 | 279 | 2 | O2MOX9_DROPS |
| 34 | 59.5 | 29.6 | 353 | 2 | O8S258_DROME |
| 35 | 59.5 | 29.6 | 353 | 2 | O9VM81_DROME |
| 36 | 59.5 | 29.6 | 484 | 2 | O5C268_HUMAN |
| 37 | 59.5 | 29.6 | 581 | 2 | O8NAV8_HUMAN |
| 38 | 59.5 | 29.6 | 852 | 2 | O5C2B3_HUMAN |
| 39 | 59.5 | 29.6 | 861 | 2 | O5SN15_CRYNE |
| 40 | 59.5 | 29.6 | 880 | 2 | O8NAV9_HUMAN |
| 41 | 59.5 | 29.6 | 992 | 2 | O86U29_HUMAN |
| 42 | 59.5 | 29.6 | 993 | 2 | O81X30_HUMAN |
| 43 | 59.5 | 29.6 | 995 | 1 | WKS3_HUMAN |
| 44 | 59 | 29.4 | 184 | 2 | O4S4Q3_TETNG |
| 45 | 59 | 29.4 | 247 | 2 | O321X4_HUMAN |
| 46 | 59 | 29.4 | 937 | 2 | O9G9Y5_CAEBL |
| 47 | 59 | 29.4 | 1917 | 2 | O51ED6_ENTHI |
| 48 | 58.5 | 29.1 | 248 | 2 | O5DDB6_SCHTA |
| 49 | 58.5 | 29.1 | 345 | 2 | O2TW70_ASPOR |
| 50 | 58.5 | 29.1 | 827 | 2 | O68FG9_MOUSE |
| 51 | 58.5 | 29.1 | 993 | 2 | O66PY1_MOUSE |
| 52 | 58 | 28.9 | 101 | 2 | O8BR19_MOUSE |
| 53 | 58 | 28.9 | 164 | 2 | O3XSX7_MOUSE |
| 54 | 58 | 28.9 | 175 | 1 | TR13C_MOUSE |
| 55 | 58 | 28.9 | 175 | 2 | O3XSX6_MOUSE |
| 56 | 58 | 28.9 | 175 | 2 | O8R4W8_MOUSE |
| 57 | 58 | 28.9 | 200 | 2 | O3U106_MOUSE |
| 58 | 58 | 28.9 | 289 | 2 | O678B7_YAIRU |
| 59 | 58 | 28.9 | 1299 | 2 | O26489_SPOPR |
| 60 | 57.5 | 28.6 | 63 | 1 | ICB1_AEGSU |
| 61 | 57.5 | 28.6 | 1061 | 2 | O5B110_DROME |
| 62 | 57.5 | 28.6 | 1679 | 1 | FUR2_DROME |
| 63 | 57 | 28.4 | 304 | 2 | O51AP4_ENTHI |
| 64 | 57 | 28.4 | 321 | 2 | O9MAM0_ARATH |
| 65 | 57 | 28.4 | 919 | 2 | O61V24_CAEBR |
| 66 | 57 | 28.4 | 1210 | 2 | O7R165_GIALA |
| 67 | 57 | 28.4 | 1717 | 2 | O26566_SCHTA |
| 68 | 56.5 | 28.1 | 1476 | 2 | O8WRF4_MOUSE |
| 69 | 56.5 | 28.1 | 1704 | 2 | O51EF3_ENTHI |
| 70 | 56 | 27.9 | 135 | 2 | O60WC9_CAEBR |
| 71 | 56 | 27.9 | 341 | 1 | ZN393_MOUSE |
| 72 | 56 | 27.9 | 387 | 2 | O4K1X7_XENLA |
| 73 | 56 | 27.9 | 387 | 2 | O9PYD4_XENLA |
| 74 | 56 | 27.9 | 392 | 2 | O6NUF1_XENLA |
| 75 | 56 | 27.9 | 544 | 2 | O3CKX7_ALYAT |
| 76 | 56 | 27.9 | 938 | 2 | O60X18_CAEBR |
| 77 | 56 | 27.9 | 2476 | 1 | ZAN_PIG |
| 78 | 55.5 | 27.6 | 146 | 2 | O9BE28_9HPC |
| 79 | 55.5 | 27.6 | 225 | 2 | O9VE40_DROME |
| 80 | 55.5 | 27.6 | 436 | 2 | O41W6_GIBZE |
| 81 | 55.5 | 27.6 | 673 | 2 | O86WK8_HUMAN |
| 82 | 55.5 | 27.6 | 929 | 2 | O3U515_MOUSE |
| 83 | 55.5 | 27.6 | 955 | 2 | O96DN2_HUMAN |
| 84 | 55.5 | 27.6 | 989 | 2 | O9ZU00_ARATH |
| 85 | 55.5 | 27.6 | 1084 | 2 | O61RM7_XENLA |
| 86 | 55.5 | 27.6 | 2898 | 2 | O9V1T6_DROME |
| 87 | 55 | 27.4 | 147 | 1 | MSRB_VIBPA |
| 88 | 55 | 27.4 | 330 | 2 | O18118_CAEBL |
| 89 | 55 | 27.4 | 344 | 2 | O924K7_MERUN |
| 90 | 55 | 27.4 | 469 | 2 | O2UP68_ASPOR |
| 91 | 55 | 27.4 | 663 | 2 | O81YX8_HUMAN |
| 92 | 55 | 27.4 | 686 | 2 | O6R0M3_HUMAN |
| 93 | 55 | 27.4 | 724 | 2 | O6B0V7_DDEBA |
| 94 | 55 | 27.4 | 858 | 1 | TTCT7A_HUMAN |
| 95 | 55 | 27.4 | 882 | 2 | O2CT9J9_HUMAN |
| 96 | 55 | 27.4 | 923 | 2 | O17970_CAEBL |
| 97 | 55 | 27.4 | 1073 | 2 | O6O157_RAT |
| 98 | 55 | 27.4 | 1074 | 2 | O964D1_ENTHI |
| 99 | 55 | 27.4 | 1090 | 2 | O50RX4_ENTHI |
| 100 | 55 | 27.4 | 1101 | 2 | O517S0_ENTHI |
| 101 | 55 | 27.4 | 1101 | 2 | O964D2_ENTHI |
| 102 | 55 | 27.4 | 1105 | 2 | O50ZK2_ENTHI |
| 103 | 55 | 27.4 | 1127 | 2 | O993K9_9GAMA |
| 104 | 55 | 27.4 | 1277 | 2 | O50RX0_ENTHI |

| | |
|---------|---------------|
| O8SPM4 | bos taurus |
| O2MOX9 | drosophila |
| O8S258 | drosophila |
| O9VM81 | drosophila |
| O5C268 | homo sapien |
| O8NAV8 | homo sapien |
| O5C2B3 | homo sapien |
| O5SN15 | cryptococcu |
| O8NAV9 | homo sapien |
| O86U29 | homo sapien |
| O81X30 | homo sapien |
| WKS3 | homo sapien |
| O4S4Q3 | tetradodon n |
| O321X4 | homo sapien |
| O9G9Y5 | caenorhabdi |
| O51ED6 | entamoeba h |
| O5DDB6 | schistosoma |
| O2TW70 | aspergillus |
| O68FG9 | mus musculu |
| O66PY1 | mus musculu |
| O8BR19 | mus musculu |
| O3XSX7 | mus musculu |
| TR13C | mus musculu |
| O3XSX6 | mus musculu |
| O8R4W8 | mus musculu |
| O3U106 | mus musculu |
| O678B7 | lymphocyti |
| O26489 | spodoptera |
| ICB1 | ascaris suu |
| O5B110 | drosophila |
| FUR2 | drosophila |
| O51AP4 | entamoeba h |
| O9MAM0 | arabidopsis |
| O61V24 | caenorhabdi |
| O7R165 | giardia lam |
| O26566 | schistosoma |
| O8WRF4 | monosiga br |
| O51EF3 | entamoeba h |
| O60WC9 | caenorhabdi |
| O8CF47 | mus musculu |
| O4K1X7 | xenopus lae |
| O9PYD4 | xenopus lae |
| O6NUF1 | xenopus lae |
| O3CKX7 | pseudoscalter |
| O60X18 | caenorhabdi |
| O9BE28 | sus scrofa |
| O9VE40 | hepatitis c |
| O41W6 | drosophila |
| O86WK8 | homo sapien |
| O3U515 | mus musculu |
| O96DN2 | homo sapien |
| O9ZU00 | arabidopsis |
| O61RM7 | xenopus lae |
| O9V1T6 | drosophila |
| MSRB | vibrio para |
| O18118 | caenorhabdi |
| O924K7 | meriones un |
| O2UP68 | aspergillus |
| O81YX8 | homo sapien |
| O6R0M3 | homo sapien |
| O6B0V7 | debaromyce |
| O2CT9J9 | homo sapien |
| O17970 | caenorhabdi |
| O6O157 | rattus norv |
| O964D1 | entamoeba h |
| O50RX4 | entamoeba h |
| O517S0 | entamoeba h |
| O964D2 | entamoeba h |
| O50ZK2 | entamoeba h |
| O993K9 | callitrichi |
| O50RX0 | entamoeba h |


```

981 47 23.4 4753 1 LBP_CABEL.
982 47 23.4 5542 2 O7YXX_CRYPV
983 46.5 23.1 63 1 IBB2_ARAHY
984 46.5 23.1 64 2 Q3LTD9_9D1PT
985 46.5 23.1 69 2 Q8WX86_GLOMR
986 46.5 23.1 93 2 Q64W05_BACFR
987 46.5 23.1 102 2 Q8MS92_DROME
988 46.5 23.1 117 2 Q80KP7_9HEPC
989 46.5 23.1 117 2 Q80KP7_9HEPC
990 46.5 23.1 117 2 Q80KR3_9HEPC
991 46.5 23.1 122 2 Q3QNU0_9HOB
992 46.5 23.1 128 2 Q68185_9HEPC
993 46.5 23.1 132 2 Q4CJ14_CLOTM
994 46.5 23.1 135 1 MSRB_AGR75
995 46.5 23.1 137 2 Q5FXF2_9HEPC
996 46.5 23.1 137 2 Q5FXF9_9HEPC
997 46.5 23.1 137 2 Q5FXH0_9HEPC
998 46.5 23.1 146 2 Q9ENZ6_9HEPC
999 46.5 23.1 146 2 Q9ENZ9_9HEPC
1000 46.5 23.1 146 2 Q9EP06_9HEPC

```

ALIGNMENTS

RESULT 1

Q2T040 HUMAN PRELIMINARY; PRT; 135 AA.

AC Q2T040; 24-JAN-2006, integrated into UniProtKB/TrEMBL.

DT 24-JAN-2006, sequence version 1.

DT 07-FEB-2006, entry version 2.

DE Tumor necrosis factor receptor superfamily member 17.

GN Name=TNFRSF17.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Mala S., Freeman G.J., Nadler L.M., Cardoso A.A.;

RT "Novel, Secreted Isoform of Human Tumor Necrosis Factor Receptor

RT Superfamily, Member 17 (TNFRSF17).";

RL Submitted (Jul-2004) to the EMBL/GenBank/DBJ databases.

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CC -----

DR EMBL: AY684975; AAV92616.1; -; mRNA.

DR GO: GO:0004872; F:receptor activity; IEA.

KW Receptor.

SQ SEQUENCE 135 AA; 14843 MW; FC31DDBB1195989 CRC64;

Query Match 100.0%; Score 201; DB 2; Length 135;

Best Local Similarity 100.0%; Pred. No. 1.3e-18;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSONEYFDSLHACIPQALRCSNTPTLCORYC 34
 DB 8 CSONEYFDSLHACIPQALRCSNTPTLCORYC 41

RESULT 2
 TNFR17 HUMAN STANDARD; PRT; 184 AA.

AC Q02223;

DT 01-JUL-1993, integrated into UniProtKB/Swiss-Prot.

DT 01-JUL-1993, sequence version 1.

DT 07-FEB-2006, entry version 59.

DE Tumor necrosis factor receptor superfamily member 17 (B-cell

DE maturation protein) (CD269 antigen).

*GN Name=TNFRSF17; Synonyms=BCM, BCMA;

*GN

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE, AND CHROMOSOMAL TRANSLOCATION.

RA Tissue=Lymph node, and Peripheral blood leukocyte;

RC MEDLINE=93010984; PubMed=1396583;

RA Laabi Y., Gros M.P., Carbonnel F., Brouet J.C., Berger R.,

RA Larsen C.-J., Tsapis A.;

RT "A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene

RT by a t(4;16)(q26;q13) translocation in a malignant T cell lymphoma.";

RL EMO J. 11:3897-3904(1992).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RA MEDLINE=94218235; PubMed=8165126;

RA Laabi Y., Gros M.P., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;

RT "The BCM gene, preferentially expressed during B lymphoid maturation,

RT is bidirectionally transcribed.";

RL Nucleic Acids Res. 22:1147-1154(1994).

RN [3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]

RA MEDLINE=99425270; PubMed=10493829; DOI=10.1006/geno.1999.5927;

RA Loftus B.J., Kim U.-J., Sneddon V.P., Kailush F., Brandon R.,

RA Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,

RA Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,

RA Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;

RT "Genome duplications and other features in 12 Mb of DNA sequence from

RT human chromosome 16p and 16q.";

RL Genomics 60:295-308(1999).

RN [4]

RP NUCLEOTIDE SEQUENCE, AND VARIANT THR-153.

RA MEDLINE=21419161; PubMed=11528522; DOI=10.1038/sj/gene/6363770;

RA Kawasaki A., Tsuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.;

RT "Presence of four major haplotypes in human BCM gene: lack of

RT association with systemic lupus erythematosus and rheumatoid

RT arthritis.";

RL Genes Immun. 2:276-279(2001).

RN [5]

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS VAL-54; VAL-65;

RA VAL-75; ASN-81 AND SER-165.

RA Livingston R.J., Rider M.J., Chung M.-W., Ritchie T.K., Olson A.N.,

RA Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.,

RA Sherwood J.K., Sherwood A.M., Leithauser B.J., Nickerson D.A.;

RT "NIH-SNPs, environmental genome project, NIHES ES15478. Department

RT of Genome Sciences, Seattle, WA (URL: <http://egp.gs.washington.edu>).";

RL Submitted (Dec-2003) to the EMBL/GenBank/DBJ databases.

RN [6]

RP FUNCTION, AND INTERACTIONS WITH TRAF1 AND TRAF3.

RA MEDLINE=20363816; PubMed=10903733;

RA Hatzioglou A., Roussel J., Bourgeade M.-F., Rogier E., Madry C.,

RA Inoue J., Devergne O., Tsapis A.;

RT "TNF receptor family member BCMA (B cell maturation) associates with

RT TNF receptor-associated factor (TRAF) 1, TRAF2, and TRAF3 and

RT activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38 mitogen-

RT activated protein kinase.";

RL J. Immunol. 165:1322-1330(2000).

RN [7]

RP FUNCTION.

RA MEDLINE=20259066; PubMed=10801128; DOI=10.1038/35010115;

RA Gross J.A., Johnston J., Mudri S., Enselman R., Dillon S.R.,

RA Madden K., Xu W., Parrish-Novak J., Foster D., Lotton-Day C.,

RA Moore M., Litalau A., Grossman A., Haugen H., Foley K., Blumberg H.,

RA Harrison K., Kindsvogel W., Clegg C.H.;

RT "TRAF1 and BCMA are receptors for a TNF homologue implicated in B-cell

RT autoimmune disease.";

RL Nature 404:995-999(2000).

RN [8]

RP FUNCTION, AND INTERACTIONS WITH APRIL AND BAFF.

RA MEDLINE=21170294; PubMed=10973284; DOI=10.1038/79802;

RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M.,

RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolima M.,

DR Ensemble: ENSG0000048462; Homo sapiens.
 DR GO: GO:0004872; F:receptor activity; IEA.
 KW Receptor.
 SQ SEQUENCE 184 AA, 20139 MW, C7ACF9940FC5531A CRC64;
 Query Match 100.0%; Score 201; DB 2; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.8e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSONEYFDSLHACIPCCRCSSNMPPLTCQRCY 34
 DB 8 CSONEYFDSLHACIPCCRCSSNMPPLTCQRCY 41

RESULT 4
 TNR17 MOUSE STANDARD; PRT, 185 AA.
 AC O88472;
 DT 27-MAY-2002, integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1998, sequence version 1.
 DT 07-FEB-2006, entry version 34.
 DE Tumor necrosis factor receptor superfamily member 17 (B-cell maturation protein).
 DE Name=tnfrsf17; Synonyms=Bcm, Bcma,
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RX MEDLINE=99061155; PubMed=9846698; DOI=10.1093/intimm/10.11.1693;
 RA Madry C, Laati Y, Callebaut I, Roussel J, Hatzoglou A,
 RA Le Contat M, Morron J.P, Berger R, Tsapis A;
 RT "The characterization of murine BCMA gene defines it as a new member
 RT of the tumor necrosis factor receptor superfamily.";
 RT Int. Immunol. 10:1693-1702(1998).
 [2]

NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
 RP STRAIN=C57BL/6J; TISSUE=Colon;
 RC PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P, Kasukawa T, Katayama S, Gough J, Fritch M.C, Maeda N,
 RA Oyama R, Ravasi R, Lenhard B, Wells C, Kodzius R, Shimokawa K,
 RA Bajic V.B, Brenner S.E, Batalov S, Forrest A.R, Zavolan M,
 RA Davis M.J, Wilming L.G, Aidinis V, Allen J.E,
 RA Abassi J, Ambrosio A, Appweiler R, Aturaliya R.N, Bailey T.L,
 RA Banal M, Baxter L, Belsel K.W, Bersano T, Bono H, Chalk A.M,
 RA Chin K.P, Choudhary V, Christofideis A, Clutterbuck D.R,
 RA Crowe M.L, Dalla E, Dalrymple B.P, de Bono B, Della Gatta G,
 RA di Bernardo D, Down T, Engstrom P, Fagioli M, Faulkner G,
 RA Flecher C.F, Fukushima T, Furum M, Futaki S, Gariboldi M,
 RA Georgii-Hemming P, Gingeras T.R, Gojobori T, Green R.E,
 RA Gusninch S, Habers M, Hayashi Y, Hensch T.K, Hirokawa N,
 RA Hill D, Hummel L, Iacono M, Ikeo K, Iwama A, Ishikawa T,
 RA Jakt M, Kanapin A, Katoh M, Kawasawa Y, Kelson J, Kitamura H,
 RA Kitano H, Kojima G, Krishnan S.P, Kruger A, Kummerfeld S.K,
 RA Kurochkin I.V, Lareau L.F, Lazarevic D, Lipovich L, Liu J,
 RA Liuni S, McMilliam S, Madan Babu M, Madera M, Marchionni L,
 RA Matcuca H, Matsuzawa S, Miki H, Mignone F, Miyake S, Morris K,
 RA Mottagui-Tabar S, Mulder N, Nakano N, Nakuchi H, Ng P,
 RA Nilsson R, Nishiguchi S, Nishikawa S, Nori F, Ohara O,
 RA Okazaki Y, Orlando V, Pang K.C, Pavan W.U, Pavese G, Pesole G,
 RA Petrovsky N, Piazza S, Reed J, Reid J.F, Ring B.Z, Ringwald M,
 RA Rost B, Ruan Y, Salzberg S.L, Sandelin A, Schneider C,
 RA Schonbach C, Sekiguchi K, Sempile C.A, Seno S, Sessa L, Sheng Y,
 RA Shibata Y, Shimada K, Shimada K, Silva D, Singhal B,
 RA Sperling S, Stupka E, Sugita K, Sultana R, Takenaka Y, Taki K,
 RA Tamanoi K, Tan S.L, Tang S, Taylor M.S, Tegner J, Teichmann S.A,
 RA Ueda H.R, van Nimwegen E, Verardo R, Wei C.L, Yangi K,
 RA Yamashiki H, Zdobych E, Zenger A, Zimmer A, Hilde M, Bult C,
 RA Grimmond S.M, Tesdale R.D, Liu E.T, Brusic V, Quekeshush J,
 RA Wahlestedt C, Wackick J.S, Hume D.A, Kai C, Sasaki D, Tomaru Y,

RA Fukuda S, Kanamori-Katayama M, Suzuki M, Aoki J, Arakawa T,
 RA Iida Y, Imamura K, Itoh M, Kawai H, Kawaguchi N,
 RA Kawashima T, Kojima M, Kondo S, Konno H, Nakano K, Niinomiya N,
 RA Nishio T, Okada M, Plessey C, Shibata K, Shiraki T, Suzuki S,
 RA Tagami M, Waki K, Wachihi A, Okamura-Ohno Y, Suzuki H, Kawai J,
 RA Hayashizaki Y;
 RT "The transcriptional landscape of the mammalian genome.";
 RT Science 309:1559-1563 (2005).
 [3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L, Feingold E.A, Grouse L.H, Derge J.G,
 RA Klausner R.D, Collins F.S, Wagner L, Shenmen G.M, Schuler G.D,
 RA Altschul S.F, Zeeberg B, Buetow K.H, Schaefer C.F, Bhat N.K,
 RA Hopkins R.F, Jordan H, Moore T, Max S.I, Wang J, Heise F,
 RA Diatchenko L, Marusina K, Farmer A.A, Rubin G.M, Hong L,
 RA Stapleton M, Soares M.B, Bonaldo M.F, Casavant T.L, Scheetz T.E,
 RA Brownstein M.J, Usslin T.B, Toshiyuki S, Carninci P, Prange C,
 RA Raha S.S, Loquellano N.A, Peters G.J, Abramson R.D, Mullany S.J,
 RA Bosak S.A, McKernan P.J, McKernan K.J, Malek J.A, Gunaratne P.H,
 RA Richards S, Worley K.C, Hale S, Garcia A.M, Gay L.J, Hulik S.W,
 RA Villalón D.K, Muzny D.M, Sodergren E.J, Lu X, Gibbs R.A,
 RA Fahy U, Helton E, Kettelman M, Madan A, Rodriguez S, Sanchez A,
 RA Whiting M, Madan A, Young A.C, Shevchenko Y, Bouffard G.G,
 RA Blakesley R.W, Touchman J.W, Green E.D, Dickson M.C,
 RA Rodriguez A.C, Grimwood J, Schmutz J, Myers R.M,
 RA Boudreghien Y.S.N, Krzywinski M.I, Skalske U, Smalins D.E,
 RA Scherch A, Schein J.E, Jones S.J.M, Marra M.A;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -I- FUNCTION: Receptor for TNFSF13B/BLyS/BAF and TNFSF13/APRIL.
 CC Promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK (By similarity).
 CC -I- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (By
 CC similarity).
 CC -I- SUBCELLULAR LOCATION: Membrane; single-pass type III membrane
 CC protein (Probable).
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=O88472-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=O88472-2; Sequence=VSP_006507;
 CC -I- TISSUE SPECIFICITY: Detected in spleen, thymus, bone marrow and
 CC heart and at lower levels in kidney and lung.
 CC -I- SIMILARITY: Contains 1 TNFR-Cys repeat.

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 CC -----

DR EMBL, AF061505; AAC37399.1; -; mRNA.
 DR EMBL, AK020247; BAB32038.1; -; mRNA.
 DR EMBL, BC027519; AAH27519.1; -; mRNA.
 DR HSSP; Q02223; 100D.
 DR Ensemble; ENSMUSG0000022496; Mus musculus.
 DR MGI; MGI:1343050; Tnfrsf17.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR InterPro; IPR001368; TNFR_C6.
 DR PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.
 DR PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.
 KW Alternative splicing; Immune response; Membrane; Receptor;
 KW Signal-anchor; Transmembrane.
 FT CHAIN 1 185
 FT Tumor necrosis factor receptor
 FT Superfamily member 17.
 FT /FTId=PRO_0000058936.
 FT TOPO_DOM 1 49
 FT Extracellular (Potential).
 FT TRANSMEM 50 70
 FT Signal-anchor for type III membrane
 FT protein (Potential).
 FT TOPO_DOM 71 185
 FT Cytoplasmic (Potential).
 FT REPEAT 4 36
 FT TNFR-Cys.
 FT DISUFID 5 18
 FT By similarity.

FT DISULFID 21 32 By similarity.
 FT DISULFID 25 36 By similarity.
 FT VARSPLIC 87 91 Missing (in isoform 2).
 FT SEQUENCE 185 AA; 20442 MW; 8806352E4FD26A8 CRC64;

Query Match 67.7%; Score 136; DB 1; Length 185;
 Best Local Similarity 70.6%; Pred. No. 7.5e-10;
 Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

Qy 1 CSQNEFYDLSLHACIPQRCSSNTPLTCRC 34
 Db 5 CFHSEYFDLSLHACKPCPKRCSN--PPATCPYC 36

RESULT 5
 088714 MOUSE
 ID 088714_MOUSE PRELIMINARY; PRT; 499 AA.
 AC 088714;
 DT 01-NOV-1998, integrated into UniProtKB/TrEMBL.
 DT 01-NOV-1998, sequence version 1.
 DT 07-FEB-2006, entry version 26.
 DE Gastric mucin-like protein (Fragment).
 GN Name=Muc6; Synonyms=gastric mucin-like;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC Tissue=Stomach;
 RA Tomasetto C., Masson R., Wendling C., Lefebvre O., Chenard M.P.,
 RA Rio M.C.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC Tissue=Stomach;
 RA Tomasetto C.L.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
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 CC EMBL; AJ010752; CA09343.1; -; mRNA.
 CC HSSP; P56682; 1CV.
 DR Ensemble; ENSMUSG00000048191; Mus musculus.
 DR MGI; MGI:2663233; Muc6.
 DR InterPro; IPR002919; Prot_Inh_CR_TTL.
 DR InterPro; IPR001846; VWF_D.
 DR Pfam; PF01826; TIL; 1.
 DR Pfam; PF00094; VMD; 1.
 DR SMART; SM00216; VMD; 1.
 FT NON_TER 1
 FT NON_TER 499
 FT SEQUENCE 499 AA; 54191 MW; 04F89EF4F23EB61E CRC64;

Query Match 36.1%; Score 72.5; DB 2; Length 499;
 Best Local Similarity 48.3%; Pred. No. 0.53;
 Matches 14; Conservative 1; Mismatches 7; Indels 7; Gaps 1;

Qy 1 CSQNEFYDLSLHACIPQRCSSNTPLT 29
 Db 430 CSQNEFYDHSSEGTVCPC-----APPT 451

RESULT 6
 080218 MOUSE
 ID 080218_MOUSE PRELIMINARY; PRT; 1674 AA.
 AC 080218;
 DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2003, sequence version 1.
 DT 07-FEB-2006, entry version 15.

DE Secreted gel-forming mucin (Fragment).
 GN Name=Muc6;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J;
 RC PubMed=14984930; DOI=10.1016/j.bbaexp.2004.01.001;
 RA Escande F., Bulsine M.P.;
 RT "The mouse secreted gel-forming mucin gene cluster."
 RL Biochim. Biophys. Acta 1676:240-250(2004).

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 CC EMBL; AJ511867; CAD54415.1; -; Genomic_DNA.
 DR EMBL; AJ511868; CAD54415.1; JOINED; Genomic_DNA.
 DR HSSP; O46162; 1KJ0.
 DR MGI; MGI:2663233; Muc6.
 DR InterPro; IPR002919; Prot_Inh_CR_TTL.
 DR InterPro; IPR006552; VWC_out.
 DR InterPro; IPR001846; VWF_D.
 DR Pfam; PF01826; TIL; 2.
 DR Pfam; PF00094; VMD; 3.
 DR SMART; SM00216; VMD; 3.
 FT NON_TER 1674
 FT SEQUENCE 1674 AA; 181170 MW; 3BC42CB004476309 CRC64;

Query Match 36.1%; Score 72.5; DB 2; Length 1674;
 Best Local Similarity 48.3%; Pred. No. 1.8;
 Matches 14; Conservative 1; Mismatches 7; Indels 7; Gaps 1;

Qy 1 CSQNEFYDLSLHACIPQRCSSNTPLT 29
 Db 1181 CSQNEFYDHSSEGTVCPC-----APPT 1202

RESULT 7
 080703 MOUSE
 ID 080703_MOUSE PRELIMINARY; PRT; 2850 AA.
 AC 080703;
 DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2003, sequence version 1.
 DT 07-FEB-2006, entry version 17.
 DE MUC6.
 GN Name=Muc6;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RC MEDLINE=22563400; PubMed=12676567; DOI=10.1016/S0888-7543(03)00036-3;
 RA Desseyn J.-L., Laine A.;
 RT "Characterization of mouse muc6 and evidence of conservation of the
 RT gel-forming mucin gene cluster between human and mouse."
 RL Genomics 81:433-436(2003).
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 CC EMBL; AY184388; AAO47735.1; -; Genomic_DNA.
 DR EMBL; AY184385; AAO47735.1; JOINED; Genomic_DNA.
 DR EMBL; AY184386; AAO47735.1; JOINED; Genomic_DNA.
 DR EMBL; AY184387; AAO47735.1; JOINED; Genomic_DNA.
 DR HSSP; O46162; 1KJ0.
 DR MGI; MGI:2663233; Muc6.
 DR InterPro; IPR006207; Cys_knot_C.

| | |
|----|---|
| RA | Tamajo A., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Ueda H.R., van Nieuwen E., Verdaro R., Wei C.L., Yagi K., Yamamoto H., Zhabrovsky B., Zhu S., Zimmer A., Hide W., Bulc C., Grimond S.W., Resdale R.D., Liu E.T., Brustle V., Quakenbush J., Wahlestedt C., Matlock J.S., Hume D.A., Kat C., Saeki D., Tomaru Y., Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Akakawa T., Iida J., Inamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Niinomiya N., Nishio T., Okada M., Plessey C., Shibata K., Shitaki T., Suzuki S., Tagami M., Waki K., Watanishi A., Okamura-Oho Y., Suzuki H., Kawai J., Hayashizaki Y., The transcriptional landscape of the mammalian genome." ; Science 309:1559-1563(2005). |
| RT | [3] |
| RL | FUNCTION. |
| RN | MEDLINE=20341628; PubMed=10860535; DOI=10.1084/jem.192.1.137; |
| RX | Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Bone T., Kelley M., Thell L.E., Colombo A., Solovlev I., Lee F., McCabe S., Elliott R., Miner K., Hawkins N., Guo Y., Stolina M., Yu G., Wang Y., Delaney J., Meng S.-Y., Boyle W.J., Hsu H.; "TAC1 is a TRAF-interacting receptor for TALL-1, a tumor necrosis factor family member involved in B cell regulation." ; J. Exp. Med. 192:137-143(2000). |
| SA | (4) |
| SB | FUNCTION. |
| SC | MEDLINE=21322748; PubMed=11429548; DOI=10.1038/89782; |
| SD | Wang H., Marceters S.A., Baker T., Chan B., Lee W.P., Xu L., Tunas D., Yang M., Dixit V.M., Ashkenazi A., Grewal I.S.; "TAC1-ligand interactions are required for T cell activation and collagen-induced arthritis in mice." ; Nat. Immunol. 2:632-637(2001). |
| SE | -1- FUNCTION: Receptor for TNFSF13/APRII and TNFSF13B/TAL1/BAPF/BLYS that binds both ligands with similar high affinity. Mediates calineurin-dependent activation of NF-AT, as well as activation of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-cell function and the regulation of humoral immunity (By similarity). |
| SF | -1- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal domain of CMLG with its C-terminus (By similarity). |
| SG | -1- SUBCELLULAR LOCATION: Membrane; single-pass type III membrane protein (Probable). |
| SH | -1- SIMILARITY: Contains 2 TNFR-Cys repeats. |
| SI | Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs license |
| SM | EMBL, AF257673; AAC00081.1; -; mRNA. |
| SN | EMBL, AK004668; BAB23457.1; -; mRNA. |
| SO | Ensembl: ENSMUSG0000010142; Mus musculus. |
| SP | MGI, MGI:1889411, Tnfrsf13b. |
| SQ | GO, GO:0009897; C:external side of plasma membrane, IDA. |
| SR | GO, GO:0005887; C:integral to plasma membrane, IDA. |
| SS | GO, GO:0001782; P:B cell homeostasis, IMP. |
| ST | GO, GO:0030889; P:negative regulation of B cell proliferation, IMP. |
| SV | InterPro: IPRO01368; TNFR_C6. |
| SW | PROSITE, PS00652; TNFR_NGFR_1, FALSE NEG. |
| SX | PROSITE, PS00650; TNFR_NGFR_2, FALSE NEG. |
| SY | Kw Immune response; Membrane; Receptor; Repeat; Signal-anchor; Transmembrane. |
| TA | CHAIN 1 249 |
| TB | superfamily member 13B. |
| TC | /FTID-PRO 0000058932. |
| TD | Extracellular (Potential). |
| TE | Signal-anchor for type III membrane protein (Potential). |
| TF | Cytoplasmic (Potential). |
| TG | TOPO_DOM 150 249 |
| TH | REPEAT 5 38 |
| TI | REPEAT 42 76 |
| TJ | DISULFID 6 19 |
| TK | DISULFID 22 34 |
| TL | DISULFID 26 38 |
| TM | DISULFID 43 52 |
| TN | DISULFID 61 72 |
| TO | By similarity. |
| TP | By similarity. |
| TP | By similarity. |
| TR | By similarity. |
| TS | By similarity. |
| TT | By similarity. |
| TU | By similarity. |
| TV | By similarity. |
| TW | By similarity. |
| TX | By similarity. |
| TY | By similarity. |
| TZ | By similarity. |
| UA | By similarity. |
| UB | By similarity. |
| UC | By similarity. |
| UD | By similarity. |
| UE | By similarity. |
| UF | By similarity. |
| UG | By similarity. |
| UH | By similarity. |
| UI | By similarity. |
| UJ | By similarity. |
| UK | By similarity. |
| UL | By similarity. |
| UM | By similarity. |
| UN | By similarity. |
| UR | By similarity. |
| US | By similarity. |
| UT | By similarity. |
| UU | By similarity. |
| UV | By similarity. |
| UX | By similarity. |
| UY | By similarity. |
| UZ | By similarity. |
| VA | By similarity. |
| VB | By similarity. |
| VC | By similarity. |
| VD | By similarity. |
| VE | By similarity. |
| VF | By similarity. |
| VG | By similarity. |
| VH | By similarity. |
| VI | By similarity. |
| VJ | By similarity. |
| VK | By similarity. |
| VL | By similarity. |
| VM | By similarity. |
| VN | By similarity. |
| VO | By similarity. |
| VP | By similarity. |
| VQ | By similarity. |
| VR | By similarity. |
| VS | By similarity. |
| VT | By similarity. |
| VU | By similarity. |
| VV | By similarity. |
| UV | By similarity. |
| UX | By similarity. |
| UY | By similarity. |
| UZ | By similarity. |
| VA | By similarity. |
| VB | By similarity. |
| VC | By similarity. |
| VD | By similarity. |
| VE | By similarity. |
| VF | By similarity. |
| VG | By similarity. |
| VH | By similarity. |
| VI | By similarity. |
| VJ | By similarity. |
| VK | By similarity. |
| VL | By similarity. |
| VM | By similarity. |
| VN | By similarity. |
| VO | By similarity. |
| VP | By similarity. |
| VQ | By similarity. |
| VR | By similarity. |
| VS | By similarity. |
| VT | By similarity. |
| VU | By similarity. |
| VV | By similarity. |
| UV | By similarity. |
| UX | By similarity. |
| UY | By similarity. |
| UZ | By similarity. |
| VA | By similarity. |
| VB | By similarity. |
| VC | By similarity. |
| VD | By similarity. |
| VE | By similarity. |
| VF | By similarity. |
| VG | By similarity. |
| VH | By similarity. |
| VI | By similarity. |
| VJ | By similarity. |
| VK | By similarity. |
| VL | By similarity. |
| VM | By similarity. |
| VN | By similarity. |
| VO | By similarity. |
| VP | By similarity. |
| VQ | By similarity. |
| VR | By similarity. |
| VS | By similarity. |
| VT | By similarity. |
| VU | By similarity. |
| VV | By similarity. |
| UV | By similarity. |
| UX | By similarity. |
| UY | By similarity. |
| UZ | By similarity. |
| VA | By similarity. |
| VB | By similarity. |
| VC | By similarity. |
| VD | By similarity. |
| VE | By similarity. |
| VF | By similarity. |
| VG | By similarity. |
| VH | By similarity. |
| VI | By similarity. |
| VJ | By similarity. |
| VK | By similarity. |
| VL | By similarity. |
| VM | By similarity. |
| VN | By similarity. |
| VO | By similarity. |
| | |

```

QY      FT DISUFID    65      76          By similarity.  

       FT CONFLICT   137    137          I -> F (in Ref. 2).  

Db      SQ SEQUENCE    249 AA; 26947 MW; CB2F2D61C2931DB1 CRC64;  

  

Query Match                                     35.6%; Score 71.5; DB 1; Length 249;  

Best Local Similarity                          35.3%; Pred. No. 0.35;  

Matches 12; Conservative                       8; Mismatches 13; Indels 1; Gaps 1;  

  

1 CSONEYFDLSLHACIPCOLRCSNTPLPTCORVC 34  

|::|||::|::|::|::|::|:  

6 CPKQDYWDSRKSCVSCALTCGQRS-QRTCTDFC 38  

  

RESULT 11  

ID OSU82 MOUSE PRELIMINARY; PRT; 249 AA.  

OSU82_1  

AC OSU82_1  

DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.  

DT 07-FEB-2006, sequence version 1.  

DE Tumor necrosis factor receptor superfamily, member 13b.  

GN Name=TNFRSF13b; ORFNames=RP23-55I2.2-001;  

OS Mus musculus (Mouse).  

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  

OC Muridae; Muridae; Murinae; Mus.  

OX NCBI_TaxID=10090;  

RN [1]  

RP NUCLEOTIDE SEQUENCE.  

RL Holt K.;  

RU Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.  

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CC -----  

CC EMBL: AL646093; CAI25896.1; ? Genomic DNA.  

DR ENSEMBL: ENSMUSG00000010142; Mus musculus.  

DR GO: GO:0004872; F:receptor activity; IEA.  

DR KW Receptor.  

SQ SEQUENCE    249 AA; 26947 MW; CB2F2D61C2931DB1 CRC64;  

  

Query Match                                     35.6%; Score 71.5; DB 2; Length 249;  

Best Local Similarity                          35.3%; Pred. No. 0.35;  

Matches 12; Conservative                       8; Mismatches 13; Indels 1; Gaps 1;  

  

1 CSONEYFDLSLHACIPCOLRCSNTPLPTCORVC 34  

|::|||::|::|::|::|::|:  

6 CPKQDYWDSRKSCVSCALTCGQRS-QRTCTDFC 38  

  

RESULT 12  

ID Q6W4X9 HUMAN PRELIMINARY; PRT; 1569 AA.  

AC Q6W4X9_1  

DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  

DT 05-JUL-2004, sequence version 1.  

DT 07-FEB-2006, entry version 10.  

DE Mucin glycoprotein (Fragment).  

DN Name=MUC6;  

OS Homo sapiens (Human).  

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  

OC Homo.  

OX NCBI_TaxID=9606;  

RN [1]  

RP NUCLEOTIDE SEQUENCE.  

RX PubMed=15081123; DOI=10.1016/j.ygeno.2003.11.003;  

RA Roussseau K., Byrne C., Kim Y.S., Gum J.R., Swallow D.M.,  

RA Toribara N.W.;  

RT "The complete genomic organization of the human MUC6 and MUC2 mucin  

genes.";  

EL genomics 83:936-939(2004).  

CC -----

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CC EMBL: AY312160; AAC82434.1; -; mRNA.
 CC DR HGNc; HGNc:7517; MUC6.
 CC DR InterPro: IPR002919; Prot_Inh_CR_TIL.
 CC DR InterPro: IPR006552; VWC_out.
 CC DR InterPro: IPR001846; VWF_D.
 CC DR Pfam: PF01826; TIL; 2.
 CC DR Pfam: PF00094; VMD; 3.
 CC DR SMART; SM00216; VMD; 3.
 CC DR NON_TER 1569 1569
 CC FT SEQUENCE 1569 AA; 168066 MW; 6AEDEE143ECB855B CRC64;
 CC SQ

Query Match 34.1%; Score 68.5; DB 2; Length 1569;
 Best Local Similarity 45.2%; Pred. No. 5.8;
 Matches 14; Conservative 2; Mismatches 8; Indels 7; Gaps 1;

Oy 1 CSQNEYPDSLHACIPQCLRCSSNTPPLTCQ 31
 Db 1179 CSQDEYFDEEGVCPWM-----PPTTPQ 1202

RESULT 13
 PCSK5_MOUSE STANDARD; PRT; 1877 AA.
 ID PCSK5_MOUSE Q04592; Q62040;
 AC Q04592; Q62040; Integrated into UniProtKB/Swiss-Prot.
 DT 01-FEB-1995, sequence version 2.
 DT 11-JAN-2001, sequence version 59.
 DT 07-MAR-2006, entry version 59.
 DE Proprotein convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-)
 DE (Protein convertase PCS5) (Subtilisin/kexin-like protease PCS5) (PC6)
 DE (Subtilisin-like proprotein convertase 6) (SPC6).
 GN Name=PCSK5;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 GN [1]
 RN NUCLEOTIDE SEQUENCE [MRNA] OF 330-1877 (ISOFORM PCSB).
 RP STRAIN=ICR; TISSUE=Intestine;
 RC MEDLINE=93327934; PubMed=8335106; DOI=10.1016/0014-5793(93)80163-O;
 RA Nakagawa T., Murakami K., Nakayama K.;
 RT "Identification of an isoform with an extremely large Cys-rich region
 of PC6, a Kex2-like processing endoprotease.";
 RT FEBS Lett. 327:165-171(1993).
 RL [2]
 RN NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM PCSA).
 RP TISSUE=Brain, and Intestine;
 RC MEDLINE=93324489; PubMed=8468318;
 RA Nakagawa T., Hosaka M., Torii S., Watanabe T., Murakami K.,
 RA Nakayama K.;
 RT "Identification and functional expression of a new member of the
 mammalian Kex2-like processing endoprotease family: its striking
 structural similarity to PACE4.";
 RT J. Biochem. 113:132-135(1993).
 RL [3]
 RN NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM PCSA).
 RP TISSUE=Adrenal cortex;
 RC MEDLINE=93342056; PubMed=831687;
 RA Lusson J., Vileau D., Hamelin J., Day R., Chretien M., Seidah N.G.;
 RT "cDNA structure of the mouse and rat subtilisin/kexin-like PCS: a
 candidate proprotein convertase expressed in endocrine and
 nonendocrine cells.";
 RT Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695(1993).
 RL [4]
 RN PARTIAL PROTEIN SEQUENCE AND SUBCELLULAR LOCATION.
 RP MEDLINE=97103178; PubMed=8947550; DOI=10.1083/jcb.135.5.1261;
 RA De Bie I., Marcinkiewicz M., Malide D., Lazure C., Nakayama K.,
 RA Bendayan M., Seidah N.G.;
 RT "The isoforms of proprotein convertase PCS are sorted to different
 subcellular compartments.";

RL J. Cell Biol. 135:1261-1275(1996).
 RN [5]
 RN DEVELOPMENTAL EXPRESSION.
 RP MEDLINE=96293359; PubMed=8698813; DOI=10.1083/jcb.134.1.181;
 RA Constam D.B., Galfon M., Robertson R.J.;
 RT "SPC4, SPC6, and the novel protease SPC7 are coexpressed with bone
 morphogenetic proteins at distinct sites during embryogenesis.";
 RL J. Cell Biol. 134:181-191(1996).
 RN [6]
 RN DEVELOPMENTAL EXPRESSION.
 RP MEDLINE=97436919; PubMed=9291583;
 RX DOI=10.1002/(SICI)1520-6408(1997)21:1<75::AID-DVG9>3.3.CO;2-T;
 RA Rancourt S.L., Rancourt D.E.;
 RT "Murine subtilisin-like proteinase SPC6 is expressed during embryonic
 implantation, somitogenesis, and skeletal formation.";
 RL Dev. Genet. 21:75-81(1997).
 CC -1- FUNCTION: Likely to represent a widespread endoprotease activity
 within the constitutive and regulated secretory pathway. Capable
 of cleavage at the RX(K/R)R consensus motif. May be responsible
 for the maturation of gastrointestinal peptides. May be involved
 in the cellular proliferation of adrenal cortex via the activation
 of growth factors.
 CC -1- CATALYTIC ACTIVITY: Release of mature proteins from their
 propeptides by cleavage of Arg-Xaa-Yaa-Arg-|-Zaa bonds, where Xaa
 can be any amino acid and Yaa is Arg or Lys.
 CC -1- SUBCELLULAR LOCATION: PCSA is secreted through the regulated
 secretory pathway. PCSB is a type I membrane protein localized to
 a paracuticular post-Golgi network compartment in communication with
 early endosomes.
 CC -1- ALTERNATIVE PRODUCTS:
 Event=Alternative splicing; Named isoforms=2;
 Comment=Additional isoforms seem to exist;
 Name=PCSB; Synonyms=Iong;
 IsoId=Q04592-1; Sequence=Displayed;
 Name=PCSA; Synonyms=Short;
 IsoId=Q04592-2; Sequence=VSP_005438, VSP_005439;
 CC -1- TISSUE SPECIFICITY: PCSA is expressed in most tissues but is most
 abundant in the intestine and adrenals. PCSB is expressed in the
 intestine, adrenals and lung but not in the brain.
 CC -1- DEVELOPMENTAL STAGE: Weakly expressed throughout the embryo,
 except in the developing nervous system, the ribs and the liver,
 but markedly up-regulated at discrete sites during development. At
 E6.5, prominent expression observed in differentiated decidua. At
 E7.5, intense expression in extraembryonic endoderm, amnion and
 nascent mesoderm. At E8.5, abundant expression in somites and yolk
 sac followed by a confinement to dermamyotome compartment. Between
 E9.5 and E11.5, abundant expression in AER (thickened ectodermal
 cells of limb buds). At E12.5, expression in the limbs is confined
 to the condensing mesenchym surrounding the cartilage. At this
 stage, strong expression also detected in vertebral and facial
 cartilage primordia and in the muscle of the tongue. At E16.5,
 abundant expression in epithelial cells of the intestinal villi.
 CC Isoform A is most abundant at all stages but significant levels of
 isoform B occur at E12.5.
 CC -1- DOMAIN: The propeptide domain acts as an intramolecular chaperone
 assisting the folding of the zymogen within the endoplasmic
 reticulum.
 CC -1- DOMAIN: AC 1 and AC 2 (clusters of acidic amino acids) contain
 sorting information. AC 1 directs TGN localization and interacts
 with the TGN sorting protein PACS-1.
 CC -1- SIMILARITY: Belongs to the peptidase S8 family.
 CC -1- SIMILARITY: Contains 1 home B/P domain.
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EMBL: D17583; BA004507.1; -; mRNA.
 EMBL: D12619; BA002143.1; -; mRNA.
 EMBL: D14932; AAA74636.1; -; mRNA.
 PIR: A48225; A48225.
 PIR: S34583; S34583.
 HSSP: P23188; 1P8J.
 MEROPS: S08.076; -.

Nat. Genet. 37:829-834(2005).

-1- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAFF/BLYS that binds both ligands with similar high affinity. Mediates calcineurin-dependent activation of NF-AT, as well as activation of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-cell function and the regulation of humoral immunity.

-1- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal domain of CAMLG with its C-terminus.

-1- INTERACTION: O75888:TNFSF13; NbExp=1; Interact=EBI-519160, EBI-519208; O92725:TNFSF13; NbExp=4; Interact=EBI-519160, EBI-519169;

-1- SUBCELLULAR LOCATION: Membrane; single-pass type III membrane protein.

-1- ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=2; Name=1; IsoId=014836-1; Sequence=Displayed;

Name=2; IsoId=014836-2; Sequence=VSP_013798;

-1- TISSUE SPECIFICITY: Highly expressed in spleen, thymus, small intestine and peripheral blood leukocytes. Expressed in resting B-cells and activated T-cells, but not in resting T-cells.

-1- DISEASE: Defects in TNFSF13B are a cause of common variable immunodeficiency (CVID) [MIM:240500]. CVID is characterized by a deficiency in all immunoglobulin (Ig) isotypes. Individuals with CVID suffer from recurrent sinopulmonary and gastrointestinal infections and have an increased incidence of autoimmune disorders and of lymphoid and nonlymphoid malignancies. There is evidence for a global isotype switching defect in some individuals with CVID. But CVID is a complex and heterogeneous disease in which defects in B-cell survival, number of circulating CD27+ memory B cells (including IgM+CD27+ B cells), B-cell activation after antigen receptor cross-linking, T-cell signaling and cytokine expression have been observed.

-1- DISEASE: Defects in TNFSF13B are a cause of immunoglobulin A deficiency 2 (IGAD2) [MIM:609529]. Selective deficiency of immunoglobulin A (IgA) is the most common form of primary immunodeficiency, with an incidence of approximately 1 in 600 individuals in the western world. Individuals with symptomatic IGAD often have deficiency of IgG subclasses or decreased antibody response to carbohydrate antigens such as pneumococcal polysaccharide vaccine. Individuals with IGAD also suffer from recurrent sinopulmonary and gastrointestinal infections and have an increased incidence of autoimmune disorders and of lymphoid and nonlymphoid malignancies. In vitro studies have suggested that some individuals with IGAD have impaired isotype class switching to IgA and others may have a post-switch defect. IGAD and CVID have been known to coexist in families. Some individuals initially present with IGAD1 and then develop CVID. These observations suggest that some cases of IGAD and CVID may have a common etiology.

-1- SIMILARITY: Contains 2 TNFR-Cys repeats.

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EMBL; AF023614; AAC51790.1; -; mRNA.
 EMBL; AY302137; AAP57629.1; -; mRNA.
 PDB; 1XU1; X-ray; R/S/T=68-109.
 PDB; 1XUT; NMR; A=68-109.
 Interact: O14836; -
 Ensembl; ENSG00000108516; Homo sapiens.
 HGNC; HGNC:18153; TNFSF13B.
 MIM; 240500; phenotype.
 MIM; 609529; gene.
 MIM; 609529; phenotype.
 GO; GO:0005887; C:integral to plasma membrane; TAS.
 GO; GO:0005515; F:protein binding; IP.
 GO; GO:0004872; F:receptor activity; TAS.
 GO; GO:0007166; F:cell surface receptor linked signal transdu. .; TAS.
 InterPro; IPR001368; TNFR_C6.
 PROSITE; PS00652; TNFR_NGFR_1; 1.
 PROSITE; PS00650; TNFR_NGFR_2; FALSE_NEG.

KM 3D-structure; Alternative splicing; Disease mutation; Glycoprotein;
 KW Immune response; Membrane; Receptor; Repeat; Signal-anchor;
 KW Transmembrane.
 FT CHAIN 1 293 Tumor necrosis factor receptor
 FT TOPO_DOM 1 165 /FTId=PRO_000058931.
 FT TRANSMEM 166 186 Extracellular (Potential).
 FT TOPO_DOM 187 293 Signal-anchor for type III membrane
 FT REPEAT 33 67 protein (Potential).
 FT REPEAT 70 104 Cytoplasmic (Potential).
 FT CARBOHYD 128 128 TNFR-Cys 1.
 FT DISULFID 34 47 N-linked (GlcNAc...) (Potential).
 FT DISULFID 50 62 By similarity.
 FT DISULFID 54 66 By similarity.
 FT DISULFID 71 86 By similarity.
 FT DISULFID 89 100
 FT DISULFID 93 104
 FT VARSPLIC 21 67
 FT VARIANT 104 104 PPGIMTGVAMRSCPEQYWDPLIGTMCCKTICNHOSQRT
 FT VARIANT 181 181 CAAPCR -> W (in isoform 2).
 FT VARIANT 202 202 /FTId=VSP_013798.
 FT STRAND 66 66 C -> R (in CVID and IGAD2).
 FT TURN 67 68 /FTId=VAR_024027.
 FT HELIX 73 75 A -> G (in CVID).
 FT TURN 76 76 /FTId=VAR_024028.
 FT STRAND 77 80 R -> H (in CVID).
 FT TURN 81 84 /FTId=VAR_024029.
 FT STRAND 85 88
 FT HELIX 89 92
 FT TURN 93 94
 FT STRAND 95 95
 FT HELIX 98 104
 SQ SEQUENCE 293 AA; 31816 MW; 411799F3DE17A5EB CRC64;

Query Match 33.1%; Score 66.5; DB 1; Length 293;
 Best Local Similarity 32.4%; Pred. No. 1.9;
 Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSONEYFDLSLHACIPCOLRCSNTPPTCORYC 34
 DB 34 CPREGYWDPLIGTMCCKTICNHOS-QRTCAAPC 66

RESULT 15
 Q4ACX1 HUMAN PRELIMINARY; PRT; 293 AA.
 ID Q4ACX1
 AC Q4ACX1
 DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
 DT 13-SEP-2005, sequence version 1.
 DT 07-FEB-2006, entry version 2.
 DE TACI.
 DE Name=TACI;
 OS Homo sapiens (Human).
 OS Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Eukaryota; Metazoa; Chordata; Euteleostomi; Primates; Catarrhini; Hominiidae;
 OC Homo.
 OC NCBI_TaxId=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Kawasaki A., Tsuchiya N., Kusaoi M., Murakami Y., Fukazawa T.,
 RA Matsuda K., Hashimoto H., Tokunaga K.,
 RT "New polymorphisms of human BAFF-R gene."
 RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
 RP NUCLEOTIDE SEQUENCE.
 RA Kawasaki A., Tsuchiya N., Kusaoi M., Murakami T., Fukazawa T.,

RA Matsuta H., Hashimoto H., Tokunaga K.;
 RT "New polymorphisms of human TAC1 gene."
 RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL: AB222991; BAE16555.1; -; Genomic_DNA.
 DR InterPro: IPR001368; TNFR_c6.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN 1.
 SQ SEQUENCE 293 AA; 31816 MW; 4117993DE17A5EB CRC64;
 QY Query Match 33.1%; Score 66.5; DB 2; Length 293;
 DB Best Local Similarity 32.4%; Pred. No. 1.9;
 Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;
 QY 1 CSQNEYFDSLHACIPQQLRCSSNTPPLTCQRYC 34
 DB 34 CPBEQYMDPLGTGCMSCKTICNHOS-QRTCAAF 66
 RESULT 16
 Q53F36 HUMAN PRELIMINARY; PRT; 293 AA.
 AC Q53F36;
 DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 24-MAY-2005, sequence version 1.
 DT 07-FEB-2006, entry version 4.
 DE Tumor necrosis factor receptor 13B variant (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Small intestine;
 RX MEDLINE=94171032; PubMed=8125298; DOI=10.1016/0378-1119(94)90802-8;
 RA Maruyama K., Sugano S.;
 RT "Oligo-capping: a simple method to replace the cap structure of
 RT eucaryotic mRNAs with oligoribonucleotides."
 RL Gene 138:171-174(1994).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Small intestine;
 RX MEDLINE=98038986; PubMed=9373149; DOI=10.1016/S0378-1119(97)00411-3;
 RA Suzuki Y., Yoshimoto K., Maruyama K., Sugano S.;
 RT "Construction and characterization of a full length-enriched and a 5'-
 RT end-enriched cDNA library."
 RL Gene 200:149-156(1997).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Small intestine;
 RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL: AK223453; BAD97173.1; -; mRNA.
 DR Ensembl: ENSG00000108516; Homo sapiens.
 DR GO: GO:0004872; F:receptor activity; IEA.
 DR InterPro: IPR001368; TNFR_c6.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN 1.
 KW Receptor.
 FT NON TER 1
 SQ SEQUENCE 293 AA; 31846 MW; D9EA2F28B3BF466D CRC64;
 QY Query Match 33.1%; Score 66.5; DB 2; Length 293;
 DB Best Local Similarity 32.4%; Pred. No. 1.9;
 Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;
 QY 1 CSQNEYFDSLHACIPQQLRCSSNTPPLTCQRYC 34

DB 34 CPBEQYMDPLGTGCMSCKTICNHOS-QRTCAAF 66
 RESULT 17
 Q7R6J7 GIALA PRELIMINARY; PRT; 1025 AA.
 ID Q7R6J7;
 AC Q7R6J7;
 DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
 DT 15-DEC-2003, sequence version 1.
 DT 07-FEB-2006, entry version 16.
 DE GLP_170_141434_144511.
 OS Giardia lamblia ATCC 50803.
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardinales; Giardia.
 OX NCBI_TaxID=184922;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=WB c6;
 RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
 RA Olsen G.J., Sogin M.L.;
 RT "Draft sequence of the Giardia lamblia genome."
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -----
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 CC -----
 DR EMBL: AACB01000001; EAA33000.1; -; Genomic_DNA.
 DR HSSP: Q9S7B3; 1EHD.
 DR InterPro: IPR006210; EGF.
 DR InterPro: IPR002049; EGF_laminin.
 DR InterPro: IPR006212; Furin_repeat.
 DR SMART: SM00261; FU; 2.
 DR PROSITE: PS01248; EGF_LAM_1; UNKNOWN 1.
 SQ SEQUENCE 1025 AA; 109045 MW; 36281DF3FE2DD843 CRC64;
 QY Query Match 32.6%; Score 65.5; DB 2; Length 1025;
 DB Best Local Similarity 36.1%; Pred. No. 9.4;
 Matches 13; Conservative 5; Mismatches 13; Indels 5; Gaps 1;
 QY 1 CSQNEYFDSLHACIPQQLRCSSNTPPLTCQ 31
 DB 79 CTDDFYLDLFGFCFSCHSSCSTCGSPSHFDCLTCR 114
 RESULT 18
 Q99ND0 MOUSE PRELIMINARY; PRT; 5374 AA.
 ID Q99ND0;
 AC Q99ND0;
 DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2001, sequence version 1.
 DT 07-FEB-2006, entry version 22.
 DE ZAN (Zonadhesin).
 GN Name=Zan;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=129/Sv;
 RX MEDLINE=21138439; PubMed=11239002; DOI=10.1093/nar/29.6.1352;
 RA Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,
 RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
 RA Miller W., Koop B.F.;
 RT "Comparative analysis of the gene-dense ACHE/TPR2 region on human
 RT chromosome 7q22 with the orthologous region on mouse chromosome 5."
 RL Nucleic Acids Res. 29:1352-1365(2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.

| | |
|--------------------------|--|
| RA | STRAIN=129/SV; |
| RC | Chung T.L., Wilson M.D., Koop B.F., Hardy D.M.; et al. |
| RL | Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases. |
| CC | ----- |
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| CC | Distributed under the Creative Commons Attribution-NoDerivs license |
| CC | ----- |
| DR | EMBL; AF312033; AAK28824.1; -; Genomic DNA. |
| DR | EMBL; AY046056; AAL04416.1; -; Genomic DNA. |
| DR | HSSP; Q90248; IHX2. |
| DR | Ensembl; ENSMUSG0000005973; Mus musculus. |
| DR | GO; GO:0016020; C:membrane; IEA. |
| DR | GO; GO:0007339; P:binding of sperm to zona pellucida; IEA. |
| DR | InterPro; IPR006210; EGF. |
| DR | InterPro; IPR006209; EGF_3. |
| DR | InterPro; IPR013032; EGF_like. |
| DR | InterPro; IPR03645; FOL_N. |
| DR | InterPro; IPR00998; MAM. |
| DR | InterPro; IPR002919; Prot_Inh_CR_TIL. |
| DR | InterPro; IPR003328; Tila_Cystich. |
| DR | InterPro; IPR005552; VMC_out. |
| DR | InterPro; IPR01007; VWF_C. |
| DR | InterPro; IPR001846; VWF_D. |
| DR | Pfam; PF02363; C_triplex; 20. |
| DR | Pfam; PF03128; CXCX; 11. |
| DR | Pfam; PF00008; EGF_1. |
| DR | Pfam; PF00629; MAM; 3. |
| DR | Pfam; PF01826; TIL; 25. |
| DR | Pfam; PF02345; TIL_assoc; 25. |
| DR | Pfam; PF00994; VMD; 4. |
| DR | SMART; SM00181; EGF; 2. |
| DR | SMART; SM00214; VMC; 18. |
| DR | SMART; SM00215; VMC_out; 1. |
| DR | SMART; SM00216; VMD; 4. |
| DR | PROSITE; PS00022; EGF_1; UNKNOWN_1. |
| DR | PROSITE; PS01186; EGF_2; 18. |
| DR | PROSITE; PS00026; EGF_3; 1. |
| DR | PROSITE; PS00740; MAM_1; 1. |
| DR | PROSITE; PS00060; MAM_2; 3. |
| SQ | SEQUENCE 5374 AA; 579550 MW; 90D2D8CFE5DE24EB CRC64; |
| | |
| Query Match | 32.1%; Score 64.5; DB 2; Length 5374; |
| Best local Similarity | 35.1%; Pred. No.70; |
| Matches 13; Conservative | 5; Mismatches 16; Indels 3; Gaps 2; |
| OY | 1 GSONEYPDSLTHACIP-CQLRCSNTP--PLTCQRVC 34 : : : : |
| Db | 3298 CPTNSGFTDCLPSCVPSCSNRCEVTSPGVSPSCRGCG 3334 |
| | |
| RESULT 19 | |
| ID_ZAN_MOUSE | STANDARD; PRT; 5376 AA. |
| AC | O08799; O08647; |
| CD | O08799; O08647; |
| DT | 27-APR-2001, integrated into UniProtKB/Swiss-Prot. |
| DT | 01-NOV-1998, sequence version 1. |
| DT | 07-MAR-2006, entry version 50. |
| DE | Zonadhesin precursor. |
| GN | Name=Zan; |
| OS | Mus musculus (Mouse); |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| OC | Mammalia; Murielia; Euarchontoglires; Glires; Rodentia; Sciurognathi; |
| OC | Muridea; Muridae; Murinae; Mus. |
| OX | NCBI_TaxID=10090; |
| RN | [1] |
| RP | NUCLEOTIDE SEQUENCE [mRNA]. |
| RC | Tissue=Testis; |
| RX | MEHLIN=98123114; PubMed=9452463; DOI=10.1074/jbc.273.6.3415; |
| RA | Gao Z., Garbers D.L.; |
| RT | "Species diversity in the structure of zonadhesin, a sperm-specific membrane protein containing multiple cell adhesion molecule-like |

| | |
|----|--|
| RT | domains."; |
| RN | J. Biol. Chem. 273:3415-3421(1998). |
| RN | [2] |
| RP | NUCLEOTIDE SEQUENCE [mRNA] OF 4864-5376. |
| RC | TSSUSE=Testis; |
| RX | MEDLINE=97271566; PubMed=9126492; DOI=10.1006/geno.1997.4620; |
| RA | Gao Z., Haximi T., Garbers D.L.; |
| RT | "Chromosome localization of the mouse zonadhesin gene and the human |
| RL | zonadhesin gene (ZAN)."; |
| CC | Genomics 41:119-122(1997). |
| CC | -1- FUNCTION: Binds in a species-specific manner to the zona pellucida |
| CC | of the egg. May be involved in gamete recognition and/or |
| CC | signaling. |
| CC | -1- SUBUNIT: Probably forms covalent oligomers. |
| CC | -1- SUBCELLULAR LOCATION: Type I membrane protein, exclusively on the |
| CC | apical region of the sperm head. |
| CC | -1- TISSUE SPECIFICITY: In testis, primarily in haploid spermatids. |
| CC | -1- DOMAIN: The MAM domains probably mediates sperm adhesion to the |
| CC | zona pellucida. |
| CC | -1- DOMAIN: During sperm migration through the reproductive tracts, |
| CC | the muchn-like domain might inhibit inappropriate trapping of |
| CC | spermatozoa or promoting adhesion to the oviductal isthmus. |
| CC | -1- DOMAIN: The VWFD domain 2 may mediate covalent oligomerization (By |
| CC | similarity). |
| CC | -1- SIMILARITY: Contains 1 EGF-like domain. |
| CC | -1- SIMILARITY: Contains 3 MAM domains. |
| CC | -1- SIMILARITY: Contains 25 VWFD domains. |
| CC | ----- |
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| CC | Distributed under the Creative Commons Attribution-NoDerivs License |
| CC | ----- |
| DR | EMBL, U97068; AAC26680.1; -; mRNA. |
| DR | EMBL, U83190; AAC3125.1; -; mRNA. |
| DR | HIS, T42215; T42215. |
| DR | PIR, Q90248; IHX2. |
| DR | MGI, MGI:106565; Zan. |
| DR | GO, GO:0005615; C:extracellular space; TAS. |
| DR | GO, GO:0016021; C:integral to membrane; TAS. |
| DR | InterPro: IPRO06210; EGF_3. |
| DR | InterPro: IPRO00742; EGF_3. |
| DR | InterPro: IPRO06209; EGF-like. |
| DR | InterPro: IPRO13032; EGF-like_reg. |
| DR | InterPro: IPRO03645; FOL_N. |
| DR | InterPro: IPRO00998; MAM. |
| DR | InterPro: IPRO02919; Prot_Inh_CR_TTL. |
| DR | InterPro: IPRO03328; TILA_Cystich. |
| DR | InterPro: IPRO06552; VWC_out. |
| DR | InterPro: IPRO01846; VWF_D. |
| DR | Pfam: PF02363; C triplex; 18. |
| DR | Pfam: PF03128; CXCX; 11. |
| DR | Pfam: PF00008; EGF_1. |
| DR | Pfam: PF00629; MAM_3. |
| DR | Pfam: PF01826; TTL_25. |
| DR | Pfam: PF02345; TTL_assoc; 25. |
| DR | Pfam: PF00094; VMD_4. |
| DR | SMART: SM00181; EGF; 2. |
| DR | SMART: SM00214; VWC; 17. |
| DR | SMART: SM00215; VWC_out; 1. |
| DR | SMART: SM00216; VMD; 4. |
| DR | PROSITE: PS00022; EGF_1; 1. |
| DR | PROSITE: PS00186; EGF_2; 18. |
| DR | PROSITE: PSS0026; EGF_3; 1. |
| DR | PROSITE: PS00740; MAM_1; 1. |
| DR | PROSITE: PSS0060; MAM_2; 3. |
| KW | Cell adhesion; EGF-like domain; Glycoprotein; Membrane; Repeat; |
| KW | Signal; Transmembrane. |
| FT | SIGNAL 1 17 Potential. |
| FT | CHAIN 18 5376 Zonadhesin. |
| FT | TOPO_DOM 18 5310 /FTID=PRO_0000007784. |
| FT | TRANSMEM 5311 5337 Extracellular (Potential). |
| FT | TOPO_DOM 5338 5376 Cytoplasmic (Potential). |

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FT DOMAIN 45 210 MAM 1.
FT DOMAIN 215 374 MAM 2.
FT DOMAIN 377 542 MAM 3.
FT DOMAIN 1171 1280 WFMD 1; truncated.
FT DOMAIN 1281 1669 WFMD 2.
FT DOMAIN 1670 2056 WFMD 3.
FT DOMAIN 2057 2459 WFMD 4.
FT DOMAIN 2460 2579 WFMD 5; truncated.
FT DOMAIN 2580 2699 WFMD 6; truncated.
FT DOMAIN 2700 2819 WFMD 7; truncated.
FT DOMAIN 2820 2939 WFMD 8; truncated.
FT DOMAIN 2940 3059 WFMD 9; truncated.
FT DOMAIN 3060 3179 WFMD 10; truncated.
FT DOMAIN 3180 3299 WFMD 11; truncated.
FT DOMAIN 3300 3416 WFMD 12; truncated.
FT DOMAIN 3417 3536 WFMD 13; truncated.
FT DOMAIN 3537 3656 WFMD 14; truncated.
FT DOMAIN 3657 3776 WFMD 15; truncated.
FT DOMAIN 3777 3892 WFMD 16; truncated.
FT DOMAIN 3893 4028 WFMD 17; truncated.
FT DOMAIN 4029 4148 WFMD 18; truncated.
FT DOMAIN 4149 4263 WFMD 19; truncated.
FT DOMAIN 4264 4383 WFMD 20; truncated.
FT DOMAIN 4384 4503 WFMD 21; truncated.
FT DOMAIN 4504 4623 WFMD 22; truncated.
FT DOMAIN 4624 4743 WFMD 23; truncated.
FT DOMAIN 4744 4863 WFMD 24; truncated.
FT DOMAIN 4864 5261 WFMD 25.
FT DOMAIN 5259 5295 BGF-like.
FT REGION 547 1170 80 x heptapeptide repeats (approximate)
                        (mucin-like domain).
FT CARBOHYD 339 339 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 499 499 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 1216 1216 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 1239 1239 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 1314 1314 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 1814 1814 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 1908 1908 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 1933 1933 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 2028 2028 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 2111 2111 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 2142 2142 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 2332 2332 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 2533 2533 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 2575 2575 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 2692 2692 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 2812 2812 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 3052 3052 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 3065 3065 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 3144 3144 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 3172 3172 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 3288 3288 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 3292 3292 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 3782 3782 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 4005 4005 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 4136 4136 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 4243 4243 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 4254 4254 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 4335 4335 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 4376 4376 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 4566 4566 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 5136 5136 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 5252 5252 N-linked (GlcNAc...) (Potential)
FT DISULFID 5263 5274 By similarity.
FT DISULFID 5268 5283 By similarity.
FT DISULFID 5285 5294 By similarity.
SQ SEQUENCE 5376 AA; 579913 MW; 0E44DB77DF2A2620 CRC64;

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Query Match 32.1%; Score 64.5; DB 1; Length 5376;
 Best Local Similarity 35.1%; Pred. No. 70;
 Matches 13; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

1 CSQNEYPDSLHACIP-COLRCSSNTP--PLTCQRYC 34

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Db. 3300 CPTNSQFTDCLPSCVPSCSNRCVTPSPVPSSCREGC 3336
RESULT 20
ID Q410Y5_GIBZE PRELIMINARY; PRT; 762 AA.
AC Q410Y5;
DT 16-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Hypothetical protein.
GN ORFNames=FG09123.1;
OS Gibberella zeae (Fusarium graminearum).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocorymceetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_Taxid=5518;
RN
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=PH-1 / NRRL 31084;
RA Birren B.W., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,
RA Boukhgelter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., Dearellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D.,
RA Galagan J.E., Gardyna S., Gnerre S., Graham L., Grand-Pierre N.,
RA Hafez N., Hagopian D., Hagos B., Hall J., Horton L., Hulme W.,
RA Iliev I., Jaffe D., Johnson R., Jones C., Kamai M., Kamat A.,
RA Karacas A., Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G.,
RA Lui A., Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J.,
RA Manning J., Matthews C., Mauceli E., McCarthy M., Meldrum J.,
RA Menues L., Mihova T., Mienga V., Murphy T., Naylor J., Nguyen C.,
RA Nicol R., Nielsen C.B., Norbu C., O'Connor T., O'Donnell P.,
RA O'Neill D., Oliver J., Peterson K., Phunhthang P., Pierre N.,
RA Purcell S., Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C.,
RA Rogov P., Roman J., Schauer S., Schuback R., Seaman S., Severy P.,
RA Smitrov S., Smith C., Spencer B., Stange-Thomann N., Stojanovic N.,
RA Stubbs M., Talamas J., Testafy S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Zander E.S.;
RT Fusarium graminearum genome sequence.
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
EMBL: AACM01000370; EAA7813.1; -, Genomic DNA.
DR GO:GO:0005634; C:nucleus, IEA.
DR GO:GO:0046872; F:metal ion binding, IEA.
DR GO:GO:0003700; F:transcription factor activity, IEA.
DR GO:GO:0008270; F:zinc ion binding, IEA.
DR GO:GO:0006355; P:regulation of transcription, DNA-dependent, IEA.
DR GO:GO:0006350; P:transcription, IEA.
DR InterPro: IPR001138; Fungi_Trcsrp_N.
DR Pfam: PF04082; Fungal_transf; 1.
DR Pfam: PF00172; Zn_c1us; 1.
DR SMART: SM00066; GAL4; 1.
DR PROSITE: PS50048; ZN2_Cy6_FUNGAL_2; 1.
KW Complete proteome; DNA-binding; Hypothetical protein; Metal-binding;
KW Nuclear protein; Transcription; Transcription regulation; Zinc.
SQ SEQUENCE 762 AA; 84756 MW; 55B25D037F21A35A CRC64;

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Query Match 31.8%; Score 64; DB 2; Length 762;
 Best Local Similarity 43.3%; Pred. No. 11;
 Matches 13; Conservative 3; Mismatches 6; Indels 8; Gaps 2;

13 ACIPQ---LRCSSNTPPLTCOR-----YC 34

Db 17 ACVPCONSKKRCDSQSPANCRRDIPYC 46

RESULT 21
ID Q50LY7_ENTHI PRELIMINARY; PRT; 799 AA.
AC Q50LY7_ENTHI
DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 07-JUN-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Protein Kinase, putative (Fragment).
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
NCBI_TaxID=294381;

RA NUCLEOTIDE SEQUENCE.
RP STRAIN=HM-1:IMSS;
RC PubMed=15729342; DOI=10.1038/nature03291;
RX Lotfus B.J., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
Amedeo P., Roncaglia P., Bertrian M., Hirt R.P., Mann B.J., Nozaki T.,
Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,
Chillingworth T., Churcher C.M., Hance Z., Harris B., Harris D.,
Jagels K., Moule S., Mungall K.L., Ormond D., Squares R.,
Whitehead S., Quail M.A., Rabinowitsch E., Norbertczak H., Price C.,
Wang Z., Guillen N., Gluchrist C., Stroup S.E., Bhattacharya S.,
Lohia A., Foster P.G., Sichteritz-Ponten T., Weber C., Singh U.,
Mukherjee C., El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M.,
Barrell B.G., Fraser C.M., Hall N.;
RT "The genome of the protist parasite Entamoeba histolytica."
RL Nature 433:865-868(2005).
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

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CC
EMBL: AAFB01001427; EAL42605.1; -; Genomic_DNA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0000166; F:nucleotide binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR006212; Furin_repeat.
DR InterPro: IPR000719; Prot_Kinase.
DR InterPro: IPR008271; Ser_Thr_kin_AS.
DR InterPro: IPR002290; Ser_Thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00069; Kinase_1.
DR PRINTS: PR00109; TKKINASE.
DR ProDom: PD000001; Prot_Kinase; 1.
DR SMART: SMO0261; FU; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KM ATP-binding; Kinase; Nucleotide-binding;
KM Serine/threonine-protein kinase; Transferase.
FT NON TER 1
SQ SEQUENCE 799 AA; 91662 MW; D8BFE2F2E235989E CRC64;

Query Match 31.6%; Score 63.5; DB 2; Length 799;
Best Local Similarity 35.3%; Pred. No. 13;
Matches 12; Conservative 5; Mismatches 14; Indels 3; Gaps 1;

QY 1 CSQNEYPDSLHACIPQC---LRCSNTPPLTQC 31
DB 137 CODNYVDKELQSCVGCSSSECLTCSNKDICTCK 170

RESULT 22
ID Q50Y51_ENTHI PRELIMINARY; PRT; 802 AA.
AC Q50Y51_ENTHI
DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 07-JUN-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE CXXC-rich protein (Fragment).
GN ORFNames=141.t00017;
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
NCBI_TaxID=294381;

RA NUCLEOTIDE SEQUENCE.
RP STRAIN=HM-1:IMSS;
RC PubMed=15729342; DOI=10.1038/nature03291;
RX Lotfus B.J., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
Amedeo P., Roncaglia P., Bertrian M., Hirt R.P., Mann B.J., Nozaki T.,
Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,
Chillingworth T., Churcher C.M., Hance Z., Harris B., Harris D.,
Jagels K., Moule S., Mungall K.L., Ormond D., Squares R.,
Whitehead S., Quail M.A., Rabinowitsch E., Norbertczak H., Price C.,
Wang Z., Guillen N., Gluchrist C., Stroup S.E., Bhattacharya S.,
Lohia A., Foster P.G., Sichteritz-Ponten T., Weber C., Singh U.,
Mukherjee C., El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M.,
Barrell B.G., Fraser C.M., Hall N.;
RT "The genome of the protist parasite Entamoeba histolytica."
RL Nature 433:865-868(2005).
CC -!- CAUTION: The sequence shown here is derived from an
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CC
EMBL: AAFB01000471; EAL46536.1; -; Genomic_DNA.
DR InterPro: IPR006212; Furin_repeat.
DR SMART: SMO0261; FU; 2.
FT NON TER 1
SQ SEQUENCE 802 AA; 90127 MW; 1425BF8514DED237 CRC64;

Query Match 31.6%; Score 63.5; DB 2; Length 802;
Best Local Similarity 35.3%; Pred. No. 13;
Matches 12; Conservative 5; Mismatches 14; Indels 3; Gaps 1;

QY 1 CSQNEYPDSLHACIPQC---LRCSNTPPLTQC 31
DB 654 CODNYVDKELQSCVGCSSSECLTCSNKDICTCK 687

RESULT 23
ID Q50PT4_ENTHI PRELIMINARY; PRT; 1150 AA.
AC Q50PT4_ENTHI
DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 07-JUN-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Receptor protein kinase, putative.
GN ORFNames=359.t00009;
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
NCBI_TaxID=294381;

RA NUCLEOTIDE SEQUENCE.
RP STRAIN=HM-1:IMSS;
RC PubMed=15729342; DOI=10.1038/nature03291;
RX Lotfus B.J., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
Amedeo P., Roncaglia P., Bertrian M., Hirt R.P., Mann B.J., Nozaki T.,
Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,
Chillingworth T., Churcher C.M., Hance Z., Harris B., Harris D.,
Jagels K., Moule S., Mungall K.L., Ormond D., Squares R.,

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RA Whitehead S., Quail M.A., Rabinowitsch E., Norbertczak H., Price C.,
RA Wang Z., Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S.,
RA Lohia A., Foster P.G., Sichert-Ponten T., Weber C., Singh U.,
RA Mukherjee C., El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M.,
RA Barrell B.G., Fraser C.M., Hall N., Entamoeba histolytica."
RT "The genome of the protist parasite Entamoeba histolytica."
CC CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC CC preliminary data.
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CC CC -----
DR DR EMBL, AAFB01000933; EAL43605.1; -; Genomic_DNA.
DR DR GO, GO:0005524; F:ATP binding; IEA.
DR DR GO, GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR DR GO, GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR DR GO, GO:0004872; F:receptor activity; IEA.
DR DR GO, GO:0006468; P:protein amino acid phosphorylation; IEA.
DR DR InterPro, IPR006212; Furin repeat.
DR DR InterPro, IPR000719; Prot Kinase.
DR DR InterPro, IPR008271; Ser_thr_kin_AS.
DR DR InterPro, IPR002290; Ser_thr_kinase.
DR DR Pfam, PF02420; Afp, 1.
DR DR Pfam, PF00069; Pkinase, 1.
DR DR PRINTS, PR00109; TYRKINASE.
DR DR ProDom, PD000001; Prot_kinase, 1.
DR DR SMART, SM00261; FU, 1.
DR DR PROSITE, PS00107; PROTEIN_KINASE_ATP, 1.
DR DR PROSITE, PS00011; PROTEIN_KINASE_DOM, 1.
DR DR PROSITE, PS00108; PROTEIN_KINASE_ST, 1.
KW Kinase; Receptor.
SQ SEQUENCE 1150 AA; 128939 MW; 0DBE7051D4B4E286 CRC64;

Query Match 31.3%; Score 63; DB 2; Length 1150;
Best Local Similarity 36.7%; Pred. No. 23;
Matches 11; Conservative 3; Mismatches 16; Indels 0; Gaps 0;

QY 1 CSONEYFDSLHACIPCOLRCSNTPPLTC 30
DB 138 CGINEYFVSKLCLPCKTCRCRCSAONC 167

RESULT 24
Q2UIG2_ASPOR PRELIMINARY; PRT; 442 AA.
ID Q2UIG2;
AC Q2UIG2;
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 3.
DE Predicted protein.
GN ORFNames=AO090023000067;
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eucuriales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RIB 40;
RX PubMed=16372010; DOI=10.1038/nature04300;
RA Machida M., Asai K., Sano M., Tanaka T., Kunagai T., Terai G.,
RA Kusumoto K., Arima T., Akita O., Kashiwagi Y., Abe K., Gomi K.,
RA Horiuchi H., Kitamoto K., Kobayashi T., Takeuchi M., Denning D.W.,
RA Galagan J.E., Nierman W.C., Yu J., Archer D.B., Bennett J.W.,
RA Bhattacharya D., Cleveland T.E., Fedotova N.D., Gotch O., Horikawa H.,
RA Hosoyama A., Ichihomiyama M., Igarashi R., Iwashita K., Juvvadi P.R.,
RA Kato M., Kato Y., Kin T., Kokubun A., Maeda H., Maeyama N.,
RA Maruyama J., Nagasaki H., Nakajima T., Oda K., Okada K., Paulsen I.,
RA Sakamoto K., Sawano T., Takahashi M., Takase K., Terabayashi Y.,
RA Mortman J.R., Yamada O., Yamagata Y., Anazawa H., Hata Y., Koide Y.,
RA Komori T., Koyama Y., Minekoki T., Suharnan S., Tanaka A., Isono K.,

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RA Kuhara S., Ogasawara N., Kikuchi H.;
RT "Genome sequencing and analysis of Aspergillus oryzae."
RT Nature 438:1157-1161(2005).
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CC CC -----
DR DR EMBL, AP007157; BAE58653.1; -; Genomic_DNA.
DR DR SEQUENCE 442 AA; 49080 MW; 7877DD025B08CA3 CRC64;
SQ SEQUENCE 442 AA; 49080 MW; 7877DD025B08CA3 CRC64;

Query Match 31.1%; Score 62.5; DB 2; Length 442;
Best Local Similarity 42.4%; Pred. No. 9.8;
Matches 14; Conservative 7; Mismatches 11; Indels 1; Gaps 1;

QY 2 SONEYFD-SLHACIPCOLRCSNTPPLTC 33
DB 356 ADEBAFVSMHACRAGQLKLSVPEVYHQYF 388

RESULT 25
Q7QGV0_ANOGA PRELIMINARY; PRT; 1294 AA.
ID Q7QGV0;
AC Q7QGV0;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 07-DEC-2004, sequence version 2.
DT 07-FEB-2006, entry version 13.
DE ENSANGP00000012534 (Fragment).
GN ORFNames=ENSANG00000010045;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae re-annotation."
RT Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
CC CC -!- CAUTION: The sequence shown here is derived from an
CC CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
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DR DR EMBL, AAB01008823; EAA0574.2; -; Genomic_DNA.
DR DR GO, GO:0016020; C:membrane; IEA.
DR DR GO, GO:0008565; F:protein transporter activity; IEA.
DR DR GO, GO:0006886; P:intracellular protein transport; IEA.
DR DR InterPro, IPR006210; EGF.
DR DR InterPro, IPR002860; Glyco_hydro_BNR.
DR DR InterPro, IPR002172; LDL_rcpt_A.
DR DR InterPro, IPR000033; LDLR.
DR DR InterPro, IPR006581; VPS10.
DR DR Pfam, PF02012; BNR, 6.
DR DR Pfam, PF00057; Ldl_recept_a, 7.
DR DR Pfam, PF00058; Ldl_recept_b, 4.
DR DR PRINTS, PR00261; LDLRECEPTOR.
DR DR SMART, SM00181; EGF, 1.
DR DR SMART, SM00192; LDLR, 7.
DR DR SMART, SM00135; LY, 2.
DR DR SMART, SM00602; VPS10, 1.
DR DR PROSITE, PS01209; LDLRA_1, 5.
DR DR PROSITE, PS00068; LDLRA_2, 5.
DR DR PROSITE, PS51120; LDLRB, 4.
FT NON_TER 1
FT NON_TER 1294

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SO SEQUENCE 1294 AA; 146750 MW; 10C251750A3F0586 CRC64;
Query Match 31.1%; Score 62.5; DB 2; Length 1294;
Best Local Similarity 31.7%; Pred. No. 30;
Matches 13; Conservative 8; Mismatches 13; Indels 7; Gaps 1;

OY 1 CSQNEYFDSLHACIPCOLRCSS-----NTPPLTCORYC 34
DB 1131 CRADEFRCVNTNACDPNMRCTEDKDCPDGSPPRKORTC 1171

RESULT 26
O6BFG4_PART1 PRELIMINARY; PRT; 3005 AA.
ID O6BFG4;
AC O6BFG4;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Putative surface protein with EGF domains and furin-like repeats.
GN ORFNames=PTMB.409;
OS Parametecium tetraurelia.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculiida;
OC Parametecidae; Parametecium.
CX NCBI_TaxID=5886;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Stock d4-2;
RX PubMed=15296759; DOI=10.1016/j.cub.2004.07.029;
RA Zagulski M., Nowak J.K., Le Mouel A., Nowacki M., Migdalski A.,
RA Gromadka R., Noel B., Blanc I., Dessen P., Wincker P., Keller A.M.,
RA Cohen J., Meyer E., Sperling L.,
RT "High Coding Density on the Largest Parametecium tetraurelia Somatic
RT Chromosome."
RL Curr. Biol. 14:1397-1404 (2004).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=Stock d4-2;
RA Nowak J.K., Migdalski A., Gromadka R., Zagulski M.,
RT "Parametecium megabase sequencing project."
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; CR348612; CAH03606.1; -; Genomic_DNA.
CC DR InterPro; IPR006058; 2FE2S_Fd_BS.
CC DR InterPro; IPR006210; EGF.
CC DR InterPro; IPR013032; EGF_like_reg.
CC DR InterPro; IPR006212; Furin_repeat.
CC DR SMART; SM00181; EGF; 4.
CC DR SMART; SM00261; FU; 1.
CC DR PROSITE; PS00197; 2FE2S_FER_1; UNKNOWN_1.
CC DR PROSITE; PS01186; EGF_2; 12.
CC DR PROSITE; PS01186; EGF_2; 12.
SQ SEQUENCE 3005 AA; 343824 MW; D8CCGA247876A5A5 CRC64;

Query Match 30.6%; Score 61.5; DB 2; Length 3005;
Best Local Similarity 40.6%; Pred. No. 96;
Matches 13; Conservative 3; Mismatches 7; Indels 9; Gaps 2;

OY 6 YFDSLHACIPCOLRCSSNTPPLTCO---RYC 34
DB 1190 YFESSNTOCTOCDLSC-----FTCOGSSKYC 1215

RESULT 27
O3WG13_9ACTO PRELIMINARY; PRT; 192 AA.
ID O3WG13_9ACTO
AC O3WG13_
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Hypothetical protein.
GN ORFNames=FraneandRAPT_6385;

```

```

OS Frankia sp. EANIpec.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Frankineae; Frankiaceae; Frankia.
CX NCBI_TaxID=298653;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=EANIpec;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Deter C., Glavina T.,
RA Hamon N., Israni S., Pluck S., Richardson P.
RT "Sequencing of the draft genome and assembly of Frankia sp. EANIpec."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=EANIpec;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Frankia sp. EANIpec."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
CC EMBL; AA101000007; EANI7768.1; -; Genomic_DNA.
CX NCBI_TaxID=298653;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RG MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
RT "The C. elegans sequencing consortium."
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology."
RL Science 282:2012-2018 (1998).
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CC -----
CC EMBL; U39644; AAA80360.2; -; Genomic_DNA.
CC DR PIR; T16840; T16840.
CC DR HSSP; P10969; IWGT.
CC DR Insect; O22378; -.
CC DR Ensemble; T10E10.4; Caenorhabditis elegans.
CC DR WormBase; WBGene0020421; T10E10.4.
CC DR WormPeP; T10E10.4; CE25989.
CC DR GO; GO:0005576; C:extracellular region; IEA.
CC DR GO; GO:0008061; F:chitin binding; IEA.

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DR GO:0006030; P:chitin metabolism; IEA.
DR InterPro: IPR006149; EB_region.
DR InterPro: IPR000794; Ketosacyl_synth.
DR InterPro: IPR002557; beta_chitin_bd.
DR InterPro: IPR003571; Snake_toxin.
DR InterPro: IPR006150; Worm_repeat_1.
DR Pfam: PF01607; CBM_14; 2.
DR Pfam: PF01683; EB; 1.
DR SMART: SMO0289; WR1; 7.
DR PROSITE: PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
DR PROSITE: PS00272; SNAKE_TOXIN; UNKNOWN_1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 966 AA; 102461 MW; B565A3CDD25216D9 CRC64;

QY 1 CSQNEVFDSDLLHACIPCGLR--CSGNTPPLTC 30
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 216 CSQSTFVNSDLNVCVPLAIQNSCDSTQGPC 247

RESULT 29
Q5JSG7_HUMAN PRELIMINARY; PRT; 1560 AA.
AC Q5JSG7;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Protein convertase subtilisin/kexin type 5 (Fragment).
GN Name=PCSKs; ORFNames=RP11-422M19.4-002;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Mashreghi-Mohammadi M.;
RL Submitted (May-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Pelan S.;
RL Submitted (May-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Peck A.;
RL Submitted (May-2005) to the EMBL/GenBank/DBJ databases.

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DR EMBL: AL391868; CA140809.1; JOINED; Genomic DNA.
DR EMBL: AL393607; CA141234.1; -; Genomic DNA.
DR EMBL: AL391868; CA141234.1; JOINED; Genomic DNA.
DR EMBL: AL589653; CA141234.1; JOINED; Genomic DNA.
DR EMBL: AL589653; CA140809.1; -; Genomic DNA.
DR EMBL: AL393607; CA140809.1; JOINED; Genomic DNA.
DR EMBL: AL589653; CA140675.1; JOINED; Genomic DNA.
DR EMBL: AL393607; CA140675.1; JOINED; Genomic DNA.
DR EMBL: AL391868; CA140675.1; -; Genomic DNA.
DR GO: 0008233; F:peptidase activity; IEA.
DR GO: 0004289; F:subtilase activity; IEA.
DR GO: 0006508; F:proteolysis; IEA.
DR InterPro: IPR006210; EGF.
DR InterPro: IPR006212; Furin_repeat.
DR InterPro: IPR000209; Pept_S8_553.
DR InterPro: IPR002884; Pp1rotenconvertsp.
DR Pfam: PF00420; AFP; 1.
DR Pfam: PF03860; DUF326; 2.
DR Pfam: PF01483; P_protein; 1.
DR Pfam: PF00082; Peptidase_S8; 1.

```

Query Match

Best Local Similarity 30.3%; Score 61; DB 2; Length 1560;
Matches 14; Conservative 6; Mismatches 14; Indels 16; Gaps 2;

DQ 1 CSONEFYDSLHLHACIPCOLRC-----SSNTPLP-TCORYC 34
||::|::|::|:
Db 1155 CSESEYWEDEAPGCKPCHVXCFHMCGPAEDQCOCFCMNSLLNLTCTVKDC 1204

RESULT 30

QARTB_TETNG PRELIMINARY; PRT; 830 AA.

ID QARTB_TETNG AC QARTY8; DT 19-JUL-2005, integrated into UniProtKB/TREMBL.
DT 19-JUN-2005, sequence version 1.
DI 21-FEB-2006, entry version 7.
DE Chromosome 12 SCARF4996, whole genome shotgun sequence. (Fragment).
GN ORFNAMES=GSTENG0029038001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
NC Acanthomorphi; Acanthopterygii; Percomorpha; Tetradontiformes;
OX Tetradontoidea; Tetradontiidae; Tetradon.
RN NCBI TaxID=99883;
RP Nucleotide Sequence.
RX PubMed=15496914; DOI=10.1038/nature03025;
RA Jallion O., Anny U.-M., Brunet F., Petit J.-L., Stange-Thmann N.,
R Muscari E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
R Nicard S., Jaife D., Fisher S., Lutalla G., Dossat C., Segurens B.,
R Desliva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
R Alhouarid V., Jubin C., Castel I.V., Katinka M., Vaccellaro B.,
R Blument C., Skalli Z., Catolico L., Poulain J., De Berardinis V.,
R Claud C., Duprat S., Broctier P., Couranceau J.-P., Guzy J.,
R Parra G., Landier G., Chapelle R., McKernan K.J., McEwan P., Bosak S.,
R Kelly M., Wolff J.-N., Guigo R., Zody M.C., Mesirov J.,
R Lindblad-Toh K., Birren B., Nusbaum C., Kann D., Robinson-Rechavi M.,
R Lauder P., Schachter V., Queller F., Saun W., Scarpelli C.,
R Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype." ;
RL Nature 431:946-957(2004).

[2]

NUCLEOTIDE SEQUENCE.
RP Genoscope; Whitehead Institute Centre for Genome Research;
RG Submitted (FEBS-2004) to the EMBL/GenBank/DBJ databases.
RL -! CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.

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DR EMBL; CAEE01014996; CAG08144.1; -; genomic DNA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPRO06210; EGF.
DR InterPro; IFPRO00742; EGF_3.
DR InterPro; IFPRO02049; EGF_laminin.
DR InterPro; IFPRO13032; EGF_like_reg.
DR Pfam; PF00053; laminin_EGF_1.
DR PRINTS; PROO011; EGFLAMININ.
DR SMART; SM00181; EGF_5.
DR PROSITE; PS00022; EGF_1_7.
DR PROSITE; PS01186; EGF_2; 4.
DR PROSITE; PSS0026; EGF_3; 4.


```
KM EGF-like domain.
FT NON TER 1
FT NON TER 830
SQ SEQUENCE 830 AA; 91073 MW; 94415DC15C27B26A CRC64;

Query Match
Best Local Similarity 29.9%; Score 60; DB 2; Length 830;
Matches 14; Conservative 6; Mismatches 14; Indels 24; Gaps 2;

Oy 1 CSONEYFSLAHACI-----PCQLRCSNTPLT-----TCORYC 34
Db 144 CSVNSICDAMTRCLCSPGWTRNGCIQCSCNNSPCDQFTGRCCGRKLMGPRCERYC 201

RESULT 31
SSPO_BOVIN STANDARD; PRT: 867 AA.
ID_SSPO_BOVIN
AC P96167,
DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-1996, sequence version 1.
DT 07-MAR-2006, entry version 48.
DE SCO-spondin (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN 11
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Endothocyte;
RX MEDLINE=96338614; PubMed=8743952;
RA Gobron S., Monnerie H., Meinzel R., Creveaux I., Lehmann W.,
RA Lamalle D., Domestique B., Meinzel A.;
RT "SCO-spondin: a new member of the thrombospondin family secreted by
RT the subcommissural organ is a candidate in the modulation of neuronal
RT aggregation." 109:1053-1061(1996).
RL J. Cell Sci. 109:1053-1061(1996).
CC -1- FUNCTION: Involved in the modulation of neuronal aggregation.
CC -1- SUBCELLULAR LOCATION: Secreted protein; extracellular space.
CC -1- TISSUE SPECIFICITY: Subcommissural organ.
CC -1- DEVELOPMENTAL STAGE: Embryo.
CC -1- SIMILARITY: Belongs to the thrombospondin family.
CC -1- SIMILARITY: Contains at least 2 EGF-like domains.
CC -1- SIMILARITY: Contains at least 1 F5/8 type C domain.
CC -1- SIMILARITY: Contains at least 3 LDL-receptor class A domains.
CC -1- SIMILARITY: Contains at least 4 TSP type-1 domains.
CC -1- SIMILARITY: Contains 1 VWFC domain.
CC -1- SIMILARITY: Contains 1 VWFC domain.
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EMBL: X93922; CAA63815.1; -; mRNA.
DR HSSP; P01130; IAUJ.
DR InterPro; IPR000742; EGF_3.
DR InterPro; IPR013032; EGF-like_reg.
DR InterPro; IPR000421; FAS8_C.
DR InterPro; IPR002172; LDL_rcpt_A.
DR InterPro; IPR002919; ProtInh_CR_TTL.
DR InterPro; IPR000884; TSP1_
DR InterPro; IPR008085; TSP_1.
DR InterPro; IPR001007; VWFC_C.
DR Pfam; PF00754; F5_F8_type_C; 1.
DR Pfam; PF00057; Ldl_recept_a; 3.
DR Pfam; PF01826; TIL; 1.
DR Pfam; PF00093; TSP_1; 4.
DR Pfam; PF00093; VWFC_1.
DR PRINTS; PR00261; LDLRECEPTOR.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00231; FAS8C; 1.
DR SMART; SM00192; LDLA; 3.
DR SMART; SM00209; TSP1; 4.
DR SMART; SM00214; VWFC; 1.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
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DR PROSITE; PS01186; EGF_2; FALSE_NEG.
DR PROSITE; PS50026; EGF_3; FALSE_NEG.
DR PROSITE; PS01285; FAS8C_1; 1.
DR PROSITE; PS01285; FAS8C_2; 1.
DR PROSITE; PS50022; FAS8C_3; 1.
DR PROSITE; PS01208; LDLRA_1; 3.
DR PROSITE; PS50068; LDLRA_2; 3.
DR PROSITE; PS50092; TSP1; 4.
DR PROSITE; PS50184; VWFC_2; 1.
KM Calcium; Cell adhesion; EGF-like domain; Glycoprotein; Repeat.
FT CHAIN <1>
FT DOMAIN 29 87
FT DOMAIN 103 142
FT DOMAIN 143 180
FT DOMAIN 188 244
FT DOMAIN 245 304
FT DOMAIN 344 502
FT DOMAIN 506 544
FT DOMAIN 663 701
FT DOMAIN 723 761
FT DOMAIN 761 814
FT DOMAIN 816 866
FT CARBOHYD 88 88
FT CARBOHYD 309 309
FT CARBOHYD 409 409
FT DISULFID 107 122
FT DISULFID 116 127
FT DISULFID 129 141
FT DISULFID 147 166
FT DISULFID 149 169
FT DISULFID 171 179
FT DISULFID 189 228
FT DISULFID 200 204
FT DISULFID 238 243
FT DISULFID 344 502
FT DISULFID 508 520
FT DISULFID 515 533
FT DISULFID 527 542
FT DISULFID 665 677
FT DISULFID 672 690
FT DISULFID 684 699
FT DISULFID 725 737
FT DISULFID 732 750
FT DISULFID 744 759
FT DISULFID 762 798
FT DISULFID 773 777
FT DISULFID 808 813
FT DISULFID 828 865
FT DISULFID 843 855
FT NON TER 1
FT NON TER 867
SQ SEQUENCE 867 AA; 91817 MW; 9538F2108E787B49 CRC64;

Query Match
Best Local Similarity 29.9%; Score 60; DB 1; Length 867;
Matches 9; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Oy 10 ILHACIPQLRCSNTPLTTC 30
Db 96 VFHACVPCPLTCDDISGATC 116

RESULT 32
O8SPM4_BOVIN PRELIMINARY; PRT: 5146 AA.
ID_O8SPM4_BOVIN
AC O8SPM4_
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 17.
DE SCO-spondin.
GN Name=sco-spondin;
OS Bos taurus (Bovine).
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RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; CH379069; EAL30797.1; -; Genomic_DNA.
FT NON TER 1
FT TER 1
SQ SEQUENCE 279 AA; 30682 MW; 1CA08116E04E7100 CRC64;

Query Match 29.6%; Score 59.5; DB 2; Length 279;
Best Local Similarity 34.1%; Pred. No. 15;
Matches 15; Conservative 3; Mismatches 15; Indels 11; Gaps 2;

QY 1 CSQNEYPDSLHACIPCOL-----RCSSNTP-----PLTCORY 33
Db 117 CVSGSYFDSGRACLPVALTAAHQCSCLLPDHATVBNPSDCERTY 160

RESULT 34
Q8SZ58 DROME PRELIMINARY; PRT; 353 AA.
AC Q8SZ58-
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE RE16222P.
GN ORFNames=CG7348;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN 1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkely;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champagne M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R.A., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY071103; AAL48725.1; -; mRNA.
DR FLYBase; FBgn0036940; CG7348.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008061; P:chitin binding; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Pera_Chitin_bd.
DR Pfam; PF01607; CBM_14; 4.
DR SMART; SMO0494; CHED2; 3.
DR PROSITE; PS50940; CHIT_BIND_II; 4.
SQ SEQUENCE 353 AA; 39712 MW; F5AB27B9A6FF9921 CRC64;

Query Match 29.6%; Score 59.5; DB 2; Length 353;
Best Local Similarity 31.8%; Pred. No. 19;
Matches 14; Conservative 4; Mismatches 15; Indels 11; Gaps 2;

QY 1 CSQNEYPDSLHACIPCOL-----RCSSNTP-----PLTCORY 33
Db 119 CSVGVYFDPARACLPVAISAHQCSCVLPDNTATLANPSDCERTY 162

RESULT 35
Q9VM81 DROME PRELIMINARY; PRT; 353 AA.
AC Q9VM81-
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.

DT 07-FEB-2006, entry version 23.
DE CG7348-PA.
GN ORFNames=CG7348; Dmel CG7348;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN 1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne U.D.,
RX Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RX George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RX Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RX Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RX Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RX Abdiel J.F., Agbayani A., An H.-J., Andrews-Plannkoch C., Baldwin D.,
RX Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RX Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RX Borkova D., Botchan M.R., Bouck J., Brokstein P., Bottlier P.,
RX Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RX Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RX de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RX Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunfey B.C., Dunn P.,
RX Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
RX Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RX Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RX Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RX Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibbegan C.,
RX Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RX Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RX Lasoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RX Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RX Mekhlov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RX Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RX Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle U.M.,
RX Palazolo M., Plutem G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RX Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RX Shue B.C., Siden-Kiamos I., Simpson M., Skipski M.P., Smith T.,
RX Spletter E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RX Svitskas R., Tector C., Turner C., Venter E., Wang A.H., Wang X.,
RX Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RX Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RX Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RX Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RX Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RX "The genome sequence of Drosophila melanogaster.";
RX Science 287:2185-2195 (2000).
RN 12]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RX Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RX Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodson A.,
RX George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RX Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.U.,
RX Svitskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RX Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RX "Finishing a whole-genome shotgun: release 3 of the Drosophila
RX melanogaster euchromatic genome sequence.";
RX Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
RN 13]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RX Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svitskas R.,
RX Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RX Ashburner M., Celniker S.E.;
RX "The transposable elements of the Drosophila melanogaster euchromatin:
RX a genomic perspective.";
RX Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20 (2002).
RN 14]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
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RA Miera S., Crosby M.A., Murgall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celinker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.,
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RG Berkeley Drosophila Genome Project;
RA Celinker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svilaras R., Smith E.,
RA Yu C., Rubin G.
RT "Drosophila melanogaster release 4 sequence."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RG FlyBase;
RL Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AE003514; AAF49068.1; -; Genomic_DNA.
DR FLYBase; FBGN0036940; CG7348.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Pfam; PF01607; CBM 14; 4.
DR Pfam; PF01607; CBM 14; 4.
DR SMART; SM00494; CHBD2; 3.
DR PROSITE; PS0940; CHIT_BIND II; 4.
SQ SEQUENCE 353 AA; 39713 MW; 1C6616504FD130B CRC64;

Query Match 29.6%; Score 59.5; DB 2; Length 353;
Best Local Similarity 31.8%; Pred. No. 19;
Matches 14; Conservative 4; Mismatches 15; Indels 11; Gaps 2;

QY 1 CSQNEYPDSLHACIPCOQ-----RCSSNT-----PLTCQRY 33
DB 119 CSQNEYPDPRRRACLPVISAHQCSCVLPDNTANLPSCERY 162

RESULT 36
OSQZ68 HUMAN PRELIMINARY; PRT; 484 AA.
AC OSQZ68;
DT 29-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 29-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Hypothetical protein DKFZp686D20108 (Fragment).
GN Name=DKFZp686D20108;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG Tissue=Fetal Kidney;
RA The German CDNA Consortium;
RA Bloeker H., Boecher M., Brandt P., Mewes H.W., Well B., Amid C.,
RA Osanger A., Fobio G., Han M., Wiemann S.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; CR936873; CA159785.1; -; -.
DR Ensemble; ENSG00000146197; Homo sapiens.

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DR InterPro; IPR000859; CUB.
DR InterPro; IPR011641; GCC2_GCC3.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF07699; GCC2_GCC3; 3.
DR SMART; SM00042; CUB; 1.
DR PROSITE; PS0180; CUB; 1.
KM Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 484 AA; 53895 MW; 8895A63E9DB369C CRC64;

Query Match 29.6%; Score 59.5; DB 2; Length 484;
Best Local Similarity 28.9%; Pred. No. 27;
Matches 11; Conservative 5; Mismatches 9; Indels 13; Gaps 1;

QY 1 CSQNEYPDSLHACIPCOQ-----RCSSNT 25
DB 241 CSQNEYPDSLHACIPCOQ-----RCSSNT 278

RESULT 37
OSQNAV8 HUMAN PRELIMINARY; PRT; 581 AA.
AC OSQNAV8;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-MAR-2006, entry version 17.
DE CNNA FLJ34691 fis, clone MESAN2000909, moderately similar to Homo
DE sapiens CEBP1 protein (CEBP1), mRNA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Oca T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Makamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto Y., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimura M., Watanabe M., Hirakawa K., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshioka Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe K., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hiroo M., Omori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senda T.,
RA Matsumura K., Kawakami Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togaishi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shitai Y., Takahawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuno Y., Yamashta R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Iogai T., Sugano S.,
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs."
RL Nat. Genet. 36:40-45(2004).
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CC -----
DR EMBL; AK092010; BAC03789.1; -, mRNA.
DR Ensemble; ENSG00000146197; Homo sapiens.

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DR InterPro: IPR000859; CUB.
DR InterPro: IPR011641; GCC2_GCC3.
DR Pfam: PF00431; CUB; 1.
DR Pfam: PF07699; GCC2_GCC3; 3.
DR SMART: SM00042; CUB; 1.
DR PROSITE: PS01180; CUB; 1.
SQ SEQUENCE 581 AA; 64343 MW; D17BC28CDALIE4E1 CRC64;
Query Match 29.6%; Score 59.5; DB 2; Length 581;
Best Local Similarity 28.9%; Pred. No. 32;
Matches 11; Conservative 5; Mismatches 9; Indels 13; Gaps 1;
QY 1 CSONEYPDSLHACIPCOL-----RCSNT 25
DB 337 CSPGHVYNTSIHRCIRCAMGSYQDPFRONFCRCPGNT 374
RESULT 38
ID Q5CZB3 HUMAN PRELIMINARY; PRT; 852 AA.
AC Q5CZB3;
DT 29-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 29-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Hypothetical protein DKFZp686B1223 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo;
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Testis;
RG The German cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mews H.W., Weill B., Anid C., Osanger A., Fobd G., Han M., Wiemann S.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: CR936607; CA156752.1; -; mRNA.
DR Ensemble: ENSG00000146197; Homo sapiens.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR GO: GO:0004888; F:transmembrane receptor activity; IEA.
DR GO: GO:0007596; P:blood coagulation; IEA.
DR InterPro: IPR000152; Asx_hydroxyl_S.
DR InterPro: IPR000859; CUB.
DR InterPro: IPR006210; EGF.
DR InterPro: IPR00742; EGF 3.
DR InterPro: IPR001881; EGF_Ca_bd.
DR InterPro: IPR013091; EGF_Ca_bd_2.
DR InterPro: IPR06209; EGF_like_reg.
DR InterPro: IPR013032; EGF_like_reg.
DR InterPro: IPR01641; GCC2_GCC3.
DR InterPro: IPR001491; Thrombomodulin.
DR Pfam: PF00431; CUB; 1.
DR Pfam: PF00008; EGF; 5.
DR Pfam: PF07645; EGF CA; 2.
DR Pfam: PF07699; GCC2_GCC3; 3.
DR PRINTS: PR00907; THROMBOMODULN.
DR SMART: SM00042; CUB; 1.
DR SMART: SM00181; EGF; 6.
DR SMART: SM00179; EGF CA; 3.
DR PROSITE: PS00010; ASX_HYDROXYL; 3.
DR PROSITE: PS01180; CUB; 1.
DR PROSITE: PS01186; EGF_2; 4.
DR PROSITE: PS00026; EGF_3; 3.
DR PROSITE: PS01187; EGF CA; 3.
KW EGF-like domain; Hypothetical protein.
FT NON_TER 1 1

SQ SEQUENCE 852 AA; 93812 MW; 514918COD126CTB2 CRC64;
Query Match 29.6%; Score 59.5; DB 2; Length 852;
Best Local Similarity 28.9%; Pred. No. 48;
Matches 11; Conservative 5; Mismatches 9; Indels 13; Gaps 1;
QY 1 CSONEYPDSLHACIPCOL-----RCSNT 25
DB 608 CSPGHVYNTSIHRCIRCAMGSYQDPFRONFCRCPGNT 645
RESULT 39
ID Q5NLS CRYNE PRELIMINARY; PRT; 861 AA.
AC Q5NLS;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Hypothetical protein.
GN ORNames=CNEH0730;
OS Cryococcus neoformans var. neoformans B-3501A.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=283643;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B-3501A;
RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
RA Wickes B.L., Fu J., Davis R.W.;
RT "Cryococcus neoformans serotype D sequencing."
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL: AA9Y0100041; EAL19380.1; -; Genomic_DNA.
DR InterPro: IPR006210; EGF.
DR InterPro: IPR00742; EGF 3.
DR InterPro: IPR002049; EGF_Laminin.
DR InterPro: IPR013032; EGF_like_reg.
DR InterPro: IPR006212; Furin_repeat.
DR Pfam: PF00008; EGF; 1.
DR SMART: SM00181; FU; 2.
DR SMART: SM00261; FU; 3.
DR PROSITE: PS00022; EGF 1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00026; EGF_3; 1.
DR PROSITE: PS01248; EGF_LAM_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 861 AA; 93347 MW; 8745729FBD869366 CRC64;
Query Match 29.6%; Score 59.5; DB 2; Length 861;
Best Local Similarity 37.1%; Pred. No. 49;
Matches 13; Conservative 4; Mismatches 13; Indels 5; Gaps 1;
QY 1 CSONEYPDSLHACIPCOLRCSNTPP-----LTC 30
DB 321 CSSGLYDSTRSCSCSCSPACSTCTGPTSDCLSC 355
RESULT 40
ID Q8NAU9 HUMAN PRELIMINARY; PRT; 880 AA.
AC Q8NAU9;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 01-MAR-2006, entry version 19.
DE CDNA FLJ34743 f1s, clone MESAN2009019, moderately similar to CEGP1
DE protein.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakatsuki A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Ohbayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki K.,
 RA Niimomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimeta M., Watanabe M., Hirooka S., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hottu T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Musashino K., Yuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshioka Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senon A., Mizoguchi H., Goto Y., Shimizu F., Wakabe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hiroo M., Omori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senda T.,
 RA Matsumura R., Nakajima Y., Mizuno T., Morinaga M., Sasaki K.,
 RA Toghiani T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okunura K., Nagase T., Nomura Y., Kikuchi H., Masuno Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isegawa T., Sugano S.,
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs".
 RT Nat. Genet. 36:40-45(2004).
 RL -----
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 CC -----
 CC EMBL, AK092062; BAC03798.1; -; mRNA.
 DR HSPB, P35555; 1LMJ.
 DR Ensemble; ENSG00000146197; Homo sapiens.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR GO; GO:0007596; P:blood coagulation; IEA.
 DR InterPro; IPR000152; Asx hydroxyl_S.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR006210; EGF.
 DR InterPro; IPR000742; EGF_3.
 DR InterPro; IPR001881; EGF_Ca_bd.
 DR InterPro; IPR013091; EGF_Ca_bd_2.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR013032; EGF-like_reg.
 DR InterPro; IPR01641; GCC2_GCC3.
 DR InterPro; IPR001491; Thrombomodulin.
 DR Pfam; PF00431; CUB; 1.
 DR Pfam; PF00008; EGF; 5.
 DR Pfam; PF07645; EGF_Ca; 2.
 DR Pfam; PF07699; GCC2_GCC3; 3.
 DR PRINTS; PRO0907; THROMBOMODULN.
 DR SMART; SM00042; CUB; 1.
 DR SMART; SM00181; EGF; 6.
 DR SMART; SM00179; EGF_Ca; 3.
 DR PROSITE; PS00010; ASX_HYDROXYL; 3.
 DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS01186; EGF_2; 5.
 DR PROSITE; PS50026; EGF_3; 3.
 DR PROSITE; PS01187; EGF_Ca; 3.
 DR Pfam; PF00008; EGF; 6.
 DR Pfam; PF07645; EGF_Ca; 4.
 DR SEQUENCE 880 AA; 97240 MW; F0BDE6E85266FD60 CRC64;

Query Match 29.6%; Score 59.5; DB 2; Length 880;
 Best Local Similarity 28.9%; Pred. No. 50;
 Matches 11; Conservative 5; Mismatches 9; Indels 13; Gaps 1;
 QY 1 CSQNYFDSLHACIPCOL-----RCSNT 25
 DB 636 CSPGHVYNTSHRCRCAMGSGYQDPDFRONFCRCPGNT 673
 RESULT 41
 ID 086U29 HUMAN PRELIMINARY; PRT; 992 AA.
 AC 086U29;
 DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2004, sequence version 2.
 DT 07-FEB-2006, entry version 14.
 DE Signal peptide, CUB domain, EGF-like 3.
 DE Name=SCUBE3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=pancreas;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Struhsberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buehler K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stalteron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ussid T.B., Toshiyuki S., Carrincci P., Prange C.,
 RA Rahn S.S., Loguella N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Wexley K.C., Hale S., Garcia A.M., Gay L.J., Huijck S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kerteman M., Madan A., Rodriques S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Binkley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences".
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=pancreas;
 RA Struhsberg R.;
 RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.
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 CC EMBL, BC052263; AAH52263.2; -; mRNA.
 DR HSPB, P35555; 1EMN.
 DR Ensemble; ENSG00000146197; Homo sapiens.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR InterPro; IPR000152; Asx hydroxyl_S.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR006210; EGF.
 DR InterPro; IPR000742; EGF_3.
 DR InterPro; IPR001881; EGF_Ca_bd.
 DR InterPro; IPR013091; EGF_Ca_bd_2.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR013032; EGF-like_reg.
 DR InterPro; IPR01641; GCC2_GCC3.
 DR Pfam; PF00431; CUB; 1.
 DR Pfam; PF00008; EGF; 6.
 DR Pfam; PF07645; EGF_Ca; 4.

RA Smith U.M., Consugar M., Tee L.J., McKee B.M., Maina E.N., Whelan S.,
 RA Morgan N.V., Goranson E., Gissen P., Lillquist S., Aligianis I.A.,
 RA Ward C.J., Pasia S., Punyashtchi R., Malik Sharif S., Berman P.A.,
 RA Bennett C.P., Woods C.G., McKeown C., Bucourt M., Miller C.A., Cox P.,
 RA Algrazali L., Trembach R.C., Torres V.E., Attie-Bitach T., Kelly D.A.,
 RA Maher E.R., Gatlone V.H., Harris P.C., Johnson C.A.,
 RT "The transmembrane protein meckelin (MKS3) is mutated in Meckel-Gruber
 RT syndrome and the wpr rat.";
 RL Nat. Genet. 38:191-196(2006).
 CC -1- FUNCTION: May be related to the ciliary basal body.
 CC -1- SUBCELLULAR LOCATION: Cell membrane; multi-pass membrane protein
 CC (Potential).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=QSHYAB-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=QSHYAB-2; Sequence=VSP_017415, VSP_017416;
 CC Note=No experimental confirmation available;
 CC -1- TISSUE SPECIFICITY: Widely expressed in adult and fetal tissues.
 CC Expressed at higher level in spinal cord.
 CC -1- DISBASE: Defects in TMEM67 are the cause of Meckel syndrome type 3
 CC (MKS3) [MIM:607361]. MKS3 is an autosomal recessive disorder
 CC characterized by a combination of renal cysts and variably
 CC associated features including developmental anomalies of the
 CC central nervous system (typically encephalocele), hepatic ductal
 CC dysplasia and cysts, and polydactyly.
 CC -----
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 CC -----
 DR EMBL; BX648768; CA14599.1; -; mRNA.
 DR EMBL; BC031220; AAH31220.1; -; mRNA.
 DR EMBL; BC032835; AAH32835.1; ALT_INTT; mRNA.
 DR EMBL; BC054338; AAH54338.1; ALT_INTT; mRNA.
 DR Ensembl; ENSG00000164953; Homo sapiens.
 DR HGNC; HGNC:28396; TMEM67.
 DR MIM; 607361; phenotype.
 DR InterPro; IPR000150; Hypoeth cof.
 DR Alternative splicing; Disease mutation; Glycoprotein; Membrane;
 KW Polymorphism; Transmembrane.
 FT CHAIN 1 995
 FT TRANSMEM 9 29
 FT TRANSMEM 526 546
 FT TRANSMEM 570 590
 FT TRANSMEM 609 629
 FT TRANSMEM 689 709
 FT TRANSMEM 734 754
 FT TRANSMEM 939 959
 FT CARBOHYD 242 242
 FT VARSPLIC 136 138
 FT VARSPLIC 139 995
 FT VARSPLIC 376 376
 FT VARIANT 604 604
 FT SEQUENCE 995 AA; 111731 MW; AEBDA6B84F759A8 CRC64;
 SQ
 Query Match 29.6%; Score 59.5; DB 1; Length 995;
 Best Local Similarity 21.6%; Pred. No. 56;
 Matches 11; Conservative 9; Mismatches 12; Indels 19; Gaps 1;
 QY 1 CSONEYFDSLHACIPCC-----QLACSSNTPLPTQRY 32
 DB 49 CDDNYFDISALSCVPCGANQRDARGTSCVCLPGFOMISNNGPAILCKK 99
 RESULT 44
 QAS403 TETNG PRELIMINARY; PRT; 184 AA.

AC QAS403;
 DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Chromosome 2 SCAR14738, whole genome shotgun sequence.
 GN ORFname=GSTENG00024082001;
 OS Tetradodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthopterygii; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_Taxid=99883;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15496914; DOI=10.1038/nature03025;
 RA Jallion O., Arny J.-M., Brunet F., Petit J.-L., Strange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costez C., Bernot A.,
 RA Nicoud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Caetelli V., Katinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Catolico L., Poulain J., De Bernardinis V.,
 RA Cruaud C., Duprat S., Brotilier P., Coutanceau J.-P., Gouzy J.,
 RA Parra G., Lardier G., Chappe C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Wolff J.-N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Landel V., Schachter V., Queller F., Saurin W., Scarpelli C.,
 RA Winkler P., Lander E.S., Weissbach J., Roest Croliiss H.;
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).
 RN (2)
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
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 CC -----
 DR EMBL; CAE0104738; CAG04379.1; -; Genomic DNA.
 SQ SEQUENCE 184 AA; 19133 MW; 3B2167B5E4FB1BB7 CRC64;
 QY 94 CSSEFMSDVDCVPC-----SCKRY 116
 DB 94 CSSEFMSDVDCVPC-----SCKRY 116
 RESULT 45
 Q32LX4_HUMAN
 ID Q32LX4_HUMAN PRELIMINARY; PRT; 247 AA.
 AC Q32LX4;
 DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
 DT 06-DEC-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE TNFRSF13B protein.
 GN Name=TNFRSF13B;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OX NCBI_Taxid=9606;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=PCR rescued clones;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Berger J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,


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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rahn S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McManus P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RG NIH MGC Project;
RL Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
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CC
CC EMBL; BC109392; AA109393.1; -, mRNA.
CC
CC SEQUENCE 247 AA; 26664 MW; 850B1F4C2578EBE6 CRC64;
SQ
Query Match 29.4%; Score 59; DB 2; Length 247;
Best Local Similarity 34.4%; Pred. No. 1b;
Matches 11; Conservative 5; Mismatches 14; Indels 2; Gaps 1;
OY 3 QNEVPSLIHACIPOLRCSSNTPPLTCORYC 34
DB 29 QGKRYDHLIRDCISCSICGQH--PKGCAVFC 58

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DR GO; GO:0005515; F:protein binding; IPI.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 937 AA; 106669 MW; 1C140595DFD3ACE4 CRC64;
Query Match 29.4%; Score 59; DB 2; Length 937;
Best Local Similarity 42.9%; Pred. No. 62;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
OY 8 DSLHACIPOLRCSSNTPPL 28
DB 439 ESVFHPXLPATIRCSADGPPL 459

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DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR PROSITE; PS00500; TNFR_NGFR_2; 1.
KW kinase.
SQ SEQUENCE 1917 AA; 212684 MW; 4AD7144F6A3CF30D CRC64;
OY 1 CSQNEYFDSLHACIPCOLRGSSNTPPLTTCORYC 34
Db 441 CNKGSYNTKTRCEPCGATGYSNTTATSCERC 474

RESULT 48
OSDB6 SCHUA
ID Q5DDB6 SCHUA PRELIMINARY; PRT; 248 AA.
AC Q5DDB6;
DT 29-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 29-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE SICHGCO9354 protein.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN RN NUCLEOTIDE SEQUENCE.
RA Han Z.;
RT "The full-length cDNA sequences of Schistosoma japonicum genes.";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
RN RN NUCLEOTIDE SEQUENCE.
RA Liu F., Lu W., Wang S.-Y., Cui S.-J., Chi M., Yan Q.,
RA Wang X.-R., Song H.-D., Xu X.-N., Wang J.-J., Zhang X.-L., Wang Z.-Q.,
RA Xue C.-L., Brindley P.J., McManus D.P., Yang P.-Y., Feng Z., Chen Z.,
RA Han Z.-G.;
RT "New Perspectives on Host-parasite Interplay by Comparative
RT Transcriptomic and Proteomic Analyses of the Human Blood Fluke,
RT Schistosoma japonicum.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY84458; AAM26130.1; -; mRNA.
DR InterPro; IPR006212; Furin_repeat.
DR SMART; SM00261; FU; 2.
SQ SEQUENCE 248 AA; 27757 MW; F8D8EBD4F5DD2EEB CRC64;
OY 1 CSQNEYFDSLHACIPCOLRGSSNTPP-----LTGOR 32
Db 142 CRFSEYFDPDGICRPCDSNQGSGRHPPQCTSCNR 178

RESULT 49
O2TW70 ASPOR
ID Q2TW70 ASPOR PRELIMINARY; PRT; 345 AA.
AC Q2TW70;
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 3.
DE Predicted protein.
GN ORFNames=AO090010000683;
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN RN [1]

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NUCLEOTIDE SEQUENCE.

RC STRAIN=RIE 40;
RX PubMed=16372010; DOI=10.1038/nature04300;
RA Machida M., Asai K., Sano M., Tanaka T., Kumagai T., Terai G.,
RA Kusumoto K., Saito T., Akita O., Kaishiyagi Y., Abe K., Gomi K.,
RA Horikuchi H., Kitamoto K., Kobayashi T., Takeuchi M., Denning D.W.,
RA Galagan J.E., Nieman W.C., Yu J., Archer D.B., Bennett J.W.,
RA Bhatnagar D., Cleveland T.E., Fedorova N.D., Gotch O., Horikawa H.,
RA Hooyana A., Ichinomiya M., Igarashi R., Iwashita K., Juvadi P.R.,
RA Kato W., Kato Y., Kim T., Kokubun A., Maeda H., Maeyama N.,
RA Maruyama K., Nakanasaki H., Nakajima T., Oda K., Okada K., Paulsen I.,
RA Sakamoto K., Sawano T., Takahashi M., Takase K., Terabayashi Y.,
RA Moritori T., Koyama Y., Yamada O., Yamagata Y., Anazawa H., Hata Y., Koide Y.,
RA Kihara S., Ogasawara N., Kikuchi H., Suharnan S., Tanaka A., Isono K.,
RT "Genome sequencing and analysis of *Aspergillus oryzae*,"
RL Nature 438:1157-1161(2005).

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CC

DR EMBL; AP007175; BAB6503.1; -, Genomic DNA.
SQ SEQUENCE 345 AA; 38461 MW; 81A2549BEFFP02AD CRC64;

Query Match 29.1%; Score 58.5; DB 2; Length 345;
Best Local Similarity 40.6%; Pred. No. 26;
Matches 13; Conservative 7; Mismatches 11; Indels 1; Gaps 1;

Oy 3 ONEYFD-SLHACIPCOLRCSSNTPPLTCQRY 33
Db 261 QDEAFDVSMMHACSGAKLKCISVPEVHOF 292

RESULT 50
O68FG9_MOUSE PRELIMINARY; PRT; 827 AA.

ID O68FG9_MOUSE PRELIMINARY; PRT; 827 AA.
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Scube3 protein (Fragment).
GN Name=Scube3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
[1]
NP NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6; TISSUE=Brain;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Straube-Berg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein W.J., Udell T.B., Yoshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S., Sanchez A.,
RA Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield J., Schein J.E., Krzywinski M.I., Skalka U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RP Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).
[2]
NP NUCLEOTIDE SEQUENCE.

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RC STRAIN=C57BL/6; TISSUE=Brain;
RA Director MGC Project;
RU Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC079849; AAH79849.1; -; mRNA.
DR Ensembl; ENSMUSG0000038677; Mus musculus.
DR MGI; MGI:3045253; Scube3.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR000742; EGF_3.
DR InterPro; IPR001881; EGF_Ca_bd.
DR InterPro; IPR013091; EGF_Ca_bd_2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR013032; EGF_like_reg.
DR InterPro; IPR011641; GCC2_GCC3.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 6.
DR Pfam; PF07645; EGF_CA; 3.
DR Pfam; PF07699; GCC2_GCC3; 2.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00181; EGF; 7.
DR SMART; SM00179; EGF_CA; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 5.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS01186; EGF_2; 6.
DR PROSITE; PS50026; EGF_3; 4.
DR PROSITE; PS01187; EGF_CA; 4.
KW EGF-like domain.
KW NON_TER
SQ SEQUENCE 827 AA; 90871 MW; DF6BB337B4CE91D CRC64;

Query Match 29.1%; Score 58.5; DB 2; Length 827;
Best Local Similarity 28.9%; Pred. No. 63;
Matches 11; Conservative 5; Mismatches 9; Indels 13; Gaps 1;

QY 1 CSQNEFDSLHACIPCOL-----RCSNT 25
DB 611 CSPGHYNTSIHRCIRCAVGSYQPDFRQNFCTRCPGNT 648

RESULT 51
066PY1 MOUSE PRELIMINARY; PRT; 993 AA.
AC 066PY1;
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Signal peptide, CUB and EGF-like domain containing protein 3
DE precursor.
GN Name=Scube3; Synonyms=SCUBE3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBITaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RX PubMed=15234972; DOI=10.1074/jbc.M405912200;
RA Wu B.T., Su Y.H., Tsai M.T., Wasserman S.M., Topper J.N., Yang R.B.;
RT "A novel secreted cell-surface glycoprotein containing multiple
RT epidermal growth factor-like repeats and one CUB domain is highly
RT expressed in primary osteoblasts and bones.";
RL J. Biol. Chem. 279:37485-37490(2004).
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CC -----
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DR EMBL; AY639609; AAU08348.1; -; mRNA.
DR Ensembl; ENSMUSG0000038677; Mus musculus.
DR MGI; MGI:3045253; Scube3.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR000742; EGF_3.
DR InterPro; IPR001881; EGF_Ca_bd.
DR InterPro; IPR013091; EGF_Ca_bd_2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR013032; EGF_like_reg.
DR InterPro; IPR011641; GCC2_GCC3.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 6.
DR Pfam; PF07645; EGF_CA; 4.
DR Pfam; PF07699; GCC2_GCC3; 3.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00181; EGF; 9.
DR SMART; SM00179; EGF_CA; 6.
DR PROSITE; PS00010; ASX_HYDROXYL; 6.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS50026; EGF_3; 6.
DR PROSITE; PS01187; EGF_CA; 6.
KW SIGNAL.
KW POTENTIAL.
SQ SEQUENCE 993 AA; 108984 MW; EA39899ACACCC345F CRC64;

Query Match 29.1%; Score 58.5; DB 2; Length 993;
Best Local Similarity 28.9%; Pred. No. 76;
Matches 11; Conservative 5; Mismatches 9; Indels 13; Gaps 1;

QY 1 CSQNEFDSLHACIPCOL-----RCSNT 25
DB 749 CSPGHYNTSIHRCIRCAVGSYQPDFRQNFCTRCPGNT 786

RESULT 52
08BR19 MOUSE PRELIMINARY; PRT; 101 AA.
AC 08BR19;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Adult male corpora quadrigemina cDNA, RIKEN full-length enriched
DE library, clone:B20316E19 product:hypothetical protein, full insert
DE sequence.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBITaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX PubMed=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carrinci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carrinci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Bremner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J.P., Wilming L.G., Aidinis V., Allen J.E.,
RA Ambesi-Impomatato A., Apweiler R., Atturaliya R.N., Bailey T.L.,
RA Banal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
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RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 RA Geoghegan-Hemming P., Gigeras T.R., Gojibori T., Green R.E.,
 RA Gueninch S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hill D., Hummel L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 RA Jaki M., Kanapin A., Karch M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matsuwaga S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Mortagni-Tabar S., Mulder N., Nakano N., Nakuchi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Post B., Ruan Y., Salzberg S.L., Sadelin A., Schneider C.,
 RA Schonbach C., Sekiguchi K., Sempke C.A., Sento S., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Spelling S., Stucka E., Sugura K., Sultana R., Takenaka Y., Taki K.,
 RA Tamoja K., Tan S.L., Tang S., Taylor M.S., Tegner T., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
 RA Yamaniishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmer S.M., Teasdale R.D., Liu E.T., Brusic A., Quackenbush J.,
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuoka S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Nimomiya N.,
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Wataniki A., Okamura-Ohno Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563 (2005).
 RN [3]

RA NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigenina;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 RT (Genome Network Core Team) and the FANTOM Consortium;
 RL "Antisense Transcription in the Mammalian Transcriptome";
 RN Science 309:1564-1566 (2005).
 RN [4]

RA NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigenina;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Otsu N., Saito R., Suzuki H., Yamashita H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojibori T.,
 RA Baladrelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schiml L.M., Kanapin A., Matsuda H., Baralov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chotila C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmer S., Gueninch S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kandi A., Kawaji H., Kawasawa Y., Kedziński R.M., King B.L.,
 RA Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Malais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Petosa G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravessi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sadelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wymshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hironaka-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino W., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573 (2002).
 RN [5]

RA NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigenina;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Iizawa M., Nishi K., Kiyosawa H., Kondo S., Yamashita H.,
 RA Saito T., Okazaki Y., Gojibori T., Bono H., Kawasawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Baralov S., Caavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsumoto H., Nishio T., Pesole G., Quackenbush J.,
 RA Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baladrelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein W.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gueninch W., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima T., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schonbach C., Seta T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyoko-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wymshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690 (2001).
 RN [6]

RA NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigenina;
 RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugihara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630 (2000).
 RN [7]

RA NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigenina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama Y., Nishi K., Katsunari T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishio T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuzaki S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771 (2000).
 RN [8]

RA NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigenina;
 RX Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Konda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toyoko-oka K., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBD databases.

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 CC "EMBL, AKO45875; BAC32518.1; -; mRNA.
 DR EMBL, AKO45875; BAC32518.1; -; mRNA.
 KW Hypothetical protein.
 SQ SEQUENCE 101 AA; 11571 MW; E899420B6F21D23 CRC64;

Query Match 28.9%; Score 58; DB 2; Length 101;
 Best Local Similarity 31.9%; Pred. No. 8.4;
 Matches 15; Conservative 5; Mismatches 9; Indels 18; Gaps 2;

QY 6 YFDSLHACTPC-----QLRCSSNTPP-----LTCQRYC 34

D5 YFNSLFLPLSLFCIFRILTLTRECTSHPPSPPPPSSHSLACGYC 50
|||::| : |||::| |
RESULT 53

ID Q3XSX7 MOUSE PRELIMINARY; PRT; 164 AA.

AC Q3XSX7;

DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DE 07-FEB-2006, entry version 6.
DI Trnfrsfic protein (Activated spleen cDNA, RIKEN full-length enriched library, clone:F8J0206Fj3 product:tumor necrosis factor receptor DE superfamily, member 13c, full insert sequence).

Name=Trnfrsfic3;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; OC Muridae; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

[1]

NUCLEOTIDE SEQUENCE.

RC TISSUE=PCR rescued clones;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Scott A.K., Altschuld S.F., Zeeberg B., Buetow K.H., Scheaf C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F., Diatchenko L., Matsushita K., Farmer A.A., Rubin G.M., Hong L., Brownstein W.J., Usdin I.B., Toshiyuki S., Carninci P., Franke C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallat S.J., Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W., Villalón D.K., Munz D.C., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C., Blakesley R.W., Touchman J.W., Shenn C.E., Dickinson B.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield V.S.N., Krzywicki M.I., Skalska U., Smalls D.E., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

NT [2]

NUCLEOTIDE SEQUENCE.

RC TISSUE=PCR rescued clones;

RG NIH MGC Project;

RL Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.

[3]

NUCLEOTIDE SEQUENCE.

RC STRAIN=NOD; TISSUE=Activated spleen;

RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RA Carminci P., Hayashizaki Y.;

RL "High-efficiency full-length cDNA cloning"; Methode Enzymol. 303:19-44(1999).

[4]

NUCLEOTIDE SEQUENCE.

RC STRAIN=NOD; TISSUE=Activated spleen;

RX Pubmed=16141072; DOI=10.1126/science.1112014;

RA Carminci P., Kasubawa T., Katayama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Bremner S.E., Batilov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Aidinis V., Allen J.E., Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L., Banerji M., Baxter L., Beisel K.W., Bersano T., Bono H., Chaik A.M., Chu K.P., Choudhury V., Christofels A., Clutterbuck D.R., Crowe M.L., Dalla E., Dalrymple B.P., de Bonis G., Della Gatta G., Fletcher C.F., Fluchsmann T., Fujihira T., Funari M., Futati S., Gaboldi M., Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E., Guelfinich S., Haberer M., Hayashi Y., Hensch T.K., Hirokawa N., Hill D., Hummelbeck L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Kitano H., Kollias G., Krishnan S.P., Kruger A., Kumaroff S.K., Kurochkin I.V., Larau L.F., Lazarevic D., Lipovich L., Liu J., Liuni S., McWilliam S., Madden Babu M., Madera M., Marchionni L., Matsuda H., Matsuzawa S., Miyai H., Misgione F., Miyake S., Morris K., Mottagui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P., Nilsson R., Niehuguchi S., Nishikawa S., Nori F., Ohara O., Okazaki Y., Orlando V., Pang K.C., Pavani M.J., Pavoni G., Pesole G., Petrovski Y., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M., Roost B., Ryan Y., Salzberg S.L., Sandelin A., Schneider C., Schobach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y., Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Sperling S., Stupp C.E., Sugiyura K., Sultana R., Takenaka Y., Taki K., Tamajoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teilmann S.A., Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yang J., Yamashiro H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., Grignani S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J., Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., Iida J., Imamura K., Itou M., Kato T., Kawasaki H., Kawagashira N., Kawahara T., Kohjima M., Kondō S., Konno H., Nakano K., Niimura Y., Nishio T., Okada M., Plesey C., Shibata K., Shiraki T., Suzuki S., Tagami M., Takaki M., Watashi A., Okamura-Ono Y., Suzuki H., Kawai J., Hayashizaki Y.

RT "The transcriptional landscape of the mammalian genome." Science 309:1559-1563(2005).

[5]

NUCLEOTIDE SEQUENCE.

RC STRAIN=NOD; TISSUE=Activated spleen;

RX Pubmed=16141073; DOI=10.1126/science.1112009;

RG RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;

RT "Antisense Transcription in the Mammalian Transcriptome." Science 309:1564-1566(2005).

[6]

NUCLEOTIDE SEQUENCE.

RC STRAIN=NOD; TISSUE=Activated spleen;

RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA Okazaki I., Furuno M., Kasubawa T., Adachi J., Bono H., Kondō S., Nikaido I., Osato N., Saito R., Suzuki H., Yamataka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batilov S., Beisel K.W., Blake U.A., Bradt D., Brusic V., Choitua C., Cotani L.B., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Fraser K.S., Gaasterland T., Gariboldi M., Glisi C., Godzik A., Gough J., Grimmmond S., Gustincich S., Hitokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawai H., Kawasawa Y., Kedzerki R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Malais L., Marchioni L., McKenzie L., Mikhi H., Nagashima T., Numata K., Okido T., Payan W.J., Pertea G., Petrosky N., Pillai R., Pontius U.U., Qi D., Ramchandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sardinella A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlstedt C., Wang Y., Waterhouse R., Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carminci P., Hayatsu N., Hitozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Satō K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Inotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.

RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs." Nature 420:563-573(2002).

[7]

NUCLEOTIDE SEQUENCE.

RC STRAIN=NOD; TISSUE=Activated spleen;

RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA Kawai U., Shingawa A., Shibata K., Yoshino M., Ito H., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Komoto H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Giusti C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schiml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Lyons P., Marchionni L., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Hayashaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN (8)
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Activated spleen;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN (9)
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Activated spleen;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada K.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujisaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multichannel sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN (10)
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Activated spleen;
 RA Aizawa K., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
 RA Hori F., Iida Y., Imamura K., Imotani K., Itoh M., Kanagawa S.,
 RA Kawai J., Kojima M., Kono H., Murata M., Nakamura M., Ninomiya N.,
 RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
 RA Shibata K., Shitaki T., Tagami M., Tagami Y., Waki K., Watanabe A.,
 RA Muramatsu M., Hayashizaki Y.,
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
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AC Q9DBD0,
 DT 27-MAY-2002, integrated into UniProtKB/Swiss-Prot.
 DT 01-JUN-2001, sequence version 1.
 DT 07-FEB-2006, entry version 30.
 DE Tumor necrosis factor receptor superfamily member 13C (B cell-
 DE activating factor receptor) (BAFF receptor) (BAFF-R) (Blys receptor 3)
 DE (B-cell maturation defect).
 GN Name=TNFRSF13c; Synonyms=BAFFr, Bmd, Bcr3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Euteleostomi; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN (1)
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2).
 RC STRAIN=BALB/c; TISSUE=B-cell lymphoma;
 RX MEDLINE=21442025; PubMed=11509692; DOI=10.1126/science.1061965;
 RA Thompson J.S., Bixler S.A., Qian F., Vora K., Sectt M.L.,
 RA Cachero T.G., Hession C., Schneider P., Sizing I.D., Muller C.,
 RA Struch K., Zafari M., Benjamin C.D., Tschopp J., Browning J.L.,
 RA Ambrose C.,
 RT "BAFF-R, a newly identified TNF receptor that specifically interacts
 RT with BAFF.";
 RL Science 293:2108-2111(2001).
 RN (2)
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND DISEASE.
 RC STRAIN=N/J;
 RX MEDLINE=21475520; PubMed=11591325; DOI=10.1016/S0960-9822(01)00481-X;
 RA Van M., Brady J.R., Chan B., Lee W.P., Hu B., Hartless S.M.,
 RA Canro M.P., Grewal I.S., Dixie V.M.,
 RT "Identification of a novel receptor for B lymphocyte stimulator that
 RT is mutated in a mouse strain with severe B cell deficiency.";
 RL Curr. Biol. 11:1547-1552(2001).
 RN (3)
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Small intestine;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Fritch M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aldins V., Allen J.E.,
 RA Ambesi-Impombato A., Apweiler R., Attalini R.N., Bailev T.L.,
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chin K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hill D., Hummelbeck L., Iacono M., Ikeo K., Iwama A., Itoh Y.,
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 RA Liuni S., McWilliam S., Madan Babu M., Mader M., Marchionni L.,
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakamura H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Noji F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schombach C., Sekiguchi K., Sempile C.A., Seno S., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sincalir B.,
 RA Sperling S., Stupka E., Sugita K., Sultana R., Takanaka Y., Taki K.,
 RA Tamura K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yang K.,
 RA Yamanishi H., Zdobych E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Wahlestedt C., Matick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki T., Aizawa T.,
 RA Iida Y., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Kono H., Nakano K., Ninomiya N.,
 RA Nishio T., Okada M., Plessy C., Shibata K., Shitaki T., Suzuki S.,
 RA Tagami M., Waki K., Watanabe A., Okamura-Ohno Y., Suzuki H., Kawai J.,

RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563 (2005).
 RN [4]
 RP FUNCTION.
 RX MEDLINE=21614654; PubMed=11747827; DOI=10.1016/S0960-9822(01)00598-X;
 RA Hartless S.M., Lentz V.M., Sah A.P., Hsu B.L., Clise-Dwyer K.,
 RA Hilbert D.M., Hayes C.E., Cancro M.P.;
 RT "Competition for Blygs-mediated signaling through Bcnd/BR3 regulates
 RT peripheral B lymphocyte numbers.";
 RL Curr. Biol. 11:1986-1989(2001).
 CC - FUNCTION: B-cell receptor specific for TNFRSF13B/TALL1/BAFF/Blygs.
 CC Promotes the survival of mature B-cells and the B-cell response.
 CC - SUBCELLULAR LOCATION: Membrane; single-pass type III membrane
 CC protein (Probable).
 CC - ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q9D8D0-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9D8D0-2; Sequence=VSP_006506;
 CC - TISSUE SPECIFICITY: Highly expressed in spleen and testis;
 CC detected at lower levels in lung and thymus.
 CC - DISEASE: Defects in TNFRSF13C are a cause of severe B-cell
 CC deficiency. B-cell deficient strain A/MySnJ has a 4.7 kb insertion
 CC in the BAFF gene leading to an altered C-terminus. The mutant RNA
 CC is not detectable. B-cell lymphoplasia is normal, but the life
 CC span of peripheral B-cells is much reduced.
 CC - SIMILARITY: Contains 1 TNFR-Cys repeat.
 CC -----
 CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
 CC Distributed under the Creative Commons Attribution-NonCommercial License
 CC -----
 CC EMBL; AF373847; AAK91827.1; -; mRNA.
 CC EMBL; AK008142; BAB25490.1; -; mRNA.
 CC HSSP: Q96R33: LOOE.
 DR MGI; MGI:1919299; Tnfrsf13c.
 DR GO; GO:0009897; C:external side of plasma membrane; IDA.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0031296; P:B cell costimulation; IDA.
 DR GO; GO:0001782; P:B cell homeostasis; IMP.
 DR GO; GO:0030890; P:positive regulation of B cell proliferation; IDA.
 DR GO; GO:0042102; P:positive regulation of interferon-gamma bio. ; IMP.
 DR GO; GO:0050776; P:regulation of T cell proliferation; IDA.
 DR GO; GO:0031295; P:T cell costimulation; IDA.
 DR InterPro; IPR001368; TNFR_C6.
 DR PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.
 DR PROSITE; PS00650; TNFR_NGFR_2; FALSE_NEG.
 KW Alternative splicing; Glycoprotein; Immune response; Membrane;
 KW Receptor; Signal-anchor; Transmembrane.
 FT CHAIN 1 175
 FT Tumor necrosis factor receptor
 FT superfamily member 13c.
 FT /FTId=PRO_0000058934.
 FT TRANSMEM 72 92
 FT Extracellular (Potential).
 FT Signal-anchor for type III membrane
 FT protein (Potential).
 FT TOPO_DOM 93 175
 FT REPEAT 21 38
 FT CARBOHYD 23 23
 FT DISULFID 22 35
 FT DISULFID 27 38
 FT VASSPLIC 133 143
 FT Missing (in isoform 2).
 FT /FTId=VSP_006506.
 SQ SEQUENCE 175 AA; 18798 MW; 28BC7C1A02FBB87EF CRC64;
 Query Match 28.9%; Score 58; DB 1; Length 175;
 Best Local Similarity 47.4%; Pred. No. 15;
 Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

RESULT 55
 O3XS6_MOUSE
 ID O3XS6_MOUSE PRELIMINARY; PRT; 175 AA.
 AC O3XS6.
 DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
 DT 11-OCT-2005, sequence version 1.
 DT 07-FEB-2006, entry version 5.
 DE Tumor necrosis factor receptor superfamily, member 13c (BAFF
 DE receptor).
 DE Name=TNFRSF13C;
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=PCR rescued clones;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh L.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Bask S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Roach S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=PCR rescued clones;
 RX NIH MGC Project;
 RG NIH MGC Project;
 RN Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=A.S.W. and SJL/J; TISSUE=Spleen;
 RA Libbey J.E., Peterson L.K., Tsunoda T., Fujinami R.S.;
 RT "Monoclonal MOG autoantibody from progressive EAE has the
 RT characteristics of a natural antibody.";
 RL Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
 CC -----
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 CC -----
 CC EMBL; BC104127; AA104128.1; -; mRNA.
 CC EMBL; DQ294929; ABC24674.1; -; mRNA.
 CC EMBL; DQ294928; ABC24673.1; -; mRNA.
 DR MGI; MGI:1919299; Tnfrsf13c.
 DR GO; GO:0009897; C:external side of plasma membrane; IDA.
 DR GO; GO:0016021; C:integral to membrane; RCA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0031296; P:B cell costimulation; IDA.
 DR GO; GO:0001782; P:B cell homeostasis; IMP.
 DR GO; GO:0030890; P:positive regulation of B cell proliferation; IDA.
 DR GO; GO:0042102; P:positive regulation of interferon-gamma bio. ; IMP.
 DR GO; GO:0042102; P:positive regulation of T cell proliferation; IDA.
 DR GO; GO:0050776; P:regulation of immune response; IMP.
 DR GO; GO:0031295; P:T cell costimulation; IDA.
 KW Receptor.
 SQ SEQUENCE 175 AA; 18798 MW; 28BC7C1A02FBB87EF CRC64;

RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sanderlin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Veraldo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wymshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Aekawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOB; TISSUE=Activated spleen;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aekawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochia H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Kono H., Balasubramanian R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustinich S., Hill D., Hofmann C., Hume D.A., Kamitaya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wymshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOB; TISSUE=Activated spleen;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOB; TISSUE=Activated spleen;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Katsunari T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishibe T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara B., Washiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOB; TISSUE=Activated spleen;
RA Aekawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Kono H., Murata M., Nakamura M., Nimomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watabiki A.,
RA Muramatsu M., Hayashizaki Y.;

RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AK163687; BAE33695.1; -; mRNA.
DR MG1; MG1.191299; Tinfef13c.
DR GO; GO:0009897; C:external side of plasma membrane; IDA.
DR GO; GO:0016021; C:integral to membrane; RCA.
DR GO; GO:0031296; P:B cell costimulation; IDA.
DR GO; GO:0001782; P:B cell homeostasis; IMP.
DR GO; GO:0030890; P:positive regulation of B cell proliferation; IDA.
DR GO; GO:0045078; P:positive regulation of interferon-gamma bio. .; IMP.
DR GO; GO:0042102; P:positive regulation of T cell proliferation; IDA.
DR GO; GO:0050776; P:regulation of immune response; IMP.
DR GO; GO:0031295; P:T cell costimulation; IDA.
KW Receptor.
SQ SEQUENCE 200 AA; 21596 MW; D65E52164A90DF03 CRC64;
Query Match 28.9%; Score 58; DB 2; Length 200;
Best Local Similarity 47.4%; Pred. No. 17;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 1 CSQNEFPLSLHACIPCOL 19
DB 22 CNGTECFDPLVRNCVSCBL 40
RESULT 58
ID 067887_9VIRU PRELIMINARY; PRT; 289 AA.
AC 067887;
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Hypothetical protein.
OS Lymphocystis disease virus - isolate China.
OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Lymphocystivirus;
OC Unclassified Lymphocystivirus.
OX NCBI_TaxID=256729;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15194775; DOI=10.1128/JVI.78.13.6982-6994.2004;
RA Zhang Q.Y., Xiao F., Xie U., Li Z.Q., Gui U.F.;
RT "Complete Genome Sequence of Lymphocystis Disease Virus Isolated from
RT China.";
RL J. Virol. 78:6982-6994(2004).
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CC -----
DR EMBL; AY380826; AAU10940.1; -; Genomic DNA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro: IPR013032; EGF_1like_reg.
DR InterPro: IPR01368; TNFR_c6.
DR Pfam: PF00207; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Hypothetical protein.
SQ SEQUENCE 289 AA; 32691 MW; 26B6114D4D5D6C3F CRC64;
Query Match 28.9%; Score 58; DB 2; Length 289;
Best Local Similarity 37.5%; Pred. No. 25;
Matches 12; Conservative 1; Mismatches 19; Indels 0; Gaps 0;
QY 1 CSQNEFPLSLHACIPCOLRCSSNTPPTCOR 32
DB 80 CROGYDPESEMCFPCSCNCSKVKVTKNR 111
RESULT 59


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026489_SPOFR PRELIMINARY; PRT; 1299 AA.
ID 026489_SPOFR
AC Q26489_1
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 34.
DE Endoprotease FURIN.
GN Name=FURIN;
OS Spodoptera frugiperda (Fall armyworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pelegrona;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Amphipyrinae; Spodoptera.
OX NCBI_TaxID=7108;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=SF9.
RL Clepik M., Klenk H.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; Z68888; CAA93116.1; -, mRNA.
DR PIR; T43251; T43251.
DR HSP; P23188; 1PBJ.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. .; IEA.
DR InterPro; IPR006211; Furin-like.
DR InterPro; IPR000709; Pept_58_553.
DR InterPro; IPR002884; Ptpocnconvertsp.
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF01483; P_protein; 1.
DR Pfam; PF00082; Peptidase 58; 1.
DR PRINTS; PRO0723; SUBTILISIN.
DR SMART; SMO0261; FU; 10.
DR PROSITE; PS00136; SUBTILASE_ASP; UNKNOWN_1.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KM Hydrolyase; Protease; Serine protease.
SQ SEQUENCE 1299 AA; 14202 MW; 4C3799C7B8C572AB CRC64;

Query Match 28.9%; Score 59; DB 2; Length 1299;
Best Local Similarity 37.1%; Pred. No. 1.2e+02;
Matches 13; Conservative 5; Mismatches 9; Indels 8; Gaps 2.

QY 1 CSQNEYPDSLHACIPQLRCS-----SNTPLTLC 30
b 1150 CSRPLRIDRLNNGCVC---CSERGVTMTPTDC 1181
||| | | | | | | | | | | | | | | | | | |
RESULT 60
ID ICE1_ASCSU STANDARD; PRT; 63 AA.
AC P07851; O77419;
DT 01-AUG-1988, integrated into UniProtKB/Swiss-Prot.
DT 01-AUG-1988, sequence version 1.
DT 07-FEB-2006, entry version 44.
DE Chymotrypsin/elastase inhibitor 1 (C/E-1 inhibitor) (AsC/E-1).
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP PROTEIN SEQUENCE.
RC MEDLINE=84255715; PubMed=6564898;
RX Babin D.R., Peanasky R.J., Goos S.M.;

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| | | |
|-----------|--|--|
| RT | "The isoforms of chymotrypsin/elastase from Ascaris lumbricoides: | |
| RT | the primary structure."; | |
| RL | Arch. Biochem. Biophys. | 232:143-161(1984). |
| RP | (2) | |
| RP | NUCLEOTIDE SEQUENCE [mRNA]. | |
| RA | MEBLIN=96297373; | PubMed=9635450; DOI=10.1006/exp.1998.4284; |
| RA | Lu C.C., Nguyen T., Morris S., Hill D., Sakamori J.A.; | |
| RT | "Analysis simplex: mutational bursts in the reactive site centers of | |
| RT | serine protease inhibitors from an ascarid nematode."; | |
| RL | Exp. Parasitol. | 89:257-261(1998). |
| RN | (3) | |
| RP | X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH ELASTASE. | |
| RA | MEBLIN=95006335; | PubMed=7922044; |
| RA | Huang K., Strynadka N.C., Bernard V.D., Peanaiky R.J., James M.N.; | |
| RT | "The molecular structure of the complex of Ascaris | |
| RT | chymotrypsin/elastase inhibitor with porcine elastase."; | |
| RL | Structure 2:679-689(1994). | |
| CC | - FUNCTION: Defends the organism against the host's proteinases. | |
| CC | - SUBCELLULAR LOCATION: Secreted protein. | |
| CC | - SIMILARITY: Contains 1 TIL (trypsin inhibitory-like) domain. | |
| CC | - | |
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| DR | EMBL; U94499; AAC61300.1; -; mRNA. | |
| DR | PDB; 1EAL; X-ray; C/D=1-61. | |
| DR | InterPro; IPR002919; Prot_Inh_CR_TIL. | |
| DR | Pfam; PF01826; TIL; 1 | |
| KM | 3D-structure; Direct protein sequencing; Protease inhibitor; | |
| KM | Serine protease inhibitor. | |
| FT | CHAIN | 1 63 |
| FT | Chymotrypsin/elastase isoform 1. | |
| FT | /Prid=PRO_0000174329. | |
| FT | DOMAIN | 5 60 |
| FT | SITE | 31 32 |
| FT | DISULFID | 5 38 |
| FT | DISULFID | 14 33 |
| FT | DISULFID | 17 29 |
| FT | DISULFID | 21 60 |
| FT | DISULFID | 40 54 |
| FT | CONFLICT | 4 4 |
| FT | CONFLICT | 23 24 |
| FT | TURN | 3 4 |
| FT | TURN | 7 8 |
| FT | STRAND | 10 15 |
| FT | STRAND | 20 22 |
| FT | TURN | 25 26 |
| FT | STRAND | 28 32 |
| FT | STRAND | 34 34 |
| FT | STRAND | 37 39 |
| FT | HELIX | 42 44 |
| FT | TURN | 45 45 |
| FT | STRAND | 46 48 |
| FT | TURN | 50 51 |
| FT | STRAND | 52 52 |
| FT | STRAND | 54 56 |
| FT | STRAND | 55 59 |
| FT | HELIX | 57 59 |
| SO | SEQUENCE | 63 AA; 6862 MW; 5DC10DE75B375F16 CRC64; |
| Oy | Query Match | 28.6%; Score 57.5; DB 1; Length 63; |
| Oy | Best Local Similarity | 37.1%; Pred. No. 6; |
| Oy | Matches 13; Conservative | 5; Mismatches 10; Indels 7; Gaps 3; |
| Oy | 1 CSONEYFDSLHACIPQALC--SSNP-PLTCOR 32 | |
| Oy | 1 CGNEVWTE---CTGCEMKCGPDENPCPLMKCR 35 | |
| Db | | |
| RESULT 61 | | |
| ID | OSB10_DROME | |
| AC | OSB10_DROME | PRELIMINARY; PRT; 1061 AA. |
| DT | 12-APR-2005, | integrated into UniProtKB/TrEMBL. |
| DT | 12-APR-2005, | sequence version 1. |

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DE 07-FEB-2006, entry version 5.
ID LD05524P.
GN Name=Fur2;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OX NCBI_TaxId=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkley;
RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,
RA Park S., Wan K., Yu C., Rubin G.M., Ceiniker S.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL: BT021414; AAX33562.1; -; mRNA.
DR FlyBase; FBgn004598; Fur2.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. .; IEA.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR006211; Furin-like.
DR InterPro; IPR006212; Furin repeat.
DR InterPro; IPR002093; Pept_S8_S53.
DR InterPro; IPR002884; P:protonconvertsp.
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF01483; P:proprotein; 1.
DR Pfam; PF00082; Peptidase_S8; 1.
DR SMART; SM00261; EGF; 1.
DR SMART; SM00261; FU; 10.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
DR SEQUENCE 1061 AA; 115700 MW; 4E7F1FC5386FF229 CRC64;

Query Match 28.6%; Score 57.5; DB 2; Length 1061;
Best Local Similarity 34.3%; Pred. No. 1,le+02;
Matches 12; Conservative 5; Mismatches 17; Indels 1; Gaps 1;

Qy 1 CSQNEYPDSLHACIPQQLRCSS-NTPPLTCQRYC 34
Db 580 GSESEFYQVEGQCRCRCHASCSCNGPADTSCCTSC 614

RESULT 62
ID FUR2 DROME STANDARD; PRT; 1679 AA.
AC P30432; Q24301; O8S2S2;
DT 01-APR-1993, integrated into UniProtKB/Swiss-Prot.
DT 25-NOV-2002, sequence version 2.
DT 07-MAR-2006, entry version 65.
DE Furin-like protease 2 precursor (EC 3.4.21.75) (Furin-2).
GN Name=Fur2; ORFNames=CG18734;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM D).
RC STRAIN=iso-1, Oregon-R, and Tuebingen;
RX MEDLINE=92381036; PubMed=1512259;
RA Roebroek A.J.M., Creemers J.W.M., Pauli I.G.L., Kurzik-Dumke U.,
RA Rentrop M., Gattei E.A.F., Lemissen J.A.M., van de Ven W.J.M.;
RT "Cloning and functional expression of Dfurin2, a subtilisin-like
RT proprotein processing enzyme of Drosophila melanogaster with multiple
RT repeats of a cysteine motif.";
J. Biol. Chem. 267:17208-17215(1992).

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RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORM D).
RC STRAIN=iso-1;
RX MEDLINE=95186060; PubMed=7880443;
RA Roebroek A.J.M., Ayoubi T.A.Y., Creemers J.W.M., Pauli I.G.L.,
RA van de Ven W.J.M.;
RT "The Dfur2 gene of Drosophila melanogaster: genetic organization,
RT expression during embryogenesis, and pro-protein processing activity
RT of its translational product Dfurin2.";
RN DNA Cell Biol. 14:223-234(1995).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blake J., Champ E., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Bens P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fustin K.J., Gabrieli A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwa C.,
RA Jalali B.E., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Keichum K.A.,
RA Kimmel M.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lascko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Martel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheibel F., Shen H.,
RA Shue B.C., Sider-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao O., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RN Science 287:2185-2195(2000).
RN [4]
RP GENOME REANNOTATION AND ALTERNATIVE SPLICING.
RX MEDLINE=22426069; PubMed=12537572;
RA Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochink S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Betencourt B.R., Ceiniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RN J. Genom. Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 305-1679 (ISOFORM A).
RC STRAIN=Berkley; TISSUE=Embryo;
RX MEDLINE=22426066; PubMed=12537569;
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champagne M.,
RA George R.A., Guarini H., Krommiller B., Pacleb J.M., Park S., Wan K.H.,
RA Rubin G.M., Ceiniker S.E.;
RT "A Drosophila full-length cDNA resource.";

```

RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
 CC -i- FUNCTION: Furin is likely to represent the ubiquitous endoprotease
 CC activity within constitutive secretory pathways and capable of
 CC cleavage at the RX(K/R) consensus motif (By similarity).
 CC -i- CATALYTIC ACTIVITY: Release of mature proteins from their
 CC propeptides by cleavage of -Arg-Xaa-Iaa-Arg-|-Zaa-bonds, where
 CC Xaa can be any amino acid and Yaa is Arg or Lys. Releases albumin,
 CC complement component C3 and von Willebrand factor from their
 CC respective precursors.
 CC -i- INTERACTION:
 CC Q9MAG3:CG15470; NbExp=1; InAct=EBI-496684, EBI-162037;
 CC Q94524:DI630F; NbExp=1; InAct=EBI-496684, EBI-158251;
 CC -i- ALTERNATIVE PRODUCTS:
 CC Name=D; Synonyms=E;
 CC IsoId=P30432-1; Sequence=displayed;
 CC Name=A; Synonyms=B;
 CC IsoId=P30432-2; Sequence=VSP_009365;
 CC Note=No experimental confirmation available;
 CC -i- TISSUE SPECIFICITY: Transient expression in a subset of central
 CC nervous system neurons during embryonic stages 12-13. Expression
 CC in developing tracheal tree from stage 13 to end of embryonic
 CC development.
 CC -i- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
 CC -i- SIMILARITY: Belongs to the peptidase S8 family. Furin subfamily.
 CC -----
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 CC -----
 DR EMBL: M94375; AAA28551.1; -; mRNA.
 DR EMBL: U3831; AAA69860.1; -; Genomic DNA.
 DR EMBL: AE003502; AAF48598.2; -; Genomic DNA.
 DR EMBL: AE003502; AAN09400.1; -; Genomic DNA.
 DR EMBL: AY070553; AAL48024.1; ALT_INIT; mRNA.
 DR PIR: A43434; A43434.
 DR HSP: P23186; IPR80.
 DR Interact: P30432; -.
 DR MEROPS: S08.049; -.
 DR Ensemble: CG18734; Drosophila melanogaster.
 DR Flybase: Fgn0004598; Fur2.
 DR Biocyc: DMEL-XXX-02:DMEL-XXX-02-002159-MONOMER; -.
 DR Biocyc: DMEL-XXX-02:DMEL-XXX-02-002161-MONOMER; -.
 DR Biocyc: DMEL-XXX-02:DMEL-XXX-02-002163-MONOMER; -.
 DR GO: GO:0004276; F: furin activity; IDA.
 DR GO: GO:0005515; F: protein binding; IPI.
 DR InterPro: IPR006210; EGF.
 DR InterPro: IPR006211; Furin-like.
 DR InterPro: IPR006212; Furin_repeat.
 DR InterPro: IPR002029; Pept_S8_S53.
 DR InterPro: IPR002884; Pp10nconvertsp.
 DR Pfam: PF00757; Furin-like; 1.
 DR Pfam: PF01483; P: proprotein; 2.
 DR Pfam: PF00082; Peptidase S8; 1.
 DR PRINTS: PR00723; SUBTILISIN.
 DR ProDom: PD000717; Pp10nconvertsp; 1.
 DR SMART: SM00181; EGF; 1.
 DR SMART: SM00261; FU; 10.
 DR PROSITE: PS00136; SUBTILASE ASP; 1.
 DR PROSITE: PS00137; SUBTILASE HIS; 1.
 DR PROSITE: PS00138; SUBTILASE_SER; 1.
 DR Alternative splicing: Complete proteome; Glycoprotein; Hydroxylase;
 DR Membrane; Protease; Repeat; Serine protease; Signal; Transmembrane;
 DR Zymogen.
 FT SIGNAL 1 ? 318 Potential.
 FT PROPEP ? 318 /Frida-PRO_0000027024.
 FT CHAIN 319 1679 Furin-like protease 2.
 FT TRANSMEM 1512 1532 /Frida-PRO_0000027025.
 FT TOPO_DOM 1533 1679 Potential.
 FT REPEAT 961 1006 Cytoplasmic (Potential).
 FT REPEAT 1007 1056 1.
 FT REPEAT 1057 1103 2.
 FT 3.

FT REPEAT 1104 1152 4.
 FT REPEAT 1153 1204 5.
 FT REPEAT 1205 1253 6.
 FT REPEAT 1254 1298 7.
 FT REPEAT 1299 1345 8.
 FT REPEAT 1346 1392 9.
 FT REPEAT 1393 1443 10.
 FT REGION 961 1443 10 X tandem repeats, Cys-rich.
 FT ACT_SITE 417 417 Charge relay system (By similarity).
 FT ACT_SITE 456 456 Charge relay system (By similarity).
 FT ACT_SITE 637 637 Charge relay system (By similarity).
 FT CARBOHYD 3 3 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 109 109 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 130 130 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 205 205 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 442 442 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 480 480 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 927 927 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1060 1060 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1181 1181 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1274 1274 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1277 1277 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1439 1439 N-linked (GlcNAc...) (Potential).
 FT DISULFID 473 629 By similarity.
 FT DISULFID 565 595 By similarity.
 FT VARSPPLIC 386 386 L -> LVSK (in isoform A).
 FT CONFLICT 152 153 Missing (in Ref. 1).
 FT CONFLICT 177 177 V -> F (in Ref. 1).
 FT CONFLICT 213 213 V -> VDQL (in Ref. 1).
 SQ SEQUENCE 1679 AA; 183370 MW; 3FE749F0B21CP6 CRC64;
 Query Match 28.6%; Score 57.5; DB 1; Length 1679;
 Best Local Similarity 34.3%; Pred. No. 1.8e+02;
 Matches 12; Conservative 5; Mismatches 17; Indels 1; Gaps 1;
 QY 1 CSQNEYFDSLHACIPCOLRCSS-NTPLTCORYC 34
 Db 1198 GSESEYSGVEGCRPCNASGSCNGPDTSTSC 1232
 RESULT 63
 ID OS1AP4 ENTHI PRELIMINARY; PRT; 304 AA.
 OS1AP4:
 DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
 DT 07-JUN-2005, sequence version 1.
 DE Cysteine-rich surface protein, putative.
 DE ORFname=32.t00048;
 GN Entamoeba histolytica HM-1:IMSS.
 OC Eukaryota, Entamoebidae, Entamoeba.
 OX NCBI_TaxID=294381;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=HM-1:IMSS;
 RX Pubmed=15729342; DOI=10.1038/nature03291;
 RA Lofthus B.J., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
 RA Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
 RA Suh B., Pop M., Duchene M., Ackers J., Jannich E., Leippe M.,
 RA Hofst B., Bruchhaus I., Willhoelt U., Bhattacharya A.,
 RA Chillingworth T., Churcher C.M., Hance Z., Harris B., Harris D.,
 RA Jagels K., Moulé S., Mungall K.L., Ormond D., Squares R.,
 RA Whitehead S., Quail M.A., Rabinowitsch E., Norbertczak H., Price C.,
 RA Wang Z., Gillen N., Gilchrist C., Stroup S.E., Bhattacharya S.,
 RA Lohia A., Foster P.G., Sichert-Ponten T., Weber C., Singh U.,
 RA Mukherjee C., El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M.,
 RA Barrett B.G., Fraser C.M., Hall N.;
 RT "The genome of the protist parasite Entamoeba histolytica.";
 RL Nature 433:865-868(2005).
 CC -i- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR000436; Sush1_SCR_CCP.
DR InterPro: IPR001245; Tyr_pkinase.
DR InterPro: IPR008266; Tyr_pkinase_AS.
DR Pfam: PF000008; EGF_2.
DR Pfam: PF07645; EGF_CA_1.
DR Pfam: PF07714; Kinase_Tyr_1.
DR Pfam: PF00084; Sush1_1.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00032; CCP; 1.
DR SMART: SM00181; EGF; 3.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00219; Tyrc; 1.
DR PROSITE: PS0010; ASK_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 2.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00026; EGF_3; 3.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS50109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50923; SUSH1; 1.
DR Kase: Receptor.
SQ SEQUENCE 1476 AA; 157131 MW; BEFOA03DDC3AD997 CRC64;

Query Match 28.1%; Score 56.5; DB 2; Length 1476;
Best Local Similarity 35.3%; Pred. No. 2.1e+02;
Matches 12; Conservative 4; Mismatches 15; Indels 3; Gaps 1;

Oy 1 CSONEYFDSLILACIPCOQ---RCSNTPPLTCQY 31
Db 110 CTISRNFSDLPPSCVPCPLNTRADNHAATCQ 143

RESULT 69
O51EF3_ENTH1 PRELIMINARY; PRT; 1704 AA.
ID O51EF3_ENTH1
AC O51EF3
DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 07-JUN-2005, sequence version 1.
DE 07-FEB-2006, entry version 10.
DE Protein kinase, putative.
GN ORFNames=10.t00023;
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=294381;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=HM-1:IMSS;
RX PubMed=15729342; DOI=10.1038/nature03291;
RA Loftus B.J., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
RA Amelio P., Roncaglia P., Bettman M., Hitt R.P., Mann B.J., Nozaki T.,
RA Suh B., Pop M., Duchene M., Ackers J., Tannich J., Lelepe M.,
RA Hofer M., Bruchhaus I., Willhoft U., Bhattacharya A.,
RA Chillingworth T., Churcher C.M., Hance Z., Harris B., Harris D.,
RA Jagale K., Moule S., Mungall K.L., Ormond D., Squares R.,
RA Whitehead S., Quail M.A., Rabinowitsch E., Norbertczak H., Price C.,
RA Wang Z., Gillen N., Gilchrist C., Stroup S.B., Bhattacharya S.,
RA Lohia A., Foster P.G., Sichteritz-Ponten T., Weber C., Singh U.,
RA Mukherjee C., El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M.,
RA Barrell B.G., Fraser C.M., Hall N.;
RA "The genome of the protist parasite Entamoeba histolytica.";
RT Nature 433:865-868(2005).
RL - CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC Distributed under the Creative Commons Attribution-NonDerivs license
CC

CC EMBL: AAF80100050; EAL51244.1; -; Genomic_DNA.
DR GO: GO:0005524; F:AMP binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0006468; F:protein amino acid phosphorylation; IEA.
DR InterPro: IPR006212; Furin_repeat.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_kin AS.
DR InterPro: IPR002290; Ser_thr_pkin AS.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; Kinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00261; FU; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR Kase: Kinase.
SQ SEQUENCE 1704 AA; 195112 MW; 0PDEF183DA12770E3 CRC64;

Query Match 28.1%; Score 56.5; DB 2; Length 1704;
Best Local Similarity 39.4%; Pred. No. 2.5e+02;
Matches 13; Conservative 3; Mismatches 12; Indels 5; Gaps 1;

Oy 6 YFDSLILACIPCOQ---LRCSNTPPLTCQRY 33
Db 754 YFEHKEFSCITCSQGLFTNNCSSITNVLYCOSY 786

RESULT 70
O60WC9_CABER PRELIMINARY; PRT; 135 AA.
ID O60WC9_CABER
AC O60WC9;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DE 07-FEB-2006, entry version 6.
DE Hypothetical protein CBG19174.
GN Name=CBG19174;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=AF16;
RX PubMed=14624247; DOI=10.1371/journal.pbio.0000045;
RA Stein L.D., Bao Z., Blaesar D., Blumenthal T., Brent M.R., Chen N.,
RA Chinnwalla A., Clarke L., Clee C., Coghlan A., Coulson A.,
RA D'Eustachio P., Fitch D.H.A., Fulton L.A., Fulton R.E.,
RA Griffiths-Jones S., Harris T.W., Hillier L.W., Kamath R.,
RA Kuwabara P.E., Mardis E.R., Marra W.A., Miner T.L., Mink P.,
RA Mullikin J.C., Plumb R.W., Rogers J., Schein J.E., Sommer M.,
RA Spieth J., Stajich J.E., Wei C., Willey D., Wilson R.K., Dublin R.,
RA Waterston R.H.;
RT "The genome sequence of Caenorhabditis briggsae: a platform for
RT comparative genomics.";
RL PLOS Biol. 1:166-192(2003).
RL - CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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Matches 13; Conservative 3; Mismatches 13; Indels 6; Gaps 2;
 QY 1 CSQNEYPFSLHACIP-COLRCSNTPPTTCORC 34
 DB 80 CPQNEQFRGGCTACEPTCE-----NPKPMCTKQC 109

RESULT 71
 ID ZN393 MOUSE STANDARD; PRT; 341 AA.
 AC 08CPA7; Q3JUT30; Q6P233; Q9D351;
 DT 08-NOV-2005, integrated into UniProtKB/Swiss-Prot.
 DT 08-NOV-2005, sequence version 2.
 DT 07-MAR-2006, entry version 21.
 DE Zinc finger protein 393 (germ cell-specific zinc finger protein).
 GN Name=Znf393; Synonyms=Gzf, Zfp393;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 NCBI Taxid=10090;
 [1]
 NP NUCLEOTIDE SEQUENCE [MRNA], AND TISSUE SPECIFICITY.
 RC STRAIN=129/Sv X C57BL; TISSUE=Testis;
 RC MEDLINE=22239718; PubMed=12351194; DOI=10.1016/S09925-4773(02)00258-7;
 RA Yan W., Burns K.H., Ma L., Matzuk M.M.;
 RT "Identification of Zfp393, a germ cell-specific gene encoding a novel
 zinc finger protein.";
 RL Mech. Dev. 118:233-239 (2002).
 [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6J; TISSUE=Egg;
 RC PubMed=16141072; DOI=10.1126/science.1112014;
 RA Ouyama R., Ravasi T., Lennard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilm M., Altman J., Attaluri R.N., Bailey T.L.,
 RA Ambesi-Impombato A., Apweiler R., Attaluri R.N., Banno H., Chalk A.M.,
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhary V., Christofels A., Clutterbuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
 RA Fletcher C.F., Fukushima T., Furumasa T., Gargioli M., Gariboldi M.,
 RA Georgianni-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hill D., Hummel L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 RA Jaki D., Huminicki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 RA Jaki D., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kunzendorf S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 RA Liun S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Motestegui-Tabar S., Mulder N., Nakano H., Nakachi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Tak K.,
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yang K.,
 RA Yamashita H., Zdobych E., Zhu S., Zimmer A., Hilde W., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Willemsen T., Matic J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Aizawa T.,
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Kono H., Nakano K., Ninomiya N.,
 RA Nishio T., Okada M., Plessey C., Shibata K., Shitaki T., Suzuki S.,
 RA Tagami M., Waki K., Wataniki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 [3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6J; TISSUE=Egg;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Miall S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huij S.W.,
 RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahay J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: May be a germ cell-specific transcription factor that
 CC plays important roles in spermatid differentiation and oocyte
 CC development.
 CC -1- TISSUE SPECIFICITY: Exclusively expressed in testis and ovary.
 CC localized to step 3-8 spermatids in testis and growing oocytes in
 CC ovary.
 CC -1- SIMILARITY: Contains 3 C2H2-type zinc fingers.
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 CC -----

DR EMBL: AF508984; AAN31656.1; -; mRNA.
 DR EMBL: AK018361; BAB31177.1; -; mRNA.
 DR EMBL: AK139827; BAE24150.1; -; mRNA.
 DR EMBL: BC064748; AAB64748.1; -; mRNA.
 DR Ensembl: ENSMUSG0000048626; Mus musculus.
 DR MGI: MGI:2181068; Zfp393.
 DR GO: GO:0007276; P:gametogenesis; IDA.
 DR InterPro: IPR007087; Znf_C2H2.
 DR Pfam: PF00096; Zf_C2H2; 3.
 DR ProDom: PD000003; Znf_C2H2; 2.
 DR SMART: SM00355; Znf_C2H2; 3.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 3.
 DR PROSITE: PS0157; ZINC_FINGER_C2H2_2; 3.
 KW DNA-binding; Metal-binding; Nuclear protein; Repeat; Transcription;
 KW Transcription regulation; Zinc; Zinc-finger.
 FT CHAIN 1 341
 FT /FTID=PRO_0000047556.
 FT ZN_FING 256 280
 FT C2H2-type 1.
 FT ZN_FING 286 310
 FT C2H2-type 2.
 FT ZN_FING 316 338
 FT C2H2-type 3.
 FT CONFLICT 141 141 S -> G (in Ref. 3).
 FT CONFLICT 165 165 L -> M (in Ref. 2; BAB31177).
 SQ SEQUENCE 341 AA; 38076 MW; 03F400D4485DDE3A CRC64;

Query Match 27.9%; Score 56; DB 1; Length 341;
 Best Local Similarity 29.4%; Pred. No. 54;
 Matches 10; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

QY 1 CSQNEYPFSLHACIP-COLRCSNTPPTTCORC 34
 DB 60 CNERWESQILRSLEHVRCSQALPIPFQNYC 93

RESULT 72
 ID 04KLX7 XENLA PRELIMINARY; PRT; 387 AA.
 AC 04KLX7;
 DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.

DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 15.
 DE LOC398134 protein (Fragment).
 GN Name=LOC398134.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 NCBI_Taxid=8335;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 MEDLINE=22388257; PubMed12477932; DOI=10.1073/pnas.242603899;
 RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altchul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Smalins D.E.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 MEDLINE=22341132; PubMed12454917; DOI=10.1002/4vdy.10174;
 RA Klein S.L., Strusberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RA Klein S., Strusberg R.;
 RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
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 CC -----
 CC EMBL: BC068640; AH68640.1; -; mRNA.
 DR GO:0005515; F:protein binding; IEA.
 DR GO:0004872; F:receptor activity; IEA.
 DR GO:000165; P:signal transduction; IEA.
 DR InterPro: IPR004488; Death.
 DR InterPro: IPR011029; DEATH_1like.
 DR InterPro: IPR011368; TNFR_C6.
 DR Pfam: PF00531; Death_1.
 DR Pfam: PF00020; TNFR_C6; 3.
 DR SMART: SM00005; DEATH_1.
 DR SMART: SM00208; TNFR; 4.
 DR PROSITE: PS00017; DEATH DOMAIN; 1.
 DR PROSITE: PS00652; TNFR_NGFR_1; 3.
 DR PROSITE: PS00650; TNFR_NGFR_2; 4.
 FT NON_TER 1
 SQ SEQUENCE 392 AA; 42538 MW; 0B41CED6CCE080FB CRC64;
 Query Match 27.9%; Score 56; DB 2; Length 392;
 Best Local Similarity 25.4%; Pred. No. 63;
 Matches 16; Conservative 6; Mismatches 11; Indels 30; Gaps 3;

QY 1 CSQNEYPFSLHACIPCOU-----RC-----SSNTPELTQ 31
 DB 108 CPERGYLDS-NGICLPQCLCSKGHWGVSQCTHNKNTVQCLSSGRYSVSESSPCLPCR 166
 QY 32 RYC 34
 DB 167 TEC 169
 RESULT 75
 ID 03CXH7 ALTAT PRELIMINARY; PRT; 544 AA.
 AC 03CXH7;
 DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.
 DT 22-NOV-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Electron-transferring-flavoprotein dehydrogenase (EC 1.5.5.1).
 GN ORFNames=PaclDRAPT_0751;
 OS Pseudalteromonas atlantica T6c.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
 OC Pseudalteromonadales; Pseudalteromonas.
 NCBI_Taxid=342610;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=T6c;
 RA US DOE Joint Genome Institute (JGI-PGF);
 RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler J.C., Glavina T.,
 RA Hammon N., Istrati S., Pittluck S., Richardson P.;
 RT "Sequencing of the draft genome and assembly of Pseudalteromonas
 RT atlantica T6c.";
 RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=T6c;
 RA US DOE Joint Genome Institute (JGI-ORNL);
 RA Larimer F., Land M.;
 RT "Annotation of the draft genome assembly of Pseudalteromonas
 RT atlantica T6c.";
 RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
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 CC -----
 CC EMBL: AAKP01000001; EAC069851.1; -; Genomic DNA.
 DR GO:0004174; F:electron-transferring-flavoprotein dehydrog. .; IEA.
 DR GO:0006118; F:oxidoreductase activity; IEA.
 DR GO:0006118; F:electron transport; IEA.
 DR GO:0008152; P:metabolism; IEA.
 DR GO:0009228; P:thiamin biosynthesis; IEA.
 KW Oxidoreductase.
 SQ SEQUENCE 544 AA; 60059 MW; 5322D5B507348A94 CRC64;
 Query Match 27.9%; Score 56; DB 2; Length 544;
 Best Local Similarity 26.7%; Pred. No. 88;
 Matches 16; Conservative 5; Mismatches 13; Indels 26; Gaps 3;

QY 1 CSQNEYPFSLHACIPCOU-----RC-----SSNTPELTQ 31
 DB 430 COKIDYPRXSVLSFQKLSVFLSNTNHEEDPCHLKUKDNTPITVNLPLYDEBAPQRYC 489
 RESULT 76
 ID 060K18 CAEBR PRELIMINARY; PRT; 938 AA.
 AC 060K18;
 DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
 DT 23-NOV-2004, sequence version 1.
 DT 07-FEB-2006, entry version 7.
 DE Hypothetical protein CBG24263.
 GN Name=CBG24263;


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FT CARBOHYD 1654 1654 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 1843 1843 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 1965 1965 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 2122 2122 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 2165 2165 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 2178 2178 N-linked (GlcNAc...) (Potential)
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FT CARBOHYD 2359 2359 N-linked (GlcNAc...) (Potential)
FT DISULFID 2370 2381 By similarity.
FT DISULFID 2392 2390 By similarity.
FT DISULFID 2401 2401 By similarity.
FT CONFLICT 823 823 C -> V (in Ref. 1; AA sequence).
FT CONFLICT 923 923 S -> Y (in Ref. 1; AA sequence).
FT CONFLICT 965 965 W -> Y (in Ref. 1; AA sequence).
FT CONFLICT 1241 1241 S -> K (in Ref. 1; AA sequence).
SQ SEQUENCE 2476 AA; 270365 MW; A13B690375A6546C CRC64;

Query Match 27.9%; Score 56; DB 1; Length 2476;
Best Local Similarity 31.6%; Pred. No. 4.2e+02;
Matches 12; Conservative 8; Mismatches 14; Indels 4; Gaps 2;

OY 1 CSQNEVFDLSLHACIP-CQ---LRCSNTPPLTCQRYC 34
Db 1851 CSAHSVYTCVBPSCPCDDPBGQCTGAAPSTCEGC 1888

RESULT 78
O9EP28_9HEPC PRELIMINARY; PRT; 146 AA.
AC O9EP28;
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 13.
DE Polypeptide (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_Taxid=11103;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Shizawa H., Shao L., Jiang Q., Togashi H., Zhang X., Ishibashi M.,
RA Watanabe H., Saito T., Takahashi T., Ohba K., Mizokami M.;
RA Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
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CC
DR EMBL; AB030968; BAB1770.1; -, Genomic RNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR002519; HCV env.
DR Pfam; PF01539; HCV env; I.
KM Envelope protein; Polypeptide; Transmembrane.
FT NON_TER 1
FT NON_TER 146
SQ SEQUENCE 146 AA; 15763 MW; 9C67046FD8507C30 CRC64;

Query Match 27.6%; Score 55.5; DB 2; Length 146;
Best Local Similarity 31.8%; Pred. No. 26;
Matches 14; Conservative 6; Mismatches 13; Indels 11; Gaps 3;

OY 1 CSQNEVFDLSLHACIP-CQ---LRCSNTPPLTCQRY 33
Db 34 CSNNSITWQTDVAHLPGCVCESDNGTLRCWIGVTPNVAKY 77

RESULT 79
O9VE40_DROME PRELIMINARY; PRT; 225 AA.
AC O9VE40;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 24.

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DE CG7714-PA (RH24988P).
GN ORFNames=CG7714; Dmel CG7714;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandal D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jatalin M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mounklov G., Mlshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puti V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Switskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye Y., Yeh R.-F., Zaveri J.S., Zhan M., Zhu G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhou S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
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RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Switskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatic
RT genome perspective."
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

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RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Bertram B.P.,
RA Belcounet B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
RA Stapleton M., Yandeh C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.,
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RT Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN
RN NUCLEOTIDE SEQUENCE.
RG Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Paclele J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.,
RT "Drosophila melanogaster release 4 sequence."
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN
RN NUCLEOTIDE SEQUENCE.
RG Flybase;
RU Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.
RN
RN NUCLEOTIDE SEQUENCE.
RC STRAIN-Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champagne M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarini H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungai C.J., Nunoo J., Paclele J., Pargass V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.,
RU Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
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CC
CC EMBL; AE003723; AAF55589.1; -; Genomic DNA.
DR EMBL; AY071711; AAL49333.1; -; mRNA.
DR Flybase; FBgn0038645; CG714.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002357; Pfam; Pf01607; CEM_14; 1.
DR Pfam; PF01607; CEM_14; 1.
SQ SEQUENCE 225 AA; 22568 MW; 6E6A7C3E301CB30 CRC64;
Query Match 27.6%; Score 55.5; DB 2; Length 225;
Best Local Similarity 31.4%; Pred. No. 41;
Matches 11; Conservative 6; Mismatches 13; Indels 5; Gaps 1;
QY 1 CSONEYFDSLHACIPC-----QLRCSSNTPPLTC 30
Db 75 CGEDTYFNALORCVACANYFPBAGCSSLPINVTG 109
RESULT 80
Q4IFW6 GIBZE PRELIMINARY; PRT; 436 AA.
AC Q4IFW6;
DT 16-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Hypothetical protein.
GN ORFNames=FG03892.1;
OS Gibberella zeae (Fusarium graminearum).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=5518;
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RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=PH-1 / NRRL 31084;
RA Birren B.W., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arabach H.M., Barua N., Bastien V., Bloom T., Boguslavskiy L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,

RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., Dearellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engle R.,
RA Erickson J., Fero S., Ferreira P., Fitzgerald M., Gage D.,
RA Galagan J., Gadyia S., Gnerre S., Gnanam L., Grand-Pierre N.,
RA Hatz N., Hagoopian D., Hages B., Hall U., Horton L., Hulme W.,
RA Iliev I., Jaffe D., Johnson S., Jones C., Kamel M., Kamet A.,
RA Karatas A., Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G.,
RA Lui A., Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J.,
RA Manning J., Matthews C., Mauceli E., McCarthy M., Meidrim J.,
RA Menes L., Mohova T., Mlenga V., Murphy T., Naylor J., Nguyen C.,
RA Nicol R., Nielsen C.B., Norbu C., O'Connor T., O'Donnell P.,
RA O'Neill D., Oliver J., Peterson K., Phunhthang P., Pierre N.,
RA Purcell S., Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C.,
RA Rogov P., Roman J., Schauer S., Schupbach R., Seaman S., Severy P.,
RA Smirnov S., Smith C., Spencer B., Stange-Thomann N., Stojanovic N.,
RA Stubbs M., Talmas J., Testaye S., Theodore J., Topham K., Travers M.,
RA Vasiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zemdek L., Zimmer A., Zody M.,
Lander E.S.,
RT "Fusarium graminearum genome sequence."
RT Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC
CC EMBL; AAC001000168; EAA73360.1; -; Genomic DNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR001138; Fungal_Trcrp_N.
DR Pfam; PF04082; Fungal_trans_1.
DR Pfam; PF04172; Zn_c1us; 1.
DR PRINTS; PR00054; FUNGALNCYS.
DR SMART; SM00066; GAL4_1.
DR PROSITE; PS00048; ZN2_Cy6_FUNGAL_2; 1.
KW Complete proteome; DNA-binding; Hypothetical protein; Metal-binding;
KW Nuclear protein; Transcription; Transcription regulation; Zinc.
SQ SEQUENCE 436 AA; 49023 MW; 23722102A0B89CF9 CRC64;
Query Match 27.6%; Score 55.5; DB 2; Length 436;
Best Local Similarity 36.4%; Pred. No. 82;
Matches 12; Conservative 6; Mismatches 10; Indels 5; Gaps 2;
QY 2 SQNEYFDSLHACIPC-----QLRCSSNTPPLTCQ 31
Db 10 SQRPY--KVRQACDPCRRKIRKIRNGSNPCVNCQ 40
RESULT 81
Q86WK8 HUMAN PRELIMINARY; PRT; 673 AA.
AC Q86WK8;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE URG11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN
RN NUCLEOTIDE SEQUENCE.
RP Lian Z., Liu J., Li L., Li X., Tufan S.N.L., Clayton M., Wu M.,
RA Wang H., Arbutnot P., Kew M., Feltelson M.A.,
RT Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whiteaker C., Wilming L.,
RA Wyshna-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690(2001).
[6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Thymus;
EX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carrincci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Komori H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:1617-1630(2000).
[7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Thymus;
EX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carrincci P.,
RA Komori H., Akiyama J., Nishi K., Katsunari T., Tashiro H., Itoh M.,
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RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Thymus;
EX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Komori H., Murata M., Nakamura M., Nimomiya N.,
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RA Shibata K., Shizaki T., Tagami M., Tagami Y., Waki K., Watabiki A.,
RA Muramatsu M., Hayashizaki Y.;
RT Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
[9]
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[10]
DR EMBL, AK153937; BAE32265.1; -; mRNA.
DR GO, GO:0005509; F:calcium ion binding; IEA.
DR GO, GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro, IPR000152; Asx_hydroxyl_5.
DR InterPro, IPR006210; EGF_3.
DR InterPro, IPR00742; EGF_3.
DR InterPro, IPR001881; EGF_Ca_bd.
DR InterPro, IPR013091; EGF_Ca_bd_2.
DR InterPro, IPR013111; EGF_extraCell.
DR InterPro, IPR013032; EGF_like_reg.
DR InterPro, IPR001304; Lectin_C.
DR InterPro, IPR004094; Prot_inh_antistn.
DR InterPro, IPR006552; VWC_out.
DR InterPro, IPR001007; VWF_C.
DR Pfam, PF02822; Antifibrin_1.
DR Pfam, PF07645; EGF_CA_3.
DR Pfam, PF00093; VWC_5.
DR SMART, SM00181; EGF_4.
DR SMART, SM00179; EGF_CA_3.
DR SMART, SM00214; VWC_6.
DR PROSITE, PS00010; ASX_HYDROXYL_3; UNKNOWN_1.
DR PROSITE, PS00022; EGF_1; UNKNOWN_1.
DR PROSITE, PS01186; EGF_2; 2.
DR PROSITE, PS00026; EGF_3; 3.
DR PROSITE, PS01187; EGF_CA_3.
DR PROSITE, PS01208; VWC_1; 4.

DR PROSITE, PS0184; VWC_2; 4.
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Query Match 27.6%; Score 55.5; DB 2; Length 929;
Best Local Similarity 37.5%; Pred. No. 1.8e+02;
Matches 12; Conservative 4; Mismatches 11; Indels 5; Gaps 1;
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CY 4 NEYFSLHACIPC-----QRCSSNTPPLTC 30
DB 631 NETPSPVLDPCPLSCICLLGSVACSPVDCPRTC 662
[12]
RESULT 83
ID 096DN2 HUMAN PRELIMINARY; PRT; 955 AA.
AC 096DN2-
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DE 07-MAR-2006, entry version 19.
DE CDNA FLJ32009 f16, clone NT2RP7009498, weakly similar to FIBULIN-1,
DE ISOFORM A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakematsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Ohyashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahata K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagasuma M., Shiratori A.,
RA Sudo H., Hosoki T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsura N., Sato K., Tanikawa M., Yamazaki M.,
RA Nimomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hirao K., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hoshino T., Kusanagi J.,
RA Kanehori K., Takahashi-Fuji A., Hara H., Tanase T.-O., Nomura Y.,
RA Togaya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotaka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara Y., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hiro M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Ohtani R., Kawakami T., Noguchi S., Itoh T., Shigetani K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togoishi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuo Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs";
RL Nat. Genet. 36:40-45(2004).
[13]
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[14]
DR EMBL, AK056571; BAB71219.1; -; mRNA.
DR HSP, P00743; 1CCF.
DR Ensemble, ENSG00000167992; Homo sapiens.
DR GO, GO:0005509; F:calcium ion binding; IEA.
DR GO, GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro, IPR000152; Asx_hydroxyl_5.
DR InterPro, IPR006210; EGF_3.
DR InterPro, IPR00742; EGF_3.
DR InterPro, IPR001881; EGF_CA_bd.


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DR InterPro: IPR013091; EGF_Ca_bd_2.
DR InterPro: IPR013111; EGF extracell.
DR InterPro: IPR013032; EGF like reg.
DR InterPro: IPR001304; Lectin_C.
DR InterPro: IPR006552; VWC out.
DR InterPro: IPR001007; VWF_C.
DR Pfam: PF02822; Antistasin_1.
DR Pfam: PF07974; EGF_2; 1.
DR Pfam: PF07645; EGF_CA; 3.
DR Pfam: PF00093; VWC; 5.
DR SMART: SM00181; EGF; 4.
DR SMART: SM00179; EGF_CA; 3.
DR SMART: SM00214; VWC; 6.
DR PROSITE: PS00010; ASK_HYDROXYL; 3.
DR PROSITE: PS00615; C_TYPE_LECTIN_1; UNKNOWN_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS00026; EGF_3; 3.
DR PROSITE: PS01187; EGF_CA; 3.
DR PROSITE: PS01208; VWFC_1; UNKNOWN_5.
DR PROSITE: PS0184; VWFC_2; 5.
DR SQ SEQUENCE 955 AA; 9985 MW; 88B0DCA8AABA9188 CRC64;

Query Match 27.6%; Score 55.5; DB 2; Length 955;
Best Local Similarity 37.5%; Pred. No. 1.8e+02;
Matches 12; Conservative 4; Mismatches 11; Indels 5; Gaps 1;

Qy 4 NEYFDSLLHACIPC-----QLRCSSTNPPLTC 30
Db ||| ||| ||| ||| ||| ||| ||| ||| |||
639 NETPFSVLDPCLSLCGLGVACSPVDCPITC 670

RESULT 84
Q9ZU00 ARATH
ID O9ZU00 ARATH PRELIMINARY; PRT; 989 AA.
AC O9ZU00;
DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1999, sequence version 1.
DE Putative CHP-rich zinc finger protein similar to T10M13.18.
DE F-256-2006, entry version 29.
DS Names: T10M13.24; Synonymus=AT4902180; OrderedLocusNames=At4g02180;
GS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OC NCBI_TaxID=3702;
ON [1]
RX NUCLEOTIDE SEQUENCE.
RP Johnson A.F., de la Bastide M., Lodhi M., Hoffman J., Hasegawa A.,
RA Gnoj L., Gottesman T., Granat S., Hameed A., Kaplan N., Schutz K.,
RA Shondy N., Van Keuren K., Parnell L., Dedhia N., Martienssen R.,
RA McCombie W.;
RT "The sequence of the Arabidopsis thaliana T10M13 BAC.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE.
RP Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M.,
RA Preston R.R., Matero A., Shan R., O'Shaughnessy A., Rodriguez M.,
RA Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N.,
RA Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[3]
RN NUCLEOTIDE SEQUENCE.
RP EU Arabidopsis sequencing project;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[4]
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CC -----
CC EMBL: AF001308; AAC78715.1; -; Genomic DNA.
CC EMBL: AL161493; CAB80711.1; -; Genomic DNA.
CC FIR: T01519; T01519.
CC TAIR: At4g02180; -.

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EMBL; BC070831; AAH70831.1; -; mRNA.
DR HSSP; Q02410; LAQC.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR011993; PH type.
DR InterPro; IPR006020; PTB_PTD.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00023; ANK; 6.
DR Pfam; PF00640; PTD; 1.
DR Pfam; PF00536; SAM_1; 2.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 6.
DR SMART; SM00462; PTB; 1.
DR SMART; SM00454; SAM; 2.
DR PROSITE; PS50297; ANK_REPEAT; 1.
DR PROSITE; PS50088; ANK_REPEAT; 5.
DR PROSITE; PS01179; PTD; 1.
DR PROSITE; PS50105; SAM_DOMAIN; 2.
KW ANK repeat; Repeat.
SQ SEQUENCE 1084 AA; 119307 MW; 4099971A09FFA80C CRC64;

Query Match 27.6%; Score 55.5; DB 2; Length 1084;
Best Local Similarity 37.0%; Pred. No. 2.1e+02;
Matches 10; Conservative 4; Mismatches 10; Indels 3; Gaps 1;

QY 5 EYFDSLLHACIPQLCRSNTPTLTCQ 31
Db 541 QHFSGLHGSSPV--CETKDFPLACE 564

RESULT 86
Q9VLT6 DROME
ID Q9VLT6 DROME PRELIMINARY; PRT; 2898 AA.
AC Q9VLT6;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 3.
DT 07-FEB-2006, entry version 26.
DE CG7466-PA.
GN ORFNames=CG7466, Dmel CG7466;
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anandacides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke T., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D.A., Heiman T.J., Gu Z., Guan P., Harris M.,
RA Hootin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA LaRo P., Lei Y., Levisky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

DR InterPro; IPR001881; EGF Ca bd.
DR InterPro; IPR013091; EGF Ca bd.2.
DR InterPro; IPR013111; EGF extracell.
DR InterPro; IPR002049; EGF laminin.
DR InterPro; IPR013032; EGF_like_reg.
DR InterPro; IPR011498; Kelch_2.
DR InterPro; IPR006652; Kelch_rep.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF07645; EGF CA; 1.
DR Pfam; PF01344; Kelch_1; 7.
DR Pfam; PF07646; Kelch_2; 2.
DR Pfam; PF00053; Laminin_EGF; 4.
DR Pfam; PF01437; PSI; 3.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00181; EGF; 5.
DR SMART; SM00179; EGF CA; 1.
DR SMART; SM00180; EGF_Lam; 3.
DR SMART; SM00423; PSI; 8.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS00022; EGF_1; 6.
DR PROSITE; PS01186; EGF_2; 6.
DR PROSITE; PS00026; EGF_3; 3.
DR PROSITE; PS01187; EGF CA; 1.
DR PROSITE; PS01248; EGF_LAM_1; 4.
DR PROSITE; PS00027; EGF_LAM_2; 4.
SQ SEQUENCE 2898 AA; 323734 MW; 8CE87F618C5DAA51 CRC64;

Query Match 27.6%; Score 55.5; DB 2; Length 2898;

Best Local Similarity 24.0%; Pred. No. 5.8e+02;
Matches 12; Conservative 5; Mismatches 14; Indels 19; Gaps 2;

QY 1 CSQNYFDSLHACIPCOLR-----CSNTPLTQCY 31
DB 1294 CRQSGYGNATPHGCLPCEGNGHQNGLGVNVSNGECYKDNTOGLNCE 1343

RESULT 87

MSRB_VIBPA STANDARD; PRT; 147 AA.
AC Q87MS5;
DT 16-JUN-2003, integrated into UniProtKB/Swiss-Prot.
DT 16-JUN-2003, sequence version 1.
DE PEP-2006, entry version 18.
DE Peptide methionine sulfoxide reductase msrB (EC 1.8.4.6).
GN Name=msrB; OrderedLocusNames=VP2156;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]_ NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=RIMD 2210633 / Serotype O3:K6;
RC MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Taganori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shingawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism distinct from that of V. cholerae";
RL Lancet 361:743-749(2003).
CC -!- CATALYTIC ACTIVITY: Protein L-methionine + thioredoxin disulfide = protein L-methionine S-oxide + thioredoxin.
CC -!- SIMILARITY: Belongs to the msrB Met sulfoxide reductase family.
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CC -----
DR HMBP; BA000031; BAC60419.1; -; Genomic_DNA.
DR ESPP; PI4930; 1L1D.
DR GenomeReviews; BA000031_GR; VP2156.
DR HAMAP; MF_01400; -; 1.

DR InterPro; IPR002579; MsrB.
DR Pfam; PF01641; SelR; 1.
DR ProDom; PD004057; DUF25; 1.
DR TIGRFAMs; TIGR00357; MsrB; 1.
KW Complete proteome; Oxidoreductase.
FT CHAIN 1 147 Peptide methionine sulfoxide reductase
FT msrB.
FT /FTID=PRO_0000140313.
FT By similarity.
SQ SEQUENCE 147 AA; 16644 MW; 089662190EFC3C0F CRC64;

Query Match 27.4%; Score 55; DB 1; Length 147;

Best Local Similarity 28.2%; Pred. No. 31;
Matches 11; Conservative 7; Mismatches 11; Indels 10; Gaps 1;

QY 6 YFDSLHACIPCOLRCS-----NTPPLTQCYC 34
DB 96 YLEDLSHGVMRTETRCASCDSHLGHVFEDGPKTGTGYC 134

RESULT 88

O18118 CAEL PRELIMINARY; PRT; 330 AA.
AC O18118;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DE 07-FEB-2006, entry version 32.
DE Hypothetical protein pgn-71.
GN Name=pgn-71; ORFNames=T23F1.6;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]_ NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=Bristol N2;
RC MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for investigating biology";
RL Science 282:2012-2018(1998).
CC -!- INTERACTION:
CC Q17400:abu-1; N5exp=1; IntAct=EBI-326590, EBI-313842;
CC P91419:abu-11; N5exp=1; IntAct=EBI-326590, EBI-313979;
CC O76840:ppn-1; N5exp=1; IntAct=EBI-326590, EBI-312512;
CC Q21746:R05F9.10; N5exp=1; IntAct=EBI-326590, EBI-312019;
CC P05690:vit-2; N5exp=1; IntAct=EBI-326590, EBI-313756;
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CC -----
DR EMBL; Z81129; CAB03405.1; -; Genomic_DNA.
DR PIR; T25169; T25169.
DR IntAct; O18118; -.
DR Ensemble; T23F1.6; Caenorhabditis elegans.
DR WormBase; WBGene0004153; T23F1.6.
DR WormPeP; T23F1.6; CE14080.
DR GO; GO:0005515; F:protein binding; IPI.
DR InterPro; IPR009475; DUF1096.
DR InterPro; IPR003341; DUF139_Cys_rich.
DR Pfam; PF02363; Ctriplex; 8.
DR Pfam; PF06493; DUF1096; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 330 AA; 36605 MW; F043BIA90D3A8F9 CRC64;

Query Match 27.4%; Score 55; DB 2; Length 330;

Best Local Similarity 28.6%; Pred. No. 71;
Matches 12; Conservative 7; Mismatches 15; Indels 8; Gaps 2;

QY 1 CSQNYFDSLHACIP-----COLRCSNTPLP---TCQRYC 34
DB 59 CASSQYQLOTSQCMFACQSCSCQCSQNTNTQCTQCS 100

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RESULT 89
Q924K7_MERUN PRELIMINARY; PRT; 344 AA.
AC Q924K7;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 21-FEB-2006, entry version 27.
DE Interleukin-12 p40 subunit.
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Gerbillinae; Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21290809; PubMed=11396996; DOI=10.1006/cyto.2001.0866;
RA Gaucher D., Chadee K.;
RT "Molecular cloning of gerbil interleukin 12 and its expression as a
RT bioactive single-chain protein.";
RL Cytochrome 14:177-183(2001).
CC -!- FUNCTION: Cytokine that can act as a growth factor for activated T
CC and NK cells, enhance the lytic activity of NK/lymphokine-
CC activated killer cells, and stimulate the production of IFN-gamma
CC by resting PBMC (By similarity).
CC -!- SUBUNIT: Disulfide-bonded heterodimer of 40 kDa and 35 kDa
CC subunits (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted protein (By similarity).
CC
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CC
CC EMBL; AF288612; AAK33061.1; -; mRNA.
DR HSSP; P29460; 1P45.
DR GO; GO:0005615; C:extracellular space; IEA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR InterPro; IPR003530; Hempt_rcpt_L_F3.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
DR PROSITE; PS08335; IG_LIKE; 1.
KW Cytokine; Immunoglobulin domain; Repeat.
SQ SEQUENCE 344 AA; 39375 MW; 21B513448D73E8CB CRC64;

Query Match 27.4%; Score 55; DB 2; Length 344;
Best Local Similarity 47.4%; Pred. No. 74;
Matches 9; Conservative 6; Mismatches 2; Indels 2; Gaps 1;

Qy 2 SQNEYFDSLL-HACIPQ 18
Db 326 AQDRYNSLYSKHACVPCK 344

RESULT 90
Q2UP68 ASPOR PRELIMINARY; PRT; 469 AA.
AC Q2UP68;
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 3.
DE Predicted protein.
OS Aspergillus oryzae.
OS ORFNames=AO090001000092;
GN Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurothales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=RIB 40;
RX PubMed=16372010; DOI=10.1038/nature04300;
RA Machida M., Asai K., Sano M., Tanaka T., Kumagai T., Terai G.,
RA Kusumoto K., Arima T., Akita O., Kashiwagi Y., Abe K., Gomi K.,
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RA Horiuchi H., Kitamoto K., Kobayashi T., Takeuchi M., Denning D.W.,
RA Gallagan J.E., Nierman W.C., Yu J., Archer D.B., Bennett J.W.,
RA Bhatnagar D., Cleveland T.E., Fedorova N.D., Gotoh O., Horikawa H.,
RA Hosoyama A., Ichinomiya M., Igarashi R., Iwashita K., Juvvadi P.R.,
RA Kato M., Kato Y., Kin T., Kokubun A., Maeda H., Maeyama N.,
RA Maruyama J., Nagasaki H., Nakajima T., Oda K., Okada K., Paulsen I.,
RA Sakamoto K., Sawano T., Takahashi M., Takase K., Terabayashi Y.,
RA Wortman J.R., Yamada O., Yamagata Y., Anazawa H., Hata Y., Koide Y.,
RA Komori T., Koyama Y., Minetoki T., Suharnan S., Tanaka A., Isono K.,
RA Kuhara S., Ogasawara N., Kikuchi H.;
RT "Genome sequencing and analysis of Aspergillus oryzae.";
RL Nature 438:1157-1161(2005).
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CC
CC EMBL; AP007154; BA556647.1; -; Genomic DNA.
DR DNA-binding; Metal-binding; Nuclear protein; Transcription;
KW Transcription regulation; Zinc.
SQ SEQUENCE 469 AA; 52434 MW; F67D0CB40814F00 CRC64;

Query Match 27.4%; Score 55; DB 2; Length 469;
Best Local Similarity 31.0%; Pred. No. 1e+02;
Matches 13; Conservative 6; Mismatches 11; Indels 12; Gaps 2;

Qy 3 QNEYFDSLLH-----ACIPC-----QLRCSSNTPLTQCR 32
Db 9 QRQEDVLQLKQREAKACYPQRQRKVKCDSGHPCTCQK 50

RESULT 91
Q81YJ8 HUMAN PRELIMINARY; PRT; 663 AA.
AC Q81YJ8;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE TTC7A protein (Fragment).
GN Name=TTC7A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Maria M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RA Strausberg R.;
RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: BC035708; AAH35708.1; -; mRNA.
DR Ensembl: ENSG00000068724; Homo sapiens.
DR GO: GO:0005488; F:binding; IEA.
DR InterPro: IPR001190; TPR-like_helical.
DR InterPro: IPR001440; TPR_1.
DR InterPro: IPR013105; TPR_2.
DR InterPro: IPR013026; TPR_region.
DR Pfam: PF00515; TPR_1; 6.
DR SMART: SM00028; TPR; 2.
DR PROSITE: PS50005; TPR; 7.
DR PROSITE: PS50293; TPR_REGION; 3.
DR TPR repeat.
KW NON TER
FT
SQ SEQUENCE 663 AA; 74252 MW; B1480A15D7A659DB CRC64;

Query Match 27.4%; Score 55; DB 2; Length 663;
Best Local Similarity 38.2%; Pred. No. 1.5e+02;
Matches 13; Conservative 5; Mismatches 14; Indels 2; Gaps 1;

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
DQ 232 CKSAYAVSLRECV--KLRPSDTPVPLMAAKVC 263

RESULT 92
Q6P0M3 HUMAN PRELIMINARY; PRT; 686 AA.
AC Q6P0M3;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE TTC7A protein (Fragment).
GN Name=TTTC7A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Maman A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Maman A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: BC065554; AAH65554.1; -; mRNA.
DR Ensembl: ENSG00000068724; Homo sapiens.
DR GO: GO:0005488; F:binding; IEA.
DR InterPro: IPR001190; TPR-like_helical.
DR InterPro: IPR001440; TPR_1.
DR InterPro: IPR013105; TPR_2.
DR InterPro: IPR013026; TPR_region.
DR Pfam: PF00515; TPR_1; 6.
DR SMART: SM00028; TPR; 2.
DR PROSITE: PS50005; TPR; 7.
DR PROSITE: PS50293; TPR_REGION; 3.
DR TPR repeat.
KW NON TER
FT
SQ SEQUENCE 686 AA; 76955 MW; AD4FD56D48E826D0 CRC64;

Query Match 27.4%; Score 55; DB 2; Length 686;
Best Local Similarity 38.2%; Pred. No. 1.5e+02;
Matches 13; Conservative 5; Mismatches 14; Indels 2; Gaps 1;

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
DQ 255 CKSAYAVSLRECV--KLRPSDTPVPLMAAKVC 286

RESULT 93
Q6BJV7 DEBHA PRELIMINARY; PRT; 724 AA.
AC Q6BJV7;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Similar to CA5860|IPF376 Candida albicans IPF376 transcriptional
DE regulator.
GN OrderedLocustNames=DEHA0P287219;
OS Debaryomyces hansenii (Yeast) (Torulaspora hansenii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
OX NCBI_TaxID=4959;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 36239 / CBS 767;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lottstein I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boissane A., Boyer J., Cattolico L., Confanieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekaita F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
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CC -----
DR EMBL: CR382138; CAG89942.1; -; Genomic_DNA.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0046872; F:metal ion binding; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO: GO:0006350; P:transcription; IEA.
DR InterPro: IPR007219; Fungal trans.
DR InterPro: IPR001138; Fungi_Trcrp_N.
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RESULT 98
O964D1 ENTHI

ID Q954D1_ENTHI PRELIMINARY; PRT; 1074 AA.
 AC Q954D1;
 DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
 DT 01-DEC-2001, sequence version 1.
 DT 07-FEB-2006, entry version 18.
 DE Gal/GalNac lectin Ig12 (Fragment).
 GN Name=Ig12;
 OS Entamoeba histolytica.
 OC Eukaryota; Entamoebidae; Entamoeba.
 OX NCBI_TaxID=5759;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=HM-1:IMSS;
 RX MEDLINE=21391855; PubMed=11500468;
 RX DOI=10.1128/JAI.69.9.5892-5898.2001;
 RA Cheng X.J., Hughes M.A., Huston C.D., Loftus B., Gilchrist C.A.,
 RA Lockhart L.A., Ghosh S., Miller-Sims V., Mann B.J., Petri W.A. Jr.,
 RA Tachibana H.;
 RA "Intermediate subunit of the Gal/GalNac lectin of Entamoeba
 RT histolytica is a member of a gene family containing multiple CXXC
 RT sequence motifs.";
 RL Infect. Immun. 69:5892-5898(2001).
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 CC -----
 CC EMBL; AF337951; AAK92362.1; -; mRNA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR GO; GO:0005529; F:sugar binding; IEA.
 DR InterPro; IPR006210; EGF.
 DR InterPro; IPR002049; EGF laminin.
 DR InterPro; IPR013032; EGF like reg.
 DR InterPro; IPR006212; Furin repeat.
 DR Pfam; PF00053; Laminin_EGF; 1.
 DR SMART; SM00181; EGF; 2.
 DR SMART; SM00261; FU; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 KW Lectin.
 FT NON_TER 1 1074
 FT NON_TER 1074 1074
 SQ SEQUENCE 1074 AA; 116783 MW; 1552E2D714EB450F CRC64;

 Query Match 27.4%; Score 55; DB 2; Length 1074;
 Best Local Similarity 40.9%; Pred. No. 2.4e+02;
 Matches 9; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

 QY 1 CSQNEYFDSLHACIPQCLRCS 22
 DB 900 CVDGFYFDEIKTCIPCTSPCT 921

 RESULT 99
 Q50RX4_ENTHI PRELIMINARY; PRT; 1090 AA.
 ID Q50RX4;
 AC Q50RX4;
 DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
 DT 07-JUN-2005, sequence version 1.
 DT 21-FEB-2006, entry version 7.
 DE Protein kinase, putative.
 GN ORFNames=275.t00011;
 GN Entamoeba histolytica HM-1:IMSS.
 OC Eukaryota; Entamoebidae; Entamoeba.
 OX NCBI_TaxID=294381;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=HM-1:IMSS;
 RX PubMed=15729342; DOI=10.1038/nature03291;
 RA Loftus B.J., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
 RA Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
 RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
 RA Hofer M., Bruchhaus I., Willhoef U., Bhattacharya A.,
 RA Chillingworth T., Churcher C.M., Hance Z., Harris B., Harris D.,
 RA Jagels K., Moule S., Mungall K.L., Ormond D., Squares R.,
 RA Whitehead S., Quail M.A., Rabinowitsch E., Norbertczak H., Price C.,
 RA Wang Z., Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S.,
 RA Lohia A., Foster P.G., Sichert-Ponten T., Weber C., Singh U.,
 RA Mukherjee C., El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M.,
 RA Chillingworth T., Churcher C.M., Hance Z., Harris B., Harris D.,
 RA Jagels K., Moule S., Mungall K.L., Ormond D., Squares R.,

RA Whitehead S., Quail M.A., Rabinowitsch E., Norbertczak H., Price C.,
 RA Wang Z., Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S.,
 RA Lohia A., Foster P.G., Sichert-Ponten T., Weber C., Singh U.,
 RA Mukherjee C., El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M.,
 RA Barrell B.G., Fraser C.M., Hall N.;
 RT "The genome of the protist parasite Entamoeba histolytica.";
 RL Nature 433:865-868(2005).
 CC CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 CC -----
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 CC -----
 CC EMBL; AAF01000767; EAL4349.1; -; Genomic_DNA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR006212; Furin repeat.
 DR InterPro; IPR00719; Prot_Kinase.
 DR InterPro; IPR008719; Ser_Thr_kinase.
 DR InterPro; IPR008271; Ser_Thr_kinase.
 DR InterPro; IPR002290; Ser_Thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR007087; Znf_C2H2.
 DR PRINTS; PR00109; TYRKINASE.
 DR PRODOM; PD000001; Prot_kinase; 1.
 DR PROSITE; PS01017; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
 KW ATP-binding; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 1090 AA; 122839 MW; 1E8B1C1F9640BC50 CRC64;

 Query Match 27.4%; Score 55; DB 2; Length 1090;
 Best Local Similarity 30.0%; Pred. No. 2.4e+02;
 Matches 9; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

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 DB 367 CVDGKYFDG--SSCVDCLKCTCYNSISC 394

 RESULT 100
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 ID Q517S0;
 AC Q517S0;
 DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
 DT 07-JUN-2005, sequence version 1.
 DT 07-FEB-2006, entry version 4.
 DE Gal/GalNac lectin subunit Ig11.
 GN ORFNames=53.t00006;
 OS Entamoeba histolytica HM-1:IMSS.
 OC Eukaryota; Entamoebidae; Entamoeba.
 OX NCBI_TaxID=294381;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=HM-1:IMSS;
 RX PubMed=15729342; DOI=10.1038/nature03291;
 RA Loftus B.J., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
 RA Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
 RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
 RA Hofer M., Bruchhaus I., Willhoef U., Bhattacharya A.,
 RA Chillingworth T., Churcher C.M., Hance Z., Harris B., Harris D.,
 RA Jagels K., Moule S., Mungall K.L., Ormond D., Squares R.,
 RA Whitehead S., Quail M.A., Rabinowitsch E., Norbertczak H., Price C.,
 RA Wang Z., Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S.,
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 RA Mukherjee C., El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M.,
 RA Barrell B.G., Fraser C.M., Hall N.;

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RT "The genome of the protist parasite Entamoeba histolytica.";
RL Nature 433:865-868(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC -----
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DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR013032; EGF_like_reg.
DR InterPro; IPR006212; Furin_repeat.
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DR SMART; SM00261; FU; 1.
DR PROSITE; PS01186; EGF_2; 1.
KW Lectin.
SQ SEQUENCE 1101 AA; 119513 MW; C8B6F5CBDE656AEC CRC64;

Query Match 27.4%; Score 55; DB 2; Length 1101;
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Db 916 CVDGFYDEIKGTCIPCTSPCT 937

Search completed: July 10, 2006, 16:44:25
Job time : 83.8 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:42:25 ; Search time 5.2 Seconds
(without alignments)
175.440 Million cell updates/sec

Title: US-10-077-137a-1_COPY_8_41

Perfect score: 201
Sequence: 1 CSQNYFDSLHACIPQLRCSSNTPPLTCQRYC 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112942 seqs, 26832045 residues

Total number of hits satisfying chosen parameters: 112942

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications AA New:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pcp.*
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6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pcp.*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pcp.*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 124 | 61.7 | 42 | US-11-272-521-197 |
| 2 | 66.5 | 33.1 | 166 | US-11-318-156-6 |
| 3 | 66.5 | 33.1 | 293 | US-11-318-156-2 |
| 4 | 59.5 | 29.6 | 985 | US-11-293-697-2874 |
| 5 | 59 | 29.4 | 175 | US-11-291-698A-55 |
| 6 | 59 | 29.4 | 247 | US-10-496-758-2 |
| 7 | 58.5 | 28.1 | 1182 | US-10-449-902-41231 |
| 8 | 58 | 28.9 | 175 | US-11-291-698A-38 |
| 9 | 52 | 25.9 | 95 | US-10-953-349-18161 |
| 10 | 52 | 25.9 | 102 | US-10-953-349-18160 |
| 11 | 52 | 25.9 | 115 | US-10-953-349-18159 |
| 12 | 52 | 25.9 | 513 | US-11-174-307B-3284 |
| 13 | 51.5 | 25.6 | 298 | US-11-293-697-2712 |
| 14 | 51 | 25.4 | 111 | US-10-953-349-12782 |
| 15 | 51 | 25.4 | 576 | US-10-449-902-35358 |
| 16 | 51 | 25.4 | 645 | US-10-953-349-52038 |
| 17 | 51 | 25.4 | 645 | US-10-449-902-10967 |
| 18 | 51 | 25.4 | 660 | US-10-953-349-10967 |
| 19 | 50 | 24.9 | 247 | US-10-504-973-6 |
| 20 | 50 | 24.9 | 458 | US-11-024-544A-22 |
| 21 | 50 | 24.9 | 458 | US-11-190-750-136 |
| 22 | 50 | 24.9 | 458 | US-11-264-784-88 |
| 23 | 50 | 24.9 | 458 | US-11-264-737-129 |
| 24 | 50 | 24.9 | 458 | US-11-265-761-101 |
| 25 | 49 | 24.4 | 17 | US-11-291-698A-132 |

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| 26 | 49 | 24.4 | 343 | 6 | US-10-953-349-10623 | Sequence 10623, A |
| 27 | 49 | 24.4 | 369 | 6 | US-10-953-349-10622 | Sequence 10622, A |
| 28 | 49 | 24.4 | 398 | 6 | US-10-449-902-40143 | Sequence 40143, A |
| 29 | 48 | 23.9 | 286 | 6 | US-10-449-902-31482 | Sequence 31482, A |
| 30 | 48 | 23.9 | 807 | 6 | US-10-449-902-43388 | Sequence 43388, A |
| 31 | 48 | 23.9 | 952 | 7 | US-11-221-332-86 | Sequence 86, Appl |
| 32 | 48 | 23.9 | 969 | 6 | US-10-505-928-94 | Sequence 94, Appl |
| 33 | 47.5 | 23.6 | 272 | 6 | US-10-449-902-28786 | Sequence 28786, A |
| 34 | 47.5 | 23.6 | 272 | 6 | US-10-449-902-49738 | Sequence 49738, A |
| 35 | 47.5 | 23.6 | 276 | 6 | US-10-953-349-34476 | Sequence 34476, A |
| 36 | 47 | 23.4 | 17 | 7 | US-11-291-698A-117 | Sequence 117, App |
| 37 | 47 | 23.4 | 17 | 7 | US-11-291-698A-137 | Sequence 137, App |
| 38 | 47 | 23.4 | 100 | 6 | US-10-449-902-51084 | Sequence 51084, A |
| 39 | 47 | 23.4 | 599 | 7 | US-11-293-697-3454 | Sequence 3454, Ap |
| 40 | 47 | 23.4 | 1617 | 7 | US-11-174-307B-2182 | Sequence 2182, Ap |
| 41 | 46.5 | 23.1 | 191 | 6 | US-10-953-349-24478 | Sequence 24478, A |
| 42 | 46.5 | 23.1 | 208 | 6 | US-10-953-349-24477 | Sequence 24477, A |
| 43 | 46.5 | 23.1 | 229 | 6 | US-10-953-349-24476 | Sequence 24476, A |
| 44 | 46.5 | 23.1 | 419 | 6 | US-10-505-928-436 | Sequence 436, App |
| 45 | 46.5 | 23.1 | 419 | 6 | US-10-505-928-864 | Sequence 864, App |
| 46 | 46.5 | 23.1 | 419 | 7 | US-11-346-806-3 | Sequence 3, Appli |
| 47 | 46.5 | 23.1 | 940 | 6 | US-10-449-902-40222 | Sequence 40222, A |
| 48 | 46 | 22.9 | 17 | 7 | US-11-291-698A-70 | Sequence 70, Appl |
| 49 | 46 | 22.9 | 17 | 7 | US-11-291-698A-96 | Sequence 96, Appl |
| 50 | 46 | 22.9 | 63 | 7 | US-11-178-724-13 | Sequence 13, Appl |
| 51 | 46 | 22.9 | 63 | 7 | US-11-178-724-14 | Sequence 14, Appl |
| 52 | 46 | 22.9 | 63 | 7 | US-11-178-724-15 | Sequence 15, Appl |
| 53 | 46 | 22.9 | 63 | 7 | US-11-178-724-16 | Sequence 16, Appl |
| 54 | 46 | 22.9 | 63 | 7 | US-11-071-796A-12 | Sequence 12, Appl |
| 55 | 46 | 22.9 | 63 | 7 | US-11-071-796A-13 | Sequence 13, Appl |
| 56 | 46 | 22.9 | 63 | 7 | US-11-071-796A-14 | Sequence 14, Appl |
| 57 | 46 | 22.9 | 315 | 6 | US-10-953-349-26729 | Sequence 26729, A |
| 58 | 46 | 22.9 | 430 | 6 | US-10-953-349-26728 | Sequence 26728, A |
| 59 | 46 | 22.9 | 462 | 6 | US-10-953-349-26727 | Sequence 26727, A |
| 60 | 46 | 22.9 | 820 | 6 | US-10-449-902-46698 | Sequence 46698, A |
| 61 | 46 | 22.9 | 1238 | 7 | US-11-178-724-22 | Sequence 22, Appl |
| 62 | 46 | 22.9 | 1238 | 7 | US-11-071-796A-21 | Sequence 21, Appl |
| 63 | 46 | 22.9 | 5738 | 6 | US-10-505-928-150 | Sequence 150, App |
| 64 | 46 | 22.9 | 38 | 7 | US-11-368-086-52 | Sequence 52, Appl |
| 65 | 45.5 | 22.6 | 182 | 6 | US-10-953-349-11907 | Sequence 11907, A |
| 66 | 45.5 | 22.6 | 238 | 6 | US-10-953-349-18908 | Sequence 18908, A |
| 67 | 45.5 | 22.6 | 338 | 6 | US-10-449-902-32087 | Sequence 32087, A |
| 68 | 45.5 | 22.6 | 375 | 6 | US-10-953-349-18907 | Sequence 18907, A |
| 69 | 45.5 | 22.6 | 375 | 6 | US-11-289-103-304 | Sequence 304, App |
| 70 | 45.5 | 22.6 | 388 | 6 | US-10-953-349-18906 | Sequence 18906, A |
| 71 | 45.5 | 22.6 | 390 | 6 | US-10-953-349-25217 | Sequence 25217, A |
| 72 | 45.5 | 22.6 | 531 | 6 | US-10-449-902-35813 | Sequence 35813, A |
| 73 | 45.5 | 22.6 | 630 | 6 | US-10-953-349-10969 | Sequence 10969, A |
| 74 | 45.5 | 22.6 | 17 | 7 | US-11-291-698A-114 | Sequence 114, App |
| 75 | 45 | 22.4 | 38 | 7 | US-11-272-521-195 | Sequence 195, App |
| 76 | 45 | 22.4 | 88 | 6 | US-10-953-349-34202 | Sequence 34202, A |
| 77 | 45 | 22.4 | 194 | 7 | US-11-293-697-3039 | Sequence 3039, Ap |
| 78 | 45 | 22.4 | 250 | 7 | US-11-319-953-23 | Sequence 23, Appl |
| 79 | 45 | 22.4 | 296 | 7 | US-11-319-953-22 | Sequence 22, Appl |
| 80 | 45 | 22.4 | 330 | 7 | US-11-174-307B-4590 | Sequence 4590, Ap |
| 81 | 45 | 22.4 | 801 | 6 | US-10-449-902-43722 | Sequence 43722, A |
| 82 | 45 | 22.4 | 909 | 6 | US-10-449-902-44686 | Sequence 44686, A |
| 83 | 45 | 22.4 | 1198 | 7 | US-11-217-997-14 | Sequence 14, Appl |
| 84 | 45 | 22.4 | 1450 | 7 | US-11-217-997-6 | Sequence 6, Appli |
| 85 | 45 | 22.4 | 1600 | 7 | US-11-174-307B-2584 | Sequence 2584, Ap |
| 86 | 45 | 22.4 | 1636 | 7 | US-11-174-307B-2242 | Sequence 2242, Ap |
| 87 | 45 | 22.4 | 2274 | 7 | US-11-174-307B-56 | Sequence 56, Appl |
| 88 | 45 | 22.4 | 56 | 6 | US-10-449-902-35834 | Sequence 35834, A |
| 89 | 44.5 | 22.1 | 83 | 6 | US-10-953-349-30356 | Sequence 30356, A |
| 90 | 44.5 | 22.1 | 85 | 6 | US-10-953-349-30355 | Sequence 30355, A |
| 91 | 44.5 | 22.1 | 106 | 6 | US-10-953-349-30354 | Sequence 30354, A |
| 92 | 44.5 | 22.1 | 136 | 6 | US-10-449-902-30002 | Sequence 30002, A |
| 93 | 44.5 | 22.1 | 136 | 6 | US-10-449-902-36200 | Sequence 36200, A |
| 94 | 44.5 | 22.1 | 364 | 6 | US-10-449-902-36422 | Sequence 36422, A |
| 95 | 44.5 | 22.1 | 988 | 6 | US-10-449-902-36422 | Sequence 36422, A |
| 96 | 44 | 21.9 | 17 | 7 | US-11-291-698A-105 | Sequence 105, App |
| 97 | 44 | 21.9 | 17 | 7 | US-11-291-698A-115 | Sequence 115, App |
| 98 | 44 | 21.9 | 41 | 7 | US-11-272-521-196 | Sequence 196, App |


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975 37 18.4 700 6 US-10-449-902-44580 Sequence 44580, A
976 37 18.4 715 6 US-10-533-841-60 Sequence 60, Appl
977 37 18.4 718 6 US-10-953-349-33331 Sequence 33331, A
978 37 18.4 745 7 US-11-330-582-1 Sequence 1, Appli
979 37 18.4 745 7 US-11-248-956-16 Sequence 16, Appl
980 37 18.4 758 6 US-10-449-902-41364 Sequence 41364, A
981 37 18.4 779 6 US-10-449-902-46895 Sequence 46895, A
982 37 18.4 779 6 US-10-533-841-58 Sequence 58, Appl
983 37 18.4 789 7 US-11-174-307B-818 Sequence 818, App
984 37 18.4 789 7 US-11-174-307B-1730 Sequence 1730, Ap
985 37 18.4 799 6 US-10-505-928-716 Sequence 716, App
986 37 18.4 809 7 US-11-318-939-9 Sequence 9, Appli
987 37 18.4 847 6 US-10-514-462-1 Sequence 1, Appli
988 37 18.4 856 6 US-10-506-095-1 Sequence 41610, A
989 37 18.4 881 6 US-10-449-902-41610 Sequence 41613, A
990 37 18.4 981 6 US-10-449-902-44613 Sequence 65, Appl
991 37 18.4 991 6 US-10-533-841-65 Sequence 1834, Ap
992 37 18.4 1016 6 US-10-449-902-41144 Sequence 1704, Ap
993 37 18.4 1026 7 US-11-174-307B-1834 Sequence 2356, Ap
994 37 18.4 1035 7 US-11-174-307B-1704 Sequence 1030, Ap
995 37 18.4 1038 7 US-11-174-307B-2356 Sequence 1534, Ap
996 37 18.4 1045 7 US-11-174-307B-1030 Sequence 2020, Ap
997 37 18.4 1047 7 US-11-174-307B-1534 Sequence 2718, Ap
998 37 18.4 1048 6 US-10-520-783-22
999 37 18.4 1050 7 US-11-174-307B-2020
1000 37 18.4 1067 7 US-11-174-307B-2718
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ALIGNMENTS

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RESULT 1
US-11-272-521-197
; Sequence 197, Application US/11272521
; Publication No. US20060135431A1
; GENERAL INFORMATION:
; APPLICANT: MIN, HOSUNG
; APPLICANT: HSU, HAILING
; APPLICANT: XIONG, FEI
; TITLE OF INVENTION: PEPTIDES AND RELATED MOLECULES THAT BIND TO TALL-1
; FILE REFERENCE: A-743
; CURRENT APPLICATION NUMBER: US/11/272,521
; CURRENT FILING DATE: 2005-11-10
; PRIOR APPLICATION NUMBER: US/10/145,206
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,196
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 197
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Human
US-11-272-521-197
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Query Match 61.7%; Score 124; DB 7; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.le-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 CSQNEYFDSLHACIPCOLRC 21
| | | | | | | | | | | | | | | | | | | |
Db 22 CSQNEYFDSLHACIPCOLRC 42
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RESULT 2
US-11-318-156-6
; Sequence 6, Application US/11318156
; Publication No. US2006010529A1
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: Von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; FILE REFERENCE: CAML AND METHODS OF USE THEREOF
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; FILE REFERENCE: 44158/254623
; CURRENT APPLICATION NUMBER: US/11/318,156
; CURRENT FILING DATE: 2005-12-23
; PRIOR APPLICATION NUMBER: US/10/293,816
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 09/782,857
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/290,333
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US 08/810,572
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-318-156-6
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Query Match 33.1%; Score 66.5; DB 7; Length 166;
Best Local Similarity 32.4%; Pred. No. 0.09;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;
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Qy 1 CSQNEYFDSLHACIPCOLRCSSNTPLTCQRYC 34
| | | | | | | | | | | | | | | | | | | |
Db 34 CPBEQYWDPLLGTCMSCKTCNHQS-QRTCAAF 66
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RESULT 3
US-11-318-156-2
; Sequence 2, Application US/11318156
; Publication No. US2006010529A1
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; FILE REFERENCE: CAML AND METHODS OF USE THEREOF
; FILE REFERENCE: 44158/254623
; CURRENT APPLICATION NUMBER: US/11/318,156
; CURRENT FILING DATE: 2005-12-23
; PRIOR APPLICATION NUMBER: US/10/293,816
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 09/782,857
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/290,333
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US 08/810,572
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-318-156-2
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Query Match 33.1%; Score 66.5; DB 7; Length 293;
Best Local Similarity 32.4%; Pred. No. 0.15;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;
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Qy 1 CSQNEYFDSLHACIPCOLRCSSNTPLTCQRYC 34
| | | | | | | | | | | | | | | | | | | |
Db 34 CPBEQYWDPLLGTCMSCKTCNHQS-QRTCAAF 66
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RESULT 4
US-11-293-697-2874
; Sequence 2874, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: Helix Research Institute
; TITLE OF INVENTION: Novel full length cdna
; FILE REFERENCE: HI-A0106
```


; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2874
; LENGTH: 985
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-2874

Query Match 29.6%; Score 59.5; DB 7; Length 985;
Best Local Similarity 21.6%; Pred. No. 3.8;
Matches 11; Conservative 9; Mismatches 12; Indels 19; Gaps 1;

QY 1 CSQNEYFDSLHACIPCLP-----QLRCSNTPLTCOR 32
DB 39 CDNNQYFDISALSCVPCGANQRDARGTSCVCLPFGFMISNNGGPAITCKK 89

RESULT 5

US-11-291-698A-55
; Sequence 55, Application US/11291698A
; Publication No. US20060135430A1
; GENERAL INFORMATION:
; APPLICANT: Chan, Andrew Chee-Yuen
; APPLICANT: Gordon, Nathaniel C.
; APPLICANT: Kelley, Robert F.
; APPLICANT: Koehler, Michael F.T.
; APPLICANT: Starovasnik, Melissa A.
; TITLE OF INVENTION: BLYS ANTAGONISTS AND USES THEREOF
; FILE REFERENCE: 11669.174USC1
; CURRENT APPLICATION NUMBER: US/11/291,698A
; CURRENT FILING DATE: 2005-11-30
; PRIOR APPLICATION NUMBER: PCT/US04/17682
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 55
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Rat
US-11-291-698A-55

Query Match 29.4%; Score 59; DB 7; Length 175;
Best Local Similarity 37.1%; Pred. No. 0.86;
Matches 13; Conservative 6; Mismatches 10; Indels 6; Gaps 1;

QY 1 CSQNEYFDSLHACIPCLP-----RCSNTPLT 29
DB 22 CNQTECFDPLVRNCVSCLEFYTPETRHASSLEPGT 56

RESULT 6

US-10-496-758-2
; Sequence 2, Application US/10496758
; Publication No. US20060089311A1
; GENERAL INFORMATION:
; APPLICANT: Genset
; TITLE OF INVENTION: TREATMENT OF METABOLIC DISORDERS WITH RYZN AGONISTS AND ANTAGONIS
; FILE REFERENCE: 163.WO1
; CURRENT APPLICATION NUMBER: US/10/496,758
; CURRENT FILING DATE: 2004-05-26
; PRIOR APPLICATION NUMBER: 60/334,152
; PRIOR FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-496-758-2

Query Match 29.4%; Score 59; DB 6; Length 247;
Best Local Similarity 34.4%; Pred. No. 1.2;
Matches 11; Conservative 5; Mismatches 14; Indels 2; Gaps 1;

QY 3 QNEYFDSLHACIPCLRCSNTPLTCORYC 34
DB 29 QGKFYDHLRLDCISCASICQGH--PKQCAAYFC 58

RESULT 7

US-10-449-902-41231
; Sequence 41231, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41231
; LENGTH: 1182
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-41231

Query Match 29.1%; Score 58.5; DB 6; Length 1182;
Best Local Similarity 52.0%; Pred. No. 6;
Matches 13; Conservative 2; Mismatches 7; Indels 3; Gaps 2;

QY 11 LHAC-IPCQ--LRCSNTPLTCOR 32
DB 597 LHECSIPCSKPLPCGSHCPMTCHR 621

RESULT 8

US-11-291-698A-38
; Sequence 38, Application US/11291698A
; Publication No. US20060135430A1
; GENERAL INFORMATION:
; APPLICANT: Chan, Andrew Chee-Yuen
; APPLICANT: Gordon, Nathaniel C.
; APPLICANT: Kelley, Robert F.
; APPLICANT: Koehler, Michael F.T.
; APPLICANT: Starovasnik, Melissa A.
; TITLE OF INVENTION: BLYS ANTAGONISTS AND USES THEREOF
; FILE REFERENCE: 11669.174USC1
; CURRENT APPLICATION NUMBER: US/11/291,698A
; CURRENT FILING DATE: 2005-11-30
; PRIOR APPLICATION NUMBER: PCT/US04/17682
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 216


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; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THEREY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10967
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-10967

Query Match      25.4%; Score 51; DB 6; Length 660;
Best Local Similarity 45.8%; Pred. No. 31;
Matches 11; Conservative 2; Mismatches 3; Indels 8; Gaps 2;

Qy 15 IPCQ-----LRCSSNTPP---LTC 30
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Db 22 LPCDGDGVCMBCKSNPPPEESLTC 45

RESULT 19
US-10-504-973-6
; Sequence 6, Application US/10504973
; Publication No. US20060121459A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; CHAWLA, Narinder K.;
; APPLICANT: YUE, Henry; RICHARDSON, Thomas W.;
; APPLICANT: MARQUIS, Joseph P.; GORVAD, Ann E.;
; APPLICANT: BECHA, Shanya D.; KABLE, Amy E.;
; APPLICANT: SWARNAKAR, Anita; JIN, Pei;
; APPLICANT: HAWKINS, Phillip R.; CHIEN, David;
; APPLICANT: RAMKUMAR, Jayalaxmi; LEHR-MASON, Patricia M.;
; APPLICANT: TRAN, Uyen K.; HAFALIA, April J.A.;
; APPLICANT: BAUGHN, Mariah R.; LEE, Soo Yeun;
; APPLICANT: JIAN, Xin; JACKSON, Alan A.;
; APPLICANT: KHARE, Reena; BULLOCH, Sean A.
; TITLE OF INVENTION: RECEPTORS AND MEMBRANE-ASSOCIATED PROTEINS
; FILE REFERENCE: PF-1381 PCT
; CURRENT APPLICATION NUMBER: US/10/504,973
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: US 60/358,279
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/364,338
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/375,657
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/376,669
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/379,837
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/379,853
; PRIOR FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7509361CD1
US-10-504-973-6

Query Match      24.9%; Score 50; DB 6; Length 247;
Best Local Similarity 35.3%; Pred. No. 17;
Matches 12; Conservative 5; Mismatches 13; Indels 4; Gaps 2;

Qy 1 CSONE---YFDSLHACIPCOLRCSNTPPLTCQ 31
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Db 127 CRKQRYHWSENLFQCFNCSL-CLNGTVHLSQ 159
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RESULT 20
US-11-024-544A-22
; Sequence 22, Application US/11024544A
; Publication No. US20060094086A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours and Company, Inc.
; APPLICANT: Yadav, Narendra
; APPLICANT: Xue, Zhixiong
; APPLICANT: Zhang, Hongxiang
; TITLE OF INVENTION: DIACYLGLYCEROL ACYLTRANSFERASES FOR ALTERATION OF POLYUNSATURATED
; TITLE OF INVENTION: FATTY ACIDS AND OIL CONTENT IN OLEAGINOUS ORGANISMS
; FILE REFERENCE: CL2717
; CURRENT APPLICATION NUMBER: US/11/024,544A
; CURRENT FILING DATE: 2004-12-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Aspergillus nidulans FGSC A4
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank Accession No. EAA57945
; DATABASE ENTRY DATE: 2004-09-09
; RELEVANT RESIDUES: (1)..(458)
US-11-024-544A-22

Query Match      24.9%; Score 50; DB 7; Length 458;
Best Local Similarity 45.0%; Pred. No. 30;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 3 QNEYFDSLHACIPCOLRCS 22
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Db 74 QDVVIGAILFALVPCQLLCS 93

RESULT 21
US-11-190-750-136
; Sequence 136, Application US/11190750
; Publication No. US20060094088A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours and Company, Inc.
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Yadav, Narendra
; APPLICANT: Zhang, Hongxiang
; TITLE OF INVENTION: ACYLTRANSFERASE REGULATION TO INCREASE THE PERCENT OF
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN TOTAL LIPIDS AND OILS OF
; FILE REFERENCE: CL2718
; CURRENT APPLICATION NUMBER: US/11/190,750
; CURRENT FILING DATE: 2005-07-27
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 136
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Aspergillus nidulans FGSC A4 [GenBank Accession No. EAA57945]
US-11-190-750-136

Query Match      24.9%; Score 50; DB 7; Length 458;
Best Local Similarity 45.0%; Pred. No. 30;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 3 QNEYFDSLHACIPCOLRCS 22
   | :| :||| |||
Db 74 QDVVIGAILFALVPCQLLCS 93

RESULT 22
US-11-264-784-88
; Sequence 88, Application US/11264784
; Publication No. US20060094092A1
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Db 74 QDVWIGAILFALVPCQLCS 93

RESULT 24

US-11-265-761-101

Sequence 101, Application US/11265761

Publication No. US20060115881A1

GENERAL INFORMATION:

APPLICANT: E.I. duPont de Nemours and Co., Inc.

APPLICANT: Damude, Howard Glenn

APPLICANT: Gillies, Peter John

APPLICANT: Macool, Daniel Joseph

APPLICANT: Picataggio, Stephen K.

APPLICANT: Pollak, Dana M. Walters

APPLICANT: Ragghianti, James John

APPLICANT: Xue, Zhixiong

APPLICANT: Yadav, Narendra S.

APPLICANT: Zhang, Hongxiang

APPLICANT: Zhu, Quinn

TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA

FILE REFERENCE: CL3136 USNA

CURRENT APPLICATION NUMBER: US/11/264,784

CURRENT FILING DATE: 2005-11-01

NUMBER OF SEQ ID NOS: 375

SOFTWARE: PatentIn version 3.3

SEQ ID NO 88

LENGTH: 458

TYPE: PRT

ORGANISM: Aspergillus nidulans FGSC A4 [GenBank Accession No. EAA57945]

FEATURE:

NAME/KEY: misc_feature

OTHER INFORMATION: DGAT1

US-11-264-784-88

Query Match 24.9%; Score 50; DB 7; Length 458;

Best Local Similarity 45.0%; Pred. No. 30;

Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 ONEYFDSLHACIPCOLCS 22

Db 74 QDVWIGAILFALVPCQLCS 93

RESULT 23

US-11-264-737-129

Sequence 129, Application US/11264737

Publication No. US20060110806A1

GENERAL INFORMATION:

APPLICANT: E.I. duPont de Nemours & Co., Inc.

APPLICANT: Damude, Howard Glenn

APPLICANT: Gillies, Peter J.

APPLICANT: Macool, Daniel Joseph

APPLICANT: Picataggio, Stephen K.

APPLICANT: Ragghianti, James John

APPLICANT: Seip, John E.

APPLICANT: Xue, Zhixiong

APPLICANT: Yadav, Narendra S.

APPLICANT: Zhang, Hongxiang

APPLICANT: Zhu, Quinn Qun

TITLE OF INVENTION: DCOSEAHEAENOIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA

FILE REFERENCE: CL3160 US NA

CURRENT APPLICATION NUMBER: US/11/264,737

CURRENT FILING DATE: 2005-11-01

NUMBER OF SEQ ID NOS: 467

SOFTWARE: PatentIn version 3.3

SEQ ID NO 129

LENGTH: 458

TYPE: PRT

ORGANISM: Aspergillus nidulans FGSC A4 [GenBank Accession No. EAA57945]

FEATURE:

NAME/KEY: misc_feature

OTHER INFORMATION: DGAT1

US-11-264-737-129

Query Match 24.9%; Score 50; DB 7; Length 458;

Best Local Similarity 45.0%; Pred. No. 30;

Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 ONEYFDSLHACIPCOLCS 22

Db 74 QDVWIGAILFALVPCQLCS 93

RESULT 25

US-11-291-698A-132

Sequence 132, Application US/11291698A

Publication No. US20060135430A1

GENERAL INFORMATION:

APPLICANT: Chan, Andrew Chee-Yuen

APPLICANT: Gordon, Nathaniel C.

APPLICANT: Kelley, Robert F.

APPLICANT: Koehler, Michael F.T.

APPLICANT: Starovaenik, Melissa A.

TITLE OF INVENTION: BLYS ANTAGONISTS AND USES THEREOF

FILE REFERENCE: 11669.174USC1

CURRENT APPLICATION NUMBER: US/11/291,698A

CURRENT FILING DATE: 2005-11-30

PRIOR APPLICATION NUMBER: PCT/US04/17682

PRIOR FILING DATE: 2004-06-04

PRIOR APPLICATION NUMBER: US 60/476,414

PRIOR FILING DATE: 2003-06-05

PRIOR APPLICATION NUMBER: US 60/476,531

PRIOR FILING DATE: 2003-06-06

PRIOR APPLICATION NUMBER: US 60/476,481

PRIOR FILING DATE: 2003-06-05

NUMBER OF SEQ ID NOS: 216

SOFTWARE: PatentIn version 3.3

SEQ ID NO 132

LENGTH: 17

TYPE: PRT

Db 74 QDVWIGAILFALVPCQLCS 93

RESULT 24

US-11-265-761-101

Sequence 101, Application US/11265761

Publication No. US20060115881A1

GENERAL INFORMATION:

APPLICANT: E.I. duPont de Nemours and Co., Inc.

APPLICANT: Damude, Howard Glenn

APPLICANT: Gillies, Peter John

APPLICANT: Macool, Daniel Joseph

APPLICANT: Picataggio, Stephen K.

APPLICANT: Pollak, Dana M. Walters

APPLICANT: Ragghianti, James John

APPLICANT: Xue, Zhixiong

APPLICANT: Yadav, Narendra S.

APPLICANT: Zhang, Hongxiang

APPLICANT: Zhu, Quinn

TITLE OF INVENTION: HIGH ICOSAPENTAENOIC ACID PRODUCING STRAINS OF YARROWIA

FILE REFERENCE: CL2698 USNA

CURRENT APPLICATION NUMBER: US/11/265,761

CURRENT FILING DATE: 2005-11-02

PRIOR APPLICATION NUMBER: US 60/624812

PRIOR FILING DATE: 2004-11-04

NUMBER OF SEQ ID NOS: 414

SOFTWARE: PatentIn version 3.3

SEQ ID NO 101

LENGTH: 458

TYPE: PRT

ORGANISM: Aspergillus nidulans FGSC A4 [GenBank Accession No. EAA57945]

FEATURE:

NAME/KEY: misc_feature

OTHER INFORMATION: DGAT1

US-11-265-761-101

Query Match 24.9%; Score 50; DB 7; Length 458;

Best Local Similarity 45.0%; Pred. No. 30;

Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 ONEYFDSLHACIPCOLCS 22

Db 74 QDVWIGAILFALVPCQLCS 93

RESULT 25

US-11-291-698A-132

Sequence 132, Application US/11291698A

Publication No. US20060135430A1

GENERAL INFORMATION:

APPLICANT: Chan, Andrew Chee-Yuen

APPLICANT: Gordon, Nathaniel C.

APPLICANT: Kelley, Robert F.

APPLICANT: Koehler, Michael F.T.

APPLICANT: Starovaenik, Melissa A.

TITLE OF INVENTION: BLYS ANTAGONISTS AND USES THEREOF

FILE REFERENCE: 11669.174USC1

CURRENT APPLICATION NUMBER: US/11/291,698A

CURRENT FILING DATE: 2005-11-30

PRIOR APPLICATION NUMBER: PCT/US04/17682

PRIOR FILING DATE: 2004-06-04

PRIOR APPLICATION NUMBER: US 60/476,414

PRIOR FILING DATE: 2003-06-05

PRIOR APPLICATION NUMBER: US 60/476,531

PRIOR FILING DATE: 2003-06-06

PRIOR APPLICATION NUMBER: US 60/476,481

PRIOR FILING DATE: 2003-06-05

NUMBER OF SEQ ID NOS: 216

SOFTWARE: PatentIn version 3.3

SEQ ID NO 132

LENGTH: 17

TYPE: PRT

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 91
US-11-291-698A-132

Query Match      24.4%; Score 49; DB 7; Length 17;
Best Local Similarity 53.3%; Pred. No. 1.8;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 5 EYFDSLHACIPCOL 19
Db 1 ECFDALVHRWVPCDL 15

RESULT 26
US-10-953-349-10623
; Sequence 10623, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579FUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10623
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-10623

Query Match      24.4%; Score 49; DB 6; Length 343;
Best Local Similarity 33.3%; Pred. No. 30;
Matches 9; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

Qy 7 FDSLHACIPQLRCSSNTPPLTCQRY 33
Db 91 FNSSDGCCCKACVMCSGNDGFCLCDSW 117

RESULT 27
US-10-953-349-10622
; Sequence 10622, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579FUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10622
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-10622

Query Match      24.4%; Score 49; DB 6; Length 369;
Best Local Similarity 33.3%; Pred. No. 33;
Matches 9; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

Qy 7 FDSLHACIPQLRCSSNTPPLTCQRY 33
Db 117 FNSSDGCCCKACVMCSGNDGFCLCDSW 143

RESULT 28
US-10-449-902-40143
; Sequence 40143, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40143
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-40143

Query Match      24.4%; Score 49; DB 6; Length 398;
Best Local Similarity 64.3%; Pred. No. 35;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 18 QLRCSNTPPLTCQ 31
Db 103 RLACLNTPPLTWQ 116

RESULT 29
US-10-449-902-31482
; Sequence 31482, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31482
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-31482

Query Match      23.9%; Score 48; DB 6; Length 286;
Best Local Similarity 32.1%; Pred. No. 34;
Matches 9; Conservative 4; Mismatches 15; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQLRCSSNTPPL 28
Db 22 CRLAHLQHRVHCTPCQLHSTRFSFPL 49

RESULT 30
US-10-449-902-43388
; Sequence 43388, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
```

APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 43388
LENGTH: 807

TYPE: PRT
ORGANISM: Oryza sativa
US-10-449-902-43388

Query Match 23.9%; Score 48; DB 6; Length 807;
Best Local Similarity 36.4%; Pred. No. 91;
Matches 12; Conservative 5; Mismatches 14; Indels 2; Gaps 1;

QY 1 CSQNE--YFDSLHACIPQLRCSSNTPLTQ 31
DB 505 CSEASGLVYFPLNGSLDHLACENSTPLTWQ 537

RESULT 31

US-11-221-332-86
Sequence 86, Application US/11221332
Publication No. US20060121498A1

GENERAL INFORMATION:
APPLICANT: Eirx Therapeutics
TITLE OF INVENTION: Enzymes involved in apoptosis
FILE REFERENCE: 8912/2042
CURRENT APPLICATION NUMBER: US/11/221,332
CURRENT FILING DATE: 2005-09-07
PRIOR APPLICATION NUMBER: PCT/GB2004/00957
PRIOR FILING DATE: 2004-03-05
PRIOR APPLICATION NUMBER: GB0305267.7
PRIOR FILING DATE: 2003-05-07
NUMBER OF SEQ ID NOS: 298
SOFTWARE: PatentIn version 3.0
SEQ ID NO 86

LENGTH: 952
TYPE: PRT

ORGANISM: Homo sapiens
US-11-221-332-86

Query Match 23.9%; Score 48; DB 7; Length 952;
Best Local Similarity 72.7%; Pred. No. 11e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 19 LRCSSNTPLT 29
DB 275 IOCLSNTPPLT 285

RESULT 32

US-10-505-928-94
Sequence 94, Application US/10505928
Publication No. US20060088532A1

GENERAL INFORMATION:
APPLICANT: Ludwig Institute for Cancer Research et al.
TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28967/39178
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE: PatentIn 3.2
SEQ ID NO 94
LENGTH: 969

TYPE: PRT
ORGANISM: Homo sapiens
US-10-505-928-94

Query Match 23.9%; Score 48; DB 6; Length 969;
Best Local Similarity 37.0%; Pred. No. 1.1e+02;
Matches 10; Conservative 1; Mismatches 16; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQLRCSSNTPTT 27
DB 832 CEPGTYFDSILIRCGECHHTCGTCVGP 858

RESULT 33

US-10-449-902-28786
Sequence 28786, Application US/10449902
Publication No. US20060123505A1

GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28786

LENGTH: 272
TYPE: PRT

ORGANISM: Oryza sativa
US-10-449-902-28786

Query Match 23.6%; Score 47.5; DB 6; Length 272;
Best Local Similarity 47.4%; Pred. No. 38;
Matches 9; Conservative 2; Mismatches 3; Indels 5; Gaps 1;

QY 1 CSQNEYFDSL-----HAC 14
DB 28 CSMDSYFDDILKDEHHAC 46

RESULT 34

US-10-449-902-49738
Sequence 49738, Application US/10449902
Publication No. US20060123505A1

GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 49738

LENGTH: 272
TYPE: PRT

ORGANISM: Oryza sativa
US-10-449-902-49738

Query Match 23.6%; Score 47.5; DB 6; Length 272;

```
Best Local Similarity 47.4%; Pred. No. 38;
Matches 9; Conservative 2; Mismatches 3; Indels 5; Gaps 1;

Qy 1 CSQNEYFDSL-----HAC 14
    ||:||||:|
Db 28 CSMDSYFDDILKOTHHAC 46

RESULT 35
US-10-953-349-34476
; Sequence 34476, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SOURCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579FUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34476
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-34476

Query Match 23.6%; Score 47.5; DB 6; Length 276;
Best Local Similarity 47.4%; Pred. No. 39;
Matches 9; Conservative 2; Mismatches 3; Indels 5; Gaps 1;

Qy 1 CSQNEYFDSL-----HAC 14
    ||:||||:|
Db 27 CSMDSYFDDILKOTHHAC 45

RESULT 36
US-11-291-698A-117
; Sequence 117, Application US/11291698A
; Publication No. US20060135430A1
; GENERAL INFORMATION:
; APPLICANT: Chan, Andrew Chee-Yuen
; APPLICANT: Gordon, Nathaniel C.
; APPLICANT: Kelley, Robert F.
; APPLICANT: Koehler, Michael F.T.
; APPLICANT: Starovasnik, Melissa A.
; TITLE OF INVENTION: BLYS ANTAGONISTS AND USES THEREOF
; FILE REFERENCE: 11669.174USC1
; CURRENT APPLICATION NUMBER: US/11/291,698A
; CURRENT FILING DATE: 2005-11-30
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 117
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 76
US-11-291-698A-117

Query Match 23.4%; Score 47; DB 7; Length 17;
Best Local Similarity 53.3%; Pred. No. 3.2;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 5 EYFDSLHACIPCQL 19
    |||||:|:|
Db 1 ECFDSLVAWVPCHV 15

RESULT 38
US-10-449-902-51084
; Sequence 51084, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51084
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-51084

Query Match 23.4%; Score 47; DB 6; Length 100;
Best Local Similarity 43.8%; Pred. No. 17;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 5 EYFDSLHACIPCQL 19
```

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||:||||:|
Db 1 ECFDTLVNAWVPCNL 15

RESULT 37
US-11-291-698A-137
; Sequence 137, Application US/11291698A
; Publication No. US20060135430A1
; GENERAL INFORMATION:
; APPLICANT: Chan, Andrew Chee-Yuen
; APPLICANT: Gordon, Nathaniel C.
; APPLICANT: Kelley, Robert F.
; APPLICANT: Koehler, Michael F.T.
; APPLICANT: Starovasnik, Melissa A.
; TITLE OF INVENTION: BLYS ANTAGONISTS AND USES THEREOF
; FILE REFERENCE: 11669.174USC1
; CURRENT APPLICATION NUMBER: US/11/291,698A
; CURRENT FILING DATE: 2005-11-30
; PRIOR APPLICATION NUMBER: PCT/US04/17682
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 137
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 96
US-11-291-698A-137

Query Match 23.4%; Score 47; DB 7; Length 17;
Best Local Similarity 53.3%; Pred. No. 3.2;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 5 EYFDSLHACIPCQL 19
    |||||:|:|
Db 1 ECFDSLVAWVPCHV 15

RESULT 38
US-10-449-902-51084
; Sequence 51084, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51084
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-51084

Query Match 23.4%; Score 47; DB 6; Length 100;
Best Local Similarity 43.8%; Pred. No. 17;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 5 EYFDSLHACIPCQL 19
```



```
/
/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: GI Number: 34912696; NR Description: P0686509.18 [oryza
/ OTHER INFORMATION: sativa (japonica cultivar-group)] >gi|13365580|dbj|BAB39125.1|
US-11-174-307B-2182

Query Match      23.4%; Score 47; DB 7; Length 1617;
Best Local Similarity 36.4%; Pred. No. 2.4e+02;
Matches 8; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY 13 ACIPQLRCSSNTPPLTCQRYC 34
Db 82 ACTTCTCTATTCATCTTTC 103

RESULT 41
US-10-953-349-24478
; Sequence 24478, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24478
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-24478

Query Match      23.1%; Score 46.5; DB 6; Length 191;
Best Local Similarity 46.4%; Pred. No. 37;
Matches 13; Conservative 2; Mismatches 6; Indels 7; Gaps 2;

QY 13 ACIPQL--RCSSNTP-----PLTCQRY 33
Db 158 ASIPGVCPRINSCPTPDGVISPTTCQY 185

RESULT 42
US-10-953-349-24477
; Sequence 24477, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24477
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-24477

Query Match      23.1%; Score 46.5; DB 6; Length 208;
Best Local Similarity 46.4%; Pred. No. 40;
Matches 13; Conservative 2; Mismatches 6; Indels 7; Gaps 2;

QY 13 ACIPQL--RCSSNTP-----PLTCQRY 33
Db 175 ASIPGVCPRINSCPTPDGVISPTTCQY 202

RESULT 43
```

```
/
/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: GI Number: 7239512; NR Description: Strong similarity to the
/ OTHER INFORMATION: higher plant tyrosine-specific protein phosphatases (PTPs) from A
/ OTHER INFORMATION: thaliana gi|3413424 expressed during embryogenesis. (Arabidopsis
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: GI Number: 53793176; NR Description: tyrosine-specific
/ OTHER INFORMATION: protein phosphatase-like protein [Oryza sativa (japonica
/ OTHER INFORMATION:

QY 6 YFDSLHLHACIPQLRC 21
Db 85 FPFHVQNCMPCSLAC 100

RESULT 39
US-11-293-697-3454
; Sequence 3454, Application US/11293697.
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3454
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3454

Query Match      23.4%; Score 47; DB 7; Length 599;
Best Local Similarity 40.6%; Pred. No. 93;
Matches 13; Conservative 4; Mismatches 9; Indels 6; Gaps 3;

QY 5 EYFDSLHLHACIPQLRCSSNTPP--LTCQRYC 34
Db 560 EPWDLVTRCCPCNV-CS---PPKATTKEAYC 587

RESULT 40
US-11-174-307B-2182
; Sequence 2182, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
; APPLICANT: BROVER, Vvacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
; TITLE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS
; FILE REFERENCE: 2750-1601PUS2
; CURRENT APPLICATION NUMBER: US/11/174,307B
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,671
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,781
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,651
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 2182
; LENGTH: 1617
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: GI Number: 21536812; NR Description: unknown (Arabidopsis thaliana)
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: GI Number: 7239512; NR Description: Strong similarity to the
/ OTHER INFORMATION: higher plant tyrosine-specific protein phosphatases (PTPs) from A
/ OTHER INFORMATION: thaliana gi|3413424 expressed during embryogenesis. (Arabidopsis
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: GI Number: 53793176; NR Description: tyrosine-specific
/ OTHER INFORMATION: protein phosphatase-like protein [Oryza sativa (japonica
```


Query Match 23.1%; Score 46.5; DB 6; Length 940;
Best Local Similarity 43.5%; Pred. No. 1.6e+02;
Matches 10; Conservative 2; Mismatches 8; Indels 3; Gaps 1;

QY 13 ACIPC---QLRCSNTPPLTCOR 32
| | | | : | | : | |
DB 2 ACIPKAGKARCDGHFPCRCVR 24

RESULT 48
US-11-291-698A-70
; Sequence 70, Application US/11291698A
; Publication No. US20060135430A1
; GENERAL INFORMATION:
; APPLICANT: Chan, Andrew Chee-Yuen
; APPLICANT: Gordon, Nathaniel C.
; APPLICANT: Kelley, Robert F.
; APPLICANT: Koehler, Michael F.T.
; APPLICANT: Starovasinik, Melissa A.
; TITLE OF INVENTION: BLYS ANTAGONISTS AND USES THEREOF
; FILE REFERENCE: 11669.174USC1
; CURRENT APPLICATION NUMBER: US/11/291,698A
; CURRENT FILING DATE: 2005-11-30
; PRIOR APPLICATION NUMBER: PCT/US04/17682
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 70
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15
US-11-291-698A-70

Query Match 22.9%; Score 46; DB 7; Length 17;
Best Local Similarity 56.2%; Pred. No. 4.3;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5 EYFDSLHACIPCOLR 20
| | | | : | | : | |
DB 1 ECFDILLVRAWVPCWLR 16

RESULT 49
US-11-291-698A-96
; Sequence 96, Application US/11291698A
; Publication No. US20060135430A1
; GENERAL INFORMATION:
; APPLICANT: Chan, Andrew Chee-Yuen
; APPLICANT: Gordon, Nathaniel C.
; APPLICANT: Kelley, Robert F.
; APPLICANT: Koehler, Michael F.T.
; APPLICANT: Starovasinik, Melissa A.
; TITLE OF INVENTION: BLYS ANTAGONISTS AND USES THEREOF
; FILE REFERENCE: 11669.174USC1
; CURRENT APPLICATION NUMBER: US/11/291,698A
; CURRENT FILING DATE: 2005-11-30
; PRIOR APPLICATION NUMBER: PCT/US04/17682
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05

; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 96
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 54
US-11-291-698A-96

Query Match 22.9%; Score 46; DB 7; Length 17;
Best Local Similarity 61.5%; Pred. No. 4.3;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 EYFDSLHACIPC 17
| | | | : | | : | |
DB 1 ECFDILLVRAWVPC 13

RESULT 50
US-11-178-724-13
; Sequence 13, Application US/11178724
; Publication No. US20060128619A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPEION, BRIAN R.
; APPLICANT: YOUNG, LESLEY L.
; APPLICANT: MCKENZIE, GRAHAME J.
; TITLE OF INVENTION: THERAPEUTIC USE OF MODULATORS OF NOTCH
; FILE REFERENCE: 674525-2021
; CURRENT APPLICATION NUMBER: US/11/178,724
; CURRENT FILING DATE: 2005-07-11
; PRIOR APPLICATION NUMBER: PCT/GB04/00021
; PRIOR FILING DATE: 2004-01-09
; PRIOR APPLICATION NUMBER: GB 0300428.0
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 13
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-178-724-13

Query Match 22.9%; Score 46; DB 7; Length 63;
Best Local Similarity 30.4%; Pred. No. 15;
Matches 7; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 12 HACIPCOLRCSNTPPLTCORVC 34
| | | | : | | : | |
DB 12 HLEQLQIRVRCDENYYSATCNKFC 34

RESULT 51
US-11-178-724-14
; Sequence 14, Application US/11178724
; Publication No. US20060128619A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPEION, BRIAN R.
; APPLICANT: YOUNG, LESLEY L.
; APPLICANT: MCKENZIE, GRAHAME J.
; TITLE OF INVENTION: THERAPEUTIC USE OF MODULATORS OF NOTCH
; FILE REFERENCE: 674525-2021
; CURRENT APPLICATION NUMBER: US/11/178,724
; CURRENT FILING DATE: 2005-07-11
; PRIOR APPLICATION NUMBER: PCT/GB04/00021
; PRIOR FILING DATE: 2004-01-09
; PRIOR APPLICATION NUMBER: GB 0300428.0
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 14
; LENGTH: 63
; TYPE: PRT

; ORGANISM: Homo sapiens
US-11-178-724-14
Query Match 22.9%; Score 46; DB 7; Length 63;
Best Local Similarity 30.4%; Pred. No. 15;
Matches 7; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
QY 12 HACPQLRCSSNTPPLTCORYC 34
Db 12 HLEQLRVRCNDENYSATCNKFC 34
RESULT 52
US-11-178-724-15
; Sequence 15, Application US/11178724
; Publication No. US20060128619A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN R.
; APPLICANT: YOUNG, LESLEY L.
; APPLICANT: MCKENZIE, GRAHAME J.
; TITLE OF INVENTION: THERAPEUTIC USE OF MODULATORS OF NOTCH
; FILE REFERENCE: 674525-2021
; CURRENT APPLICATION NUMBER: US/11/178,724
; CURRENT FILING DATE: 2005-07-11
; PRIOR APPLICATION NUMBER: PCT/GB04/00021
; PRIOR FILING DATE: 2004-01-09
; PRIOR APPLICATION NUMBER: GB 0300428.0
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 15
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Rattus sp.
US-11-178-724-15
Query Match 22.9%; Score 46; DB 7; Length 63;
Best Local Similarity 30.4%; Pred. No. 15;
Matches 7; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
QY 12 HACPQLRCSSNTPPLTCORYC 34
Db 12 HLEQLRVRCNDENYSATCNKFC 34
RESULT 53
US-11-178-724-16
; Sequence 16, Application US/11178724
; Publication No. US20060128619A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN R.
; APPLICANT: YOUNG, LESLEY L.
; APPLICANT: MCKENZIE, GRAHAME J.
; TITLE OF INVENTION: THERAPEUTIC USE OF MODULATORS OF NOTCH
; FILE REFERENCE: 674525-2021
; CURRENT APPLICATION NUMBER: US/11/178,724
; CURRENT FILING DATE: 2005-07-11
; PRIOR APPLICATION NUMBER: PCT/GB04/00021
; PRIOR FILING DATE: 2004-01-09
; PRIOR APPLICATION NUMBER: GB 0300428.0
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 16
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-178-724-16
Query Match 22.9%; Score 46; DB 7; Length 63;
Best Local Similarity 30.4%; Pred. No. 15;
Matches 7; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 12 HACPQLRCSSNTPPLTCORYC 34
Db 12 HLEQLRVRCNDENYSATCNKFC 34
RESULT 54
US-11-071-796A-12
; Sequence 12, Application US/11071796A
; Publication No. US20060140943A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: SOLARI, ROBERTO CELESTE ERCOLE
; APPLICANT: DALLMAN, MARGARET JANE
; APPLICANT: LAMB, JONATHAN ROBERT
; APPLICANT: HOYNE, GERARD FRANCIS
; APPLICANT: BRIEND, EMMANUEL CYRILLE PASCAL
; TITLE OF INVENTION: IMMUNOTHERAPY USING MODULATORS OF NOTCH SIGNALLING
; FILE REFERENCE: 674525-2018
; CURRENT APPLICATION NUMBER: US/11/071,796A
; CURRENT FILING DATE: 2005-03-03
; PRIOR APPLICATION NUMBER: PCT/GB03/03874
; PRIOR FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: GB 0220658.9
; PRIOR FILING DATE: 2002-09-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 12
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-071-796A-12
Query Match 22.9%; Score 46; DB 7; Length 63;
Best Local Similarity 30.4%; Pred. No. 15;
Matches 7; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
QY 12 HACPQLRCSSNTPPLTCORYC 34
Db 12 HLEQLRVRCNDENYSATCNKFC 34
RESULT 55
US-11-071-796A-13
; Sequence 13, Application US/11071796A
; Publication No. US20060140943A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: SOLARI, ROBERTO CELESTE ERCOLE
; APPLICANT: DALLMAN, MARGARET JANE
; APPLICANT: LAMB, JONATHAN ROBERT
; APPLICANT: HOYNE, GERARD FRANCIS
; APPLICANT: BRIEND, EMMANUEL CYRILLE PASCAL
; TITLE OF INVENTION: IMMUNOTHERAPY USING MODULATORS OF NOTCH SIGNALLING
; FILE REFERENCE: 674525-2018
; CURRENT APPLICATION NUMBER: US/11/071,796A
; CURRENT FILING DATE: 2005-03-03
; PRIOR APPLICATION NUMBER: PCT/GB03/03874
; PRIOR FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: GB 0220658.9
; PRIOR FILING DATE: 2002-09-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 13
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-071-796A-13
Query Match 22.9%; Score 46; DB 7; Length 63;
Best Local Similarity 30.4%; Pred. No. 15;
Matches 7; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
QY 12 HACPQLRCSSNTPPLTCORYC 34

Db 12 HLELQIRVRCDENYYSATCNKFC 34

RESULT 56

US-11-071-796A-14
; Sequence 14, Application US/11071796A
; Publication No. US20060140943A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: SOLARI, ROBERTO CELESTE ERCOLE
; APPLICANT: DALLMAN, MARGARET JANE
; APPLICANT: LAMB, JONATHAN ROBERT
; APPLICANT: HOYNE, GERARD FRANCIS
; APPLICANT: BRIEND, EMMANUEL CYRILLE PASCAL
; TITLE OF INVENTION: IMMUNOTHERAPY USING MODULATORS OF NOTCH SIGNALLING
; FILE REFERENCE: 674525-2018
; CURRENT APPLICATION NUMBER: US/11/071,796A
; CURRENT FILING DATE: 2005-03-03
; PRIOR APPLICATION NUMBER: PCT/GB03/03874
; PRIOR FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: GB 0220658.9
; PRIOR FILING DATE: 2002-09-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 14
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-071-796A-14

Query Match 22.9%; Score 46; DB 7; Length 63;
Best Local Similarity 30.4%; Pred. No. 15;
Matches 7; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 12 HACIPQLRCSSNTPPLTCQRYC 34

Db 12 HLELQIRVRCDENYYSATCNKFC 34

RESULT 57

US-11-071-796A-15
; Sequence 15, Application US/11071796A
; Publication No. US20060140943A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: SOLARI, ROBERTO CELESTE ERCOLE
; APPLICANT: DALLMAN, MARGARET JANE
; APPLICANT: LAMB, JONATHAN ROBERT
; APPLICANT: HOYNE, GERARD FRANCIS
; APPLICANT: BRIEND, EMMANUEL CYRILLE PASCAL
; TITLE OF INVENTION: IMMUNOTHERAPY USING MODULATORS OF NOTCH SIGNALLING
; FILE REFERENCE: 674525-2018
; CURRENT APPLICATION NUMBER: US/11/071,796A
; CURRENT FILING DATE: 2005-03-03
; PRIOR APPLICATION NUMBER: PCT/GB03/03874
; PRIOR FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: GB 0220658.9
; PRIOR FILING DATE: 2002-09-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 15
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-071-796A-15

Query Match 22.9%; Score 46; DB 7; Length 63;
Best Local Similarity 30.4%; Pred. No. 15;
Matches 7; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 12 HACIPQLRCSSNTPPLTCQRYC 34

Db 12 HLELQIRVRCDENYYSATCNKFC 34

RESULT 58

US-10-953-349-26729
; Sequence 26729, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 26729
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-26729

Query Match 22.9%; Score 46; DB 6; Length 315;
Best Local Similarity 42.1%; Pred. No. 68;
Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 6 YFDSLHACIPQLRCSSN 24

Db 296 YIHESLHNCPCGESQCSSS 314

RESULT 59

US-10-953-349-26728
; Sequence 26728, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 26728
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-26728

Query Match 22.9%; Score 46; DB 6; Length 430;
Best Local Similarity 42.1%; Pred. No. 91;
Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 6 YFDSLHACIPQLRCSSN 24

Db 411 YIHESLHNCPCGESQCSSS 429

RESULT 60

US-10-953-349-26727
; Sequence 26727, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 26727

```
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-26727

Query Match      22.9%; Score 46; DB 6; Length 462;
Best Local Similarity 42.1%; Pred. No. 97;
Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 6 YFDSLHACIPQLRCSN 24
Db 443 YIHESLHNCPCGSCSS 461

RESULT 61
US-10-449-902-46698
; Sequence 46698, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46698
; LENGTH: 820
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-46698

Query Match      22.9%; Score 46; DB 6; Length 820;
Best Local Similarity 30.8%; Pred. No. 1.7e+02;
Matches 8; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

Qy 1 CSONEYFDSLHACIPQLRCSNTP 26
Db 577 CADQSYLGILNCLCCSLASILHAP 602

RESULT 62
US-11-178-724-22
; Sequence 22, Application US/11178724
; Publication No. US20060128619A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN R.
; APPLICANT: YOUNG, LESLEY L.
; APPLICANT: MCKENZIE, GRAHAME J.
; TITLE OF INVENTION: THERAPEUTIC USE OF MODULATORS OF NOTCH
; FILE REFERENCE: 674525-2021
; CURRENT APPLICATION NUMBER: US/11/178,724
; CURRENT FILING DATE: 2005-07-11
; PRIOR APPLICATION NUMBER: PCT/GB04/00021
; PRIOR FILING DATE: 2004-01-09
; PRIOR APPLICATION NUMBER: GB 0300428.0
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 22
; LENGTH: 1238
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-178-724-22

Query Match      22.9%; Score 46; DB 7; Length 1238;
```

```
Best Local Similarity 30.4%; Pred. No. 2.5e+02;
Matches 7; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 12 HACIPQLRCSNTPPLTCORYC 34
Db 189 HLEQLQIRVRCDENYSATCNKFC 211

RESULT 63
US-11-071-796A-21
; Sequence 21, Application US/11071796A
; Publication No. US20060140943A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: SOLARI, ROBERTO CELESTE ERCOLE
; APPLICANT: DALLMAN, MARGARET JANE
; APPLICANT: LAMB, JONATHAN ROBERT
; APPLICANT: HOYNE, GERARD FRANCIS
; APPLICANT: BRIEND, EMMANUEL CYRILLE PASCAL
; TITLE OF INVENTION: IMMUNOTHERAPY USING MODULATORS OF NOTCH SIGNALING
; FILE REFERENCE: 674525-2018
; CURRENT APPLICATION NUMBER: US/11/071,796A
; CURRENT FILING DATE: 2005-03-03
; PRIOR APPLICATION NUMBER: PCT/GB03/03874
; PRIOR FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: GB 0220658.9
; PRIOR FILING DATE: 2002-09-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 21
; LENGTH: 1238
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-071-796A-21

Query Match      22.9%; Score 46; DB 7; Length 1238;
Best Local Similarity 30.4%; Pred. No. 2.5e+02;
Matches 7; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 12 HACIPQLRCSNTPPLTCORYC 34
Db 189 HLEQLQIRVRCDENYSATCNKFC 211

RESULT 64
US-10-505-928-150
; Sequence 150, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 150
; LENGTH: 5738
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-150

Query Match      22.9%; Score 46; DB 6; Length 5738;
Best Local Similarity 33.3%; Pred. No. 1e+03;
Matches 7; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

Qy 10 LLHACIPQLRCSNTPPLTC 30
Db 2212 MFQPCAFCLTCDDISQVTC 2232
```

RESULT 65

US-11-368-086-52
; Sequence 52, Application US/11368086
; Publication No. US20060141003A1
; GENERAL INFORMATION:
; APPLICANT: Reactive Surfaces, Ltd.
; TITLE OF INVENTION: Antifungal Paints and Coatings
; FILE REFERENCE: RACT-00400
; CURRENT APPLICATION NUMBER: US/11/368,086
; CURRENT FILING DATE: 2006-03-03
; PRIOR APPLICATION NUMBER: US/10/884,355
; PRIOR FILING DATE: 2004-07-02
; PRIOR APPLICATION NUMBER: 60/485,234
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 52
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Phytolacca americana
US-11-368-086-52

Query Match 22.6%; Score 45.5; DB 7; Length 38;
Best Local Similarity 40.9%; Pred. No. 11;
Matches 9; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 14 CIPQCLRSSNT-PPLTCQRYC 34
|||:::| | | | |
Db 3 CIKNGGRCNASAGPPYCCSSYC 24

RESULT 66

US-10-953-349-11907
; Sequence 11907, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11907
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-11907

Query Match 22.6%; Score 45.5; DB 6; Length 182;
Best Local Similarity 29.4%; Pred. No. 47;
Matches 10; Conservative 4; Mismatches 17; Indels 3; Gaps 1;

QY 4 NEYFD---SLHACIPQCLRSSNTPLTCQRYC 34
|||:::| | | | |
Db 4 NEYLSKNVNLQCGTAIELGSGVIGITILCSRFC 37

RESULT 67

US-10-953-349-18908
; Sequence 18908, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18908

; LENGTH: 238
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18908

Query Match 22.6%; Score 45.5; DB 6; Length 238;
Best Local Similarity 32.6%; Pred. No. 60;
Matches 15; Conservative 3; Mismatches 11; Indels 17; Gaps 3;

QY 1 CSQNEYFDSL-----LHACIPQCLRC-SSNTPLTQ 31
|||:::| | | | |
Db 92 CSSNVKNSLDYPLVPNATYATACVKC--KCDSSNNFIQCE 135

RESULT 68

US-10-449-902-32087
; Sequence 32087, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A020511-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32087
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-32087

Query Match 22.6%; Score 45.5; DB 6; Length 338;
Best Local Similarity 39.3%; Pred. No. 84;
Matches 11; Conservative 3; Mismatches 9; Indels 5; Gaps 1;

QY 5 EYFDSLHAC-----IPCQLRCSSNTTPP 27
|||:::| | | | |
Db 238 EFTDLLHGCAGSPPPCGEAAASATMP 265

RESULT 69

US-10-953-349-18907
; Sequence 18907, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18907
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18907

Query Match 22.6%; Score 45.5; DB 6; Length 375;
Best Local Similarity 32.6%; Pred. No. 93;
Matches 15; Conservative 3; Mismatches 11; Indels 17; Gaps 3;

QY 1 CSQNEYFDSL-----LHACIPQCLRC-SSNTPLTQ 31
|||:::| | | | |

Db 229 CSSNVKNSLDYPLLVPNTAYTAHECVKC--KCDSSNNFILOCE 272

RESULT 70

US-11-289-102-304
; Sequence 304, Application US/11289102
; Publication No. US20060121511A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Hyerim
; APPLICANT: Shaw, Peter M.
; APPLICANT: Clark, Edwin
; TITLE OF INVENTION: BIOMARKERS AND METHODS FOR DETERMINING SENSITIVITY TO
; TITLE OF INVENTION: MICROTUBULE-STABILIZING AGENTS
; FILE REFERENCE: 10338 NP
; CURRENT APPLICATION NUMBER: US/11/289,102
; CURRENT FILING DATE: 2005-11-29
; PRIOR APPLICATION NUMBER: US 60/631,993
; PRIOR FILING DATE: 2004-11-30
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 304
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-289-102-304

Query Match 22.6%; Score 45.5; DB 7; Length 375;
Best Local Similarity 22.7%; Pred. No. 93;
Matches 10; Conservative 6; Mismatches 13; Indels 15; Gaps 1;

Qy 3 QNEYFDSLHACIPCCQ-----LRCSNTPPLTCQ 31

Db 60 QDGYGFGSKGCLPCQCNRRSASCDALTGACLNCKNSKGNHCE 103

RESULT 71

US-10-953-349-18906
; Sequence 18906, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18906
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18906

Query Match 22.6%; Score 45.5; DB 6; Length 388;
Best Local Similarity 32.6%; Pred. No. 96;
Matches 15; Conservative 3; Mismatches 11; Indels 17; Gaps 3;

Qy 1 CSQNEYFDSL-----LHACIPCOLRC-SSNTPPLTCQ 31

Db 242 CSSNVKNSLDYPLLVPNTAYTAHECVKC--KCDSSNNFILOCE 285

RESULT 72

US-10-953-349-25217
; Sequence 25217, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349

; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25217
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-25217

Query Match 22.6%; Score 45.5; DB 6; Length 390;
Best Local Similarity 41.9%; Pred. No. 96;
Matches 13; Conservative 2; Mismatches 7; Indels 9; Gaps 2;

Qy 6 YFDSLHACIPC-----OLR--CSSNTPP 27

Db 12 YTRNLLHHSAPAFDASTRPQLRLFCSETPP 42

RESULT 73

US-10-449-902-35813
; Sequence 35813, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A020511-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35813
; LENGTH: 531
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-35813

Query Match 22.6%; Score 45.5; DB 6; Length 531;
Best Local Similarity 36.7%; Pred. No. 1.3e+02;
Matches 11; Conservative 3; Mismatches 13; Indels 3; Gaps 1;

Qy 4 NEYFDSLHACIPCOLRCSSNTPPLTCQRY 33

Db 38 NFYFDDIFN---PSSDTFDENTPPLSDPNY 64

RESULT 74

US-10-953-349-10969
; Sequence 10969, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10969
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-10969

Query Match 22.6%; Score 45.5; DB 6; Length 630;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;

Matches 9; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

Qy 19 LRCSSNTPP---LTC 30
:|||||:
Db 1 MRCKSNPPPESLTC 15

RESULT 75

US-11-291-698A-114
; Sequence 114, Application US/11291698A
; Publication No. US20060135430A1
; GENERAL INFORMATION:
; APPLICANT: Chan, Andrew Chee-Yuen
; APPLICANT: Gordon, Nathaniel C.
; APPLICANT: Kelley, Robert F.
; APPLICANT: Koehler, Michael F.T.
; APPLICANT: Starovasnik, Melissa A.
; TITLE OF INVENTION: BLYS ANTAGONISTS AND USES THEREOF
; FILE REFERENCE: 11669.174USC1
; CURRENT APPLICATION NUMBER: US/11/291,698A
; CURRENT FILING DATE: 2005-11-30
; PRIOR APPLICATION NUMBER: PCT/US04/17682
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 114
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 73
US-11-291-698A-114

Query Match 22.4%; Score 45; DB 7; Length 17;
Best Local Similarity 61.5%; Pred. No. 5.8;
Matches 8; Conservative 2; Mismatches 3; Indels 3; Gaps 0;

Qy 5 EYFDSLHACIPC 17
:|||||:
Db 1 ECFDSLVRWVPC 13

RESULT 76

US-11-272-521-195
; Sequence 195, Application US/11272521
; Publication No. US20060135431A1
; GENERAL INFORMATION:
; APPLICANT: MIN, HOSUNG
; APPLICANT: HSU, HAILING
; APPLICANT: XIONG, FEI
; TITLE OF INVENTION: PEPTIDES AND RELATED MOLECULES THAT BIND TO TALL-1
; FILE REFERENCE: A-743
; CURRENT APPLICATION NUMBER: US/11/272,521
; CURRENT FILING DATE: 2005-11-10
; PRIOR APPLICATION NUMBER: US/10/145,206
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,196
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 195
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Human
US-11-272-521-195

Query Match 22.4%; Score 45; DB 7; Length 38;

Best Local Similarity 36.8%; Pred. No. 12;
Matches 7; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CSONEYFDSLHACIPCQL 19
:|||||:
Db 19 CVPTCYDLLVRKVCDCRL 37

RESULT 77

US-10-953-349-34202
; Sequence 34202, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34202
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-34202

Query Match 22.4%; Score 45; DB 6; Length 88;
Best Local Similarity 45.0%; Pred. No. 27;
Matches 9; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Qy 11 LHACIPCQLRCSSNTPPLTC 30
:|||||:
Db 53 VHASATCFSRWLSRTPPSC 72

RESULT 78

US-11-293-697-3039
; Sequence 3039, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3039
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3039

Query Match 22.4%; Score 45; DB 7; Length 194;
Best Local Similarity 40.0%; Pred. No. 58;
Matches 14; Conservative 4; Mismatches 11; Indels 6; Gaps 3;

Qy 5 EYFDSLHACIPCQL---RCSSNT---PPLTCORY 33
:|||||:
Db 102 EFPDAAPFATPCLPQAWWRCSTTTGRRATLTCTAY 136

RESULT 79

US-11-319-952-23
; Sequence 23, Application US/11319952
; Publication No. US20060134114A1
; GENERAL INFORMATION:
; APPLICANT: Yousef, George M.
; APPLICANT: Diamandis, Eleftherios
; TITLE OF INVENTION: Novel Human Kallikrein-Like Genes

```
; FILE REFERENCE: MTS3USA
; CURRENT APPLICATION NUMBER: US/11/319,952
; CURRENT FILING DATE: 2005-12-28
; PRIOR APPLICATION NUMBER: US/09/936,271
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/CA00/00258
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/124,260
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/127,386
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: US 60/144,919
; PRIOR FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-319-952-23
```

```
Query Match 22.4%; Score 45; DB 7; Length 250;
Best Local Similarity 30.3%; Pred. No. 73;
Matches 10; Conservative 6; Mismatches 17; Indels 0; Gaps 0;
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QY 2 SONEVDSLHACIPCOLRCSNTPTLTQRYC 34
Db 104 SANDHNDIMLRLRQARLSPAVQPLNLSQTC 136
```

RESULT 80

```
US-11-319-952-22
; Sequence 22, Application US/11/319952
; Publication No. US20060134114A1
; GENERAL INFORMATION:
; APPLICANT: Yousef, George M.
; TITLE OF INVENTION: Novel Human Kallikrein-Like Genes
; FILE REFERENCE: MTS3USA
; CURRENT APPLICATION NUMBER: US/11/319,952
; CURRENT FILING DATE: 2005-12-28
; PRIOR APPLICATION NUMBER: US/09/936,271
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/CA00/00258
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/124,260
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/127,386
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: US 60/144,919
; PRIOR FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-319-952-22
```

```
Query Match 22.4%; Score 45; DB 7; Length 296;
Best Local Similarity 30.3%; Pred. No. 86;
Matches 10; Conservative 6; Mismatches 17; Indels 0; Gaps 0;
```

```
QY 2 SONEVDSLHACIPCOLRCSNTPTLTQRYC 34
Db 150 SANDHNDIMLRLRQARLSPAVQPLNLSQTC 182
```

RESULT 81

```
US-11-174-307B-4590
; Sequence 4590, Application US/11/174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
```

```
; APPLICANT: ALEXANDROV, Nickolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
; TITLE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS
; FILE REFERENCE: 2750-1601PUS2
; CURRENT APPLICATION NUMBER: US/11/174,307B
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,671
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,781
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,651
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 4590
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Pfam Name: 2OG-FeII_Oxy; Pfam Description: 2OG-Fe(II)
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 55771340; NR Description: putative oxidoreductase
; OTHER INFORMATION: [Oryza sativa (japonica cultivar-group)]
; OTHER INFORMATION: gi|55771331|dbj|BAD72256.1| putative oxidoreductase [Oryza sativa
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 12320957; NR Description: hyoscyamine
; OTHER INFORMATION: 6-dioxygenase hydroxylase, putative [Arabidopsis thaliana]
; OTHER INFORMATION: >gi|15219523|ref|NP_174753.1| oxidoreductase, 2OG-Fe(II) oxygenase
; OTHER INFORMATION: family protein [Arabidopsis thaliana] >gi|25285682|pir||G86472
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 42565662; NR Description: oxidoreductase,
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 42565664; NR Description: oxidoreductase,
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 37536200; NR Description: putative gibberellin
; OTHER INFORMATION: 20-oxidase [Oryza sativa (japonica cultivar-group)]
; OTHER INFORMATION: >gi|27311281|gb|AAC00707.1| putative gibberellin 20-oxidase [Oryza
; OTHER INFORMATION: sativa (japonica cultivar-group)] >gi|31433136|gb|AAP54689.1|
US-11-174-307B-4590
Query Match 22.4%; Score 45; DB 7; Length 330;
Best Local Similarity 32.4%; Pred. No. 95;
Matches 11; Conservative 4; Mismatches 13; Indels 6; Gaps 2;
QY 6 YFDSLHAC-IPCOLRCSNT-----PELTQRY 33
Db 277 YFLEPSHDLVECLPTCKSDSNPPKFPILCHDY 310
RESULT 82
US-10-449-902-43722
; Sequence 43722, Application US/10/449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
```

```
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43722
; LENGTH: 801
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-43722

Query Match      22.4%; Score 45; DB 6; Length 801;
Best Local Similarity 32.3%; Pred. No. 2.2e+02;
Matches 10; Conservative 6; Mismatches 9; Indels 6; Gaps 1;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPTLTCQ 31
Db 404 CPPPEYFANLLFGLV-----NNVIPPLSCK 428

RESULT 83
US-10-449-902-44686
; Sequence 44686, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44686
; LENGTH: 909
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-44686

Query Match      22.4%; Score 45; DB 6; Length 909;
Best Local Similarity 34.3%; Pred. No. 2.5e+02;
Matches 12; Conservative 2; Mismatches 9; Indels 12; Gaps 3;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPTLTC-QRYC 34
Db 599 CSKRQF-----PCNLGCGN---PLNGGNHYC 622

RESULT 84
US-11-217-997-14
; Sequence 14, Application US/11217997
; Publication No. US20060111561A1
; GENERAL INFORMATION:
; APPLICANT: Valerie L. Gerlach
; APPLICANT: Elma R. Fernandes
; APPLICANT: Richard A. Shinkets
; APPLICANT: Meera Patturajan
; APPLICANT: Vladimir Y. Gusev
; APPLICANT: Stacie (Casman) Navara
; APPLICANT: Velizar T. Tchernev
; APPLICANT: David W. Anderson
; APPLICANT: Xiaojia (Sasha) Guo
; APPLICANT: Luca Rastelli
; APPLICANT: Mei Zhong
; APPLICANT: Muralidhara Padigaru
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODED THEREBY
; FILE REFERENCE: Cura 551 CIP
; CURRENT APPLICATION NUMBER: US/11/217,997
; CURRENT FILING DATE: 2005-08-31
; PRIOR APPLICATION NUMBER: 10/453,372
; PRIOR FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 10/055,877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
```

```
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODED THEREBY
; FILE REFERENCE: Cura 551 CIP
; CURRENT APPLICATION NUMBER: US/11/217,997
; CURRENT FILING DATE: 2005-08-31
; PRIOR APPLICATION NUMBER: 10/453,372
; PRIOR FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 10/055,877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 14
; LENGTH: 1198
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-217-997-14

Query Match      22.4%; Score 45; DB 7; Length 1198;
Best Local Similarity 24.4%; Pred. No. 3.2e+02;
Matches 11; Conservative 5; Mismatches 17; Indels 12; Gaps 2;

QY 1 CSQNEYFDSLHACIPQ-----LRCSNTPTLTCORYC 34
Db 986 CPAGLYGDNCRHSCL-CQNGGTCDPVSGHCACPEGWAGLACEKC 1029

RESULT 85
US-11-217-997-6
; Sequence 6, Application US/11217997
; Publication No. US20060111561A1
; GENERAL INFORMATION:
; APPLICANT: Valerie L. Gerlach
; APPLICANT: Elma R. Fernandes
; APPLICANT: Richard A. Shinkets
; APPLICANT: Meera Patturajan
; APPLICANT: Vladimir Y. Gusev
; APPLICANT: Stacie (Casman) Navara
; APPLICANT: Velizar T. Tchernev
; APPLICANT: David W. Anderson
; APPLICANT: Xiaojia (Sasha) Guo
; APPLICANT: Luca Rastelli
; APPLICANT: Mei Zhong
; APPLICANT: Muralidhara Padigaru
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODED THEREBY
; FILE REFERENCE: Cura 551 CIP
; CURRENT APPLICATION NUMBER: US/11/217,997
; CURRENT FILING DATE: 2005-08-31
; PRIOR APPLICATION NUMBER: 10/453,372
; PRIOR FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 10/055,877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
```

```
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 6
; LENGTH: 1450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-217-997-6

Query Match      22.4%; Score 45; DB 7; Length 1450;
Best Local Similarity 24.4%; Pred. No. 3.8e+02;
Matches 11; Conservative 5; Mismatches 17; Indels 12; Gaps 2;

QY 1 CSQNEYFDSLHACIPCO-----LRCSNTPTPLTCQRYC 34
   | | | | | | | | | | | | | | | | | | | | |
Db 986 CPAGLYGDNCRHSCL-CQNGCTCDPVSGHCACPEGWAGLACEK 1029
   | | | | | | | | | | | | | | | | | | | | |

RESULT 86
US-11-174-307B-2584
; Sequence 2584, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
; FILE REFERENCE: 2750-1601PUS2
; CURRENT APPLICATION NUMBER: US/11/174,307B
; PRIOR FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,671
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,781
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,651
; NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 2584
; LENGTH: 1600
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Pfam Name: Chal_sti_synt_C; Pfam Description: Chalcone and
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Pfam Name: Chal_sti_synt_N; Pfam Description: Chalcone and
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Pfam Name: MMTV_SA9; Pfam Description: Mouse mammary tumour
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 50920373; NR Description: Putative fiddlehead-like
; OTHER INFORMATION: protein [Oryza sativa (japonica cultivar-group)]
; OTHER INFORMATION: >gi|24960748|gb|AA65442.1| Putative fiddlehead-like protein [Ory
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 3142289; NR Description: Strong similarity to
```

```
; OTHER INFORMATION: beta-keto-CoA synthase gbU37088 from Simmondsia chinensis.
; OTHER INFORMATION: [Arabidopsis thaliana] gi|7488037|pir||T00951 probable
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 1045614; NR Description: beta-ketoacyl-CoA synthase
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 23297625; NR Description: beta-ketoacyl-CoA
; OTHER INFORMATION: synthase [Arabidopsis thaliana] >gi|10177945|dbj|BAB11304.1|
; OTHER INFORMATION: beta-ketoacyl-CoA synthase [Arabidopsis thaliana]
; OTHER INFORMATION: >gi|15983491|gb|AAL11613.1| AT5g43760/MQD19_11 [Arabidopsis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 50932775; NR Description: putative beta-ketoacyl
; OTHER INFORMATION: synthase [Oryza sativa (japonica cultivar-group)]
; OTHER INFORMATION: >gi|50080251|gb|AAT69586.1| putative beta-ketoacyl synthase [Oryza
US-11-174-307B-2584

Query Match      22.4%; Score 45; DB 7; Length 1600;
Best Local Similarity 36.4%; Pred. No. 4.2e+02;
Matches 8; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

QY 13 ACIPQCLRCSSNTPTPLTCQRYC 34
   | | | | | | | | | | | | | | | | | | | | |
Db 1102 ACAGCATACGATTTCCTCCAAC 1123
   | | | | | | | | | | | | | | | | | | | | |

RESULT 87
US-11-174-307B-2242
; Sequence 2242, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
; FILE REFERENCE: 2750-1601PUS2
; CURRENT APPLICATION NUMBER: US/11/174,307B
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,671
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,781
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,651
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 2242
; LENGTH: 1636
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Pfam Name: Aldose_epim; Pfam Description: Aldose 1-epimerase
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 26452398; NR Description: putative aldose
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 7671483; NR Description: putative aldose
; OTHER INFORMATION: 1-epimerase-like protein [Arabidopsis thaliana]
; OTHER INFORMATION: >gi|11358633|pir||T49949 probable aldose 1-epimerase-like protein
; OTHER INFORMATION: Arabidopsis thaliana >gi|15422223|ref|NP_197018.1| aldose
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 21537069; NR Description: aldose 1-epimerase-like
; FEATURE:
```

; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 15824567; NR Description: non-cell-autonomous
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 15824565; NR Description: non-cell-autonomous
US-11-174-307B-2242

Query Match 22.4%; Score 45; DB 7; Length 1636;
Best Local Similarity 36.4%; Pred. No. 4.3e+02;
Matches 8; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

QY 13 ACIPQLRCSSNTPPLTCORYC 34
||| :|||
Db 1137 ACAGCATACGATTTCCTCAAC 1158

RESULT 88
US-11-174-307B-56
; Sequence 56, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
; TITLE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS
; FILE REFERENCE: 2750-1601PUS2
; CURRENT APPLICATION NUMBER: US/11/174,307B
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,671
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,781
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,651
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 56
; LENGTH: 2274
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Pfam Name: MFAP1_C; Pfam Description:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 50251322; NR Description: putative MFAP1 protein
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 7267500; NR Description: putative
; OTHER INFORMATION: microfilbril-associated protein [Arabidopsis thaliana]
; OTHER INFORMATION: >gi|2565010|gb|AA81880.1| putative microfilbril-associated protein
; OTHER INFORMATION: [Arabidopsis thaliana] >gi|7487954|pir||T01826
US-11-174-307B-56

Query Match 22.4%; Score 45; DB 7; Length 2274;
Best Local Similarity 36.4%; Pred. No. 5.9e+02;
Matches 8; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY 13 ACIPQLRCSSNTPPLTCORYC 34
||| :|||
Db 417 ACCTCTCACTATTTCCTCTC 438

RESULT 89
US-10-449-902-35834
; Sequence 35834, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35834
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-35834

Query Match 22.1%; Score 44.5; DB 6; Length 56;
Best Local Similarity 42.9%; Pred. No. 21;
Matches 12; Conservative 1; Mismatches 12; Indels 3; Gaps 1;

QY 1 CSQNEYFDSLHAC--IPCQLRCSSNT 25
||| :|||
Db 25 CSSLSFISLKYACSWLIACYCTCSKIT 52

RESULT 90
US-10-953-349-30356
; Sequence 30356, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30356
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-30356

Query Match 22.1%; Score 44.5; DB 6; Length 83;
Best Local Similarity 33.3%; Pred. No. 30;
Matches 9; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

QY 1 CSQNEYFDSLHACIPCQLRCSSNTPP 27
||| :|||
Db 33 CSQTOYHNACILFCNKKCKKCLC-VPP 58

RESULT 91
US-10-953-349-30355
; Sequence 30355, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30355
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Triticum aestivum

US-10-953-349-30355

Query Match 22.1%; Score 44.5; DB 6; Length 85;
Best Local Similarity 33.3%; Pred. No. 31;
Matches 9; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

Qy 1 CSQNEYFDSLHLHACIPQLRCSSTPP 27
||| : | : : | : | : ||
Db 35 CSQTQYHNACILFCNKKCRKCLC-VPP 60

RESULT 92

US-10-953-349-30354
; Sequence 30354, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30354
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-30354

| | | | | |
|-------------------------|-------|----------------|-----------|-------------|
| Query Match | 22.1% | Score 44.5; | DB 6; | Length 106; |
| Best Local Similarity | 33.3% | Pred. No. 38; | | |
| Matches 9: Conservative | 5; | Mismatches 12; | Indels 1; | Gaps 1; |

| | | | |
|----|----|-----------------------------|----|
| Qy | 1 | CSQNEYFDSLHACIPQLRCSNTPP | 27 |
| | | : : : : : | |
| Db | 56 | CSOTQYHNACILFCNKKCRKCLC-VPP | 81 |

RESULT 93

```

US-10-449-902-39002
; Sequence 39002, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39002
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-39002

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| | | | | |
|-----------------------|--------------|---------------|---------------|-------------|
| Query Match | 22.1% | Score 44.5; | DB 6; | Length 136; |
| Best Local Similarity | 33.3% | Pred. No. 48; | | |
| Matches 9; | Conservative | 3; | Mismatches 6; | Indels 9; |
| Gaps 1; | | | | |

Qy 1 CSQNEYFDSLHACIPCQLRCSNTPP 27
|:| | | :|:
Db 80 CNQNS-----IVCMVRCALTPPP 97

RESULT 94

```

US-10-449-902-36200
; Sequence 36200, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205V1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36200
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-36200

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|--------------------------|--------|--------------------|-----------|-------------|
| Query Match | 22.1%; | Score 44.5; | DB 6; | Length 364; |
| Best Local Similarity | 36.4%; | Pred. No. 1.2e+02; | | |
| Matches 12; Conservative | 4; | Mismatches 12; | Indels 5; | Gaps 2; |

QY 2 SQNEYFDSLHACIP--CQIRCSSNTPPLTCQR 32
|:| | | : | | :|:|:| |

Dp 27 SKNYLLPYLRNNVPWCC---CTSCNPPIVCVR 56

RESULT 95

```

US-10-449-902-36422
; Sequence 36422, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36422
; LENGTH: 998
; TYPE: PR1
; ORGANISM: Oryza sativa
US-10-449-902-36422

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| | | | | |
|--------------------------|-------|--------------------|------------|-------------|
| Query Match | 22.1% | Score 44.5; | DB 6; | Length 988; |
| Best Local Similarity | 33.3% | Pred. NO. 3.1e+02; | | |
| Matches 10: Conservative | 3; | Mismatches 6; | Indels 11; | Gaps 1; |

Qy 1 CSQNEYFDSLHACIPCQLRCSNTPLTC 30
|||: :|||
Db 441 CSENSHIVNL-----GSNTAPFTC 459

RESULT 96

US-11-291-698A-105
; Sequence 105, Application US/11291698A
; Publication No. US20060135430A1
; GENERAL INFORMATION:

; APPLICANT: Chan, Andrew Chee-Yuen
; APPLICANT: Gordon, Nathaniel C.
; APPLICANT: Kelley, Robert F.
; APPLICANT: Koehler, Michael F.T.
; APPLICANT: Stavovasnik, Melissa A.
; TITLE OF INVENTION: BLYS ANTAGONISTS AND USES THEREOF
; FILE REFERENCE: 11669.174USC1
; CURRENT APPLICATION NUMBER: US/11/291,698A
; PRIOR FILING DATE: 2005-11-30
; PRIOR APPLICATION NUMBER: PCT/US04/17682
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 105
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 63
US-11-291-698A-105

Query Match 21.9%; Score 44; DB 7; Length 17;
Best Local Similarity 53.3%; Pred. No. 7.8;
Matches 8; Conservative 2; Mismatches 5; Indels 5; Gaps 0;

QY 5 EYFDSLHLHACIPCOL 19
| | | | | : | | |
DB 1 ECFDVLVLRWPCNL 15

RESULT 97
US-11-291-698A-115
; Sequence 115, Application US/11291698A
; Publication No. US20060135430A1
; GENERAL INFORMATION:
; APPLICANT: Chan, Andrew Chee-Yuen
; APPLICANT: Gordon, Nathaniel C.
; APPLICANT: Kelley, Robert F.
; APPLICANT: Koehler, Michael F.T.
; APPLICANT: Stavovasnik, Melissa A.
; TITLE OF INVENTION: BLYS ANTAGONISTS AND USES THEREOF
; FILE REFERENCE: 11669.174USC1
; CURRENT APPLICATION NUMBER: US/11/291,698A
; CURRENT FILING DATE: 2005-11-30
; PRIOR APPLICATION NUMBER: PCT/US04/17682
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 115
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 74
US-11-291-698A-115

Query Match 21.9%; Score 44; DB 7; Length 17;
Best Local Similarity 53.3%; Pred. No. 7.8;
Matches 8; Conservative 2; Mismatches 5; Indels 5; Gaps 0;

QY 5 EYFDSLHLHACIPCOL 19

DB 1 ECFDVLVLRWPCGL 15
| | | | | : | | |

RESULT 98
US-11-272-521-196
; Sequence 196, Application US/11272521
; Publication No. US20060135431A1
; GENERAL INFORMATION:
; APPLICANT: MIN, HOSUNG
; APPLICANT: HSU, HAILING
; APPLICANT: XIONG, FEI
; TITLE OF INVENTION: PEPTIDES AND RELATED MOLECULES THAT BIND TO TALL-1
; FILE REFERENCE: A-743
; CURRENT APPLICATION NUMBER: US/11/272,521
; CURRENT FILING DATE: 2005-11-10
; PRIOR APPLICATION NUMBER: US/10/145,206
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,196
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 196
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Human
US-11-272-521-196

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; Publication No. US20060111296A1
; GENERAL INFORMATION:
; APPLICANT: Devy, Laetitia
; APPLICANT: Ley, Arthur C.
; APPLICANT: Ladner, Robert C.
; TITLE OF INVENTION: PLASMIN-INHIBITORY THERAPIES
; FILE REFERENCE: 10280-122001
; CURRENT APPLICATION NUMBER: US/11/287,121A
; CURRENT FILING DATE: 2005-11-22
; PRIOR APPLICATION NUMBER: US 60/630,226
; PRIOR FILING DATE: 2004-11-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
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; TYPE: PRT
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; Publication No. US20060134087A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS HNE INHIBITORS
; FILE REFERENCE: D0617.7005US03
; CURRENT APPLICATION NUMBER: US/11/253,176
; CURRENT FILING DATE: 2005-10-18
; PRIOR APPLICATION NUMBER: 10/038,722
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
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; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; PRIOR APPLICATION NUMBER: US 08/133,031
; PRIOR FILING DATE: 1992-02-28
; NUMBER OF SEQ ID NOS: 173
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Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

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Listing first 1000 summaries

Database : Published Applications AA Main:*

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Pred. No. is the number of results predicted by chance to have a
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| 445 | 50 | 24.9 | 371 | 3 | US-09-898-234-12 | Sequence 12, Appl | 517 | 50 | 24.9 | 991 | 4 | Sequence 1944, Ap | Sequence 1944, Ap |
| 446 | 50 | 24.9 | 371 | 3 | US-09-899-429A-22 | Sequence 22, Appl | 518 | 50 | 24.9 | 1200 | 4 | Sequence 325, App | Sequence 325, App |
| 447 | 50 | 24.9 | 371 | 3 | US-09-792-356-12 | Sequence 12, Appl | 519 | 50 | 24.9 | 1200 | 4 | Sequence 326, App | Sequence 326, App |
| 448 | 50 | 24.9 | 397 | 4 | US-10-436-826-79 | Sequence 79, Appl | 520 | 50 | 24.9 | 1200 | 4 | Sequence 218, App | Sequence 218, App |
| 449 | 50 | 24.9 | 417 | 4 | US-10-436-826-76 | Sequence 76, Appl | 521 | 50 | 24.9 | 1200 | 4 | Sequence 2079, Ap | Sequence 2079, Ap |
| 450 | 50 | 24.9 | 420 | 4 | US-10-436-826-76 | Sequence 76, Appl | 522 | 50 | 24.9 | 1200 | 4 | Sequence 82, Appl | Sequence 82, Appl |
| 451 | 50 | 24.9 | 426 | 4 | US-10-349-977-37 | Sequence 37, Appl | 523 | 50 | 24.9 | 1200 | 4 | Sequence 80, Appl | Sequence 80, Appl |
| 452 | 50 | 24.9 | 453 | 4 | US-10-363-427-2 | Sequence 2, Appl | 524 | 50 | 24.9 | 1200 | 4 | Sequence 74, Appl | Sequence 74, Appl |
| 453 | 50 | 24.9 | 453 | 4 | US-10-280-047-5 | Sequence 5, Appl | 525 | 50 | 24.9 | 1200 | 4 | Sequence 228, App | Sequence 228, App |
| 454 | 50 | 24.9 | 453 | 6 | US-11-185-878-5 | Sequence 5, Appl | 526 | 50 | 24.9 | 1200 | 4 | Sequence 4, Appl | Sequence 4, Appl |
| 455 | 50 | 24.9 | 455 | 3 | US-09-826-212-3 | Sequence 3, Appl | 527 | 50 | 24.9 | 1200 | 4 | Sequence 4, Appl | Sequence 4, Appl |
| 456 | 50 | 24.9 | 455 | 3 | US-09-333-966-5 | Sequence 5, Appl | 528 | 50 | 24.9 | 1200 | 4 | Sequence 76, Appl | Sequence 76, Appl |
| 457 | 50 | 24.9 | 455 | 3 | US-09-077-287-3 | Sequence 3, Appl | 529 | 50 | 24.9 | 1200 | 4 | Sequence 233, App | Sequence 233, App |
| 458 | 50 | 24.9 | 455 | 3 | US-09-874-138-3 | Sequence 3, Appl | 530 | 50 | 24.9 | 1200 | 4 | Sequence 256, App | Sequence 256, App |
| 459 | 50 | 24.9 | 455 | 3 | US-09-840-707A-16 | Sequence 16, Appl | 531 | 50 | 24.9 | 1200 | 4 | Sequence 256, App | Sequence 256, App |
| 460 | 50 | 24.9 | 455 | 3 | US-09-232-656B-3 | Sequence 3, Appl | 532 | 50 | 24.9 | 1200 | 4 | Sequence 96, Appl | Sequence 96, Appl |
| 461 | 50 | 24.9 | 455 | 3 | US-09-899-422-2 | Sequence 2, Appl | 533 | 50 | 24.9 | 1200 | 4 | Sequence 2, Appl | Sequence 2, Appl |
| 462 | 50 | 24.9 | 455 | 3 | US-09-899-422-17 | Sequence 17, Appl | 534 | 50 | 24.9 | 1200 | 4 | | |
| 463 | 50 | 24.9 | 455 | 3 | US-09-935-727-5 | Sequence 5, Appl | 535 | 50 | 24.9 | 1200 | 4 | | |
| 464 | 50 | 24.9 | 455 | 3 | US-09-898-234-2 | Sequence 2, Appl | 536 | 50 | 24.9 | 1200 | 4 | | |
| 465 | 50 | 24.9 | 455 | 3 | US-09-898-234-17 | Sequence 17, Appl | 537 | 50 | 24.9 | 1200 | 4 | | |
| | 50 | 24.9 | 455 | 3 | US-09-756-854-5 | Sequence 5, Appl | 538 | 50 | 24.9 | 1200 | 4 | | |


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777 46.5 23.1 419 4 US-10-081-126-4 Sequence 4, Appli
778 46.5 23.1 419 4 US-10-303-997B-12 Sequence 12, Appl
779 46.5 23.1 419 4 US-10-439-337A-12 Sequence 12, Appl
780 46.5 23.1 419 4 US-10-661-740-4 Sequence 2, Appli
781 46.5 23.1 419 4 US-10-326-048-2 Sequence 2, Appli
782 46.5 23.1 419 4 US-10-696-002-2 Sequence 2, Appli
783 46.5 23.1 419 4 US-10-696-002-18 Sequence 18, Appl
784 46.5 23.1 419 4 US-10-712-124-106 Sequence 106, App
785 46.5 23.1 419 4 US-10-792-480-8 Sequence 8, Appli
786 46.5 23.1 419 4 US-10-792-480-58 Sequence 58, Appl
787 46.5 23.1 419 4 US-10-792-461-8 Sequence 8, Appli
788 46.5 23.1 419 4 US-10-792-461-58 Sequence 58, Appl
789 46.5 23.1 419 4 US-10-774-802-21 Sequence 21, Appl
790 46.5 23.1 419 4 US-10-859-737-3 Sequence 3, Appli
791 46.5 23.1 419 4 US-10-669-176-24 Sequence 24, Appl
792 46.5 23.1 419 5 US-10-772-927A-14 Sequence 14, Appl
793 46.5 23.1 419 5 US-10-723-860-986 Sequence 986, App
794 46.5 23.1 419 5 US-10-868-577A-2 Sequence 2, Appli
795 46.5 23.1 419 5 US-10-868-577A-68 Sequence 68, Appl
796 46.5 23.1 419 5 US-10-868-549-2 Sequence 2, Appli
797 46.5 23.1 419 5 US-10-868-549-5 Sequence 6, Appli
798 46.5 23.1 419 5 US-10-868-549-17 Sequence 17, Appl
799 46.5 23.1 419 5 US-10-980-815-2 Sequence 2, Appli
1000 46.5 23.1 419 5 US-10-980-815-18 Sequence 18, Appl
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ALIGNMENTS

```
RESULT 1
US-09-854-864-7
; Sequence 7, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-7

Query Match 100.0%; Score 201; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.4e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPCOLRCSSNTPLTCORYC 34
Db 1 CSQNEYFDSLHACIPCOLRCSSNTPLTCORYC 34

RESULT 2
US-09-855-158-7
; Sequence 7, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
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; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-7

Query Match 100.0%; Score 201; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.4e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPCOLRCSSNTPLTCORYC 34
Db 1 CSQNEYFDSLHACIPCOLRCSSNTPLTCORYC 34

RESULT 3
US-10-967-527A-9
; Sequence 9, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; TITLE OF INVENTION: Receptor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 40
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)..(40)
; OTHER INFORMATION: cysteine rich
US-10-967-527A-9

Query Match 100.0%; Score 201; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.8e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPCOLRCSSNTPLTCORYC 34
Db 3 CSQNEYFDSLHACIPCOLRCSSNTPLTCORYC 36

RESULT 4
US-09-854-864-6
; Sequence 6, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
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US-09-854-864-21
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-854-864-6
Query Match 100.0%; Score 201; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.5e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSSTNPPLTCORYC 34
DB 5 CSQNEYFDSLHACIPCOLRCSSTNPPLTCORYC 38

RESULT 5

US-09-855-158-6
; Sequence 6, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-855-158-6
Query Match 100.0%; Score 201; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.5e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSSTNPPLTCORYC 34
DB 5 CSQNEYFDSLHACIPCOLRCSSTNPPLTCORYC 38

RESULT 6

US-09-854-864-21
; Sequence 21, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-854-864-21

Query Match 100.0%; Score 201; DB 3; Length 58;
Best Local Similarity 100.0%; Pred. No. 4e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSSTNPPLTCORYC 34
DB 1 CSQNEYFDSLHACIPCOLRCSSTNPPLTCORYC 34

RESULT 7

US-09-855-158-21
; Sequence 21, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-855-158-21
Query Match 100.0%; Score 201; DB 3; Length 58;
Best Local Similarity 100.0%; Pred. No. 4e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSSTNPPLTCORYC 34
DB 1 CSQNEYFDSLHACIPCOLRCSSTNPPLTCORYC 34

RESULT 8

US-09-854-864-13
; Sequence 13, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus

US-09-854-864-13
Query Match 100.0%; Score 201; DB 3; Length 81;
Best Local Similarity 100.0%; Pred. No. 5.4e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSSTNPPLTCORYC 34

Db 1 CSQNEFYDSLHACIPQCLRCSSNTPPLTCQRYC 34
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RESULT 9
US-09-855-158-13
; Sequence 13, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; PRIOR FILING DATE: 2001-09-11
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-855-158-13

Query Match 100.0%; Score 201; DB 3; Length 81;
Best Local Similarity 100.0%; Pred. No. 5.4e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEFYDSLHACIPQCLRCSSNTPPLTCQRYC 34
|||||

Db 1 CSQNEFYDSLHACIPQCLRCSSNTPPLTCQRYC 34
|||||

RESULT 10
US-09-854-864-5
; Sequence 5, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-5

Query Match 100.0%; Score 201; DB 3; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEFYDSLHACIPQCLRCSSNTPPLTCQRYC 34
|||||

Db 5 CSQNEFYDSLHACIPQCLRCSSNTPPLTCQRYC 38
|||||

RESULT 11
US-09-855-158-5
; Sequence 5, Application US/09855158

; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; PRIOR FILING DATE: 2001-09-11
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-5

Query Match 100.0%; Score 201; DB 3; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEFYDSLHACIPQCLRCSSNTPPLTCQRYC 34
|||||

Db 5 CSQNEFYDSLHACIPQCLRCSSNTPPLTCQRYC 38
|||||

RESULT 12
US-10-077-438-1
; Sequence 1, Application US/10077438
; Publication No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-1

Query Match 100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEFYDSLHACIPQCLRCSSNTPPLTCQRYC 34
|||||

Db 8 CSQNEFYDSLHACIPQCLRCSSNTPPLTCQRYC 41
|||||

RESULT 13
US-10-077-438-7

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; Sequence 7, Application US/10077438
; Publication NO. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-7

Query Match          100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEFYFDSLLHACIPCOLRCSSNTPPLTCQRYC 34
Db 8 CSQNEFYFDSLLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 14
US-10-077-137-1
; Sequence 1, Application US/10077137
; Publication NO. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-7

Query Match          100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEFYFDSLLHACIPCOLRCSSNTPPLTCQRYC 34
Db 8 CSQNEFYFDSLLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 15
US-10-077-137-7
; Sequence 7, Application US/10077137
; Publication NO. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-7

Query Match          100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEFYFDSLLHACIPCOLRCSSNTPPLTCQRYC 34
Db 8 CSQNEFYFDSLLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 16
US-10-068-725-2
; Sequence 2, Application US/10068725
; Publication NO. US20030012783A1
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne
; TITLE OF INVENTION: Antibodies That Bind Both BCMA and TACI
; FILE REFERENCE: 01-04
; CURRENT APPLICATION NUMBER: US/10/068,725
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/270,274
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/283,447
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-725-2

Query Match          100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CSONEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 8 CSONEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

RESULT 17
US-10-151-882-47
; Sequence 47, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554
; CURRENT APPLICATION NUMBER: US/10/151,882
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-882-47

Query Match 100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSONEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 8 CSONEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

RESULT 18
US-10-115-192-8
; Sequence 8, Application US/10115192
; Publication No. US20030082175A1
; GENERAL INFORMATION:
; APPLICANT: Apotech R & D S.A.
; TITLE OF INVENTION: April Receptor (BCVA) and Uses Thereof
; FILE REFERENCE: A083PCT
; CURRENT APPLICATION NUMBER: US/10/115,192
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 60/215688
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/181807
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/157933
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-115-192-8

Query Match 100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSONEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 8 CSONEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

RESULT 19
US-10-008-063-7
; Sequence 7, Application US/10008063
; Publication No. US20030092164A1
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Henne, Randal M.
; APPLICANT: Grant, Francis, J.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
; FILE REFERENCE: 00-103
; CURRENT APPLICATION NUMBER: US/10/008,063
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-008-063-7

Query Match 100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSONEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 8 CSONEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

RESULT 20
US-10-152-363A-27
; Sequence 27, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-152-363A-27

Query Match 100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSONEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 8 CSONEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

RESULT 21
US-10-216-074-11
; Sequence 11, Application US/10216074
; Publication No. US20030148445A1
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/10/216,074
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
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Qy 1 CSONEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 8 CSONEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

RESULT 20
US-10-152-363A-27
; Sequence 27, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-152-363A-27

Query Match 100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSONEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 8 CSONEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

RESULT 21
US-10-216-074-11
; Sequence 11, Application US/10216074
; Publication No. US20030148445A1
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/10/216,074
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
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; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-216-074-11

Query Match      100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 22
US-10-087-080-39
; Sequence 39, Application US/10087080
; Publication No. US20030235820A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Markowitz, Sanford David
; APPLICANT: Eos Biotechnology, Inc.
; APPLICANT: Case Western Reserve University
; TITLE OF INVENTION: No. US20030235820A1 Methods of Diagnosis of Metastatic Colorectal Cancer
; TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for
; TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer
; FILE REFERENCE: 018501-000840US
; CURRENT APPLICATION NUMBER: US/10/087,080
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/272,206
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/281,149
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/284,555
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: tumor necrosis factor receptor superfamily, member
US-10-087-080-39

Query Match      100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 23
US-10-742-634-9
; Sequence 9, Application US/10742634
; Publication No. US20040208924A1
; GENERAL INFORMATION:
; APPLICANT: Parmelee, David
; APPLICANT: Yeh, Ren-Hwa
; APPLICANT: Galperina, Olga
; APPLICANT: Hilbert, David
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Neutrokin-alpha Conjugate, Neutrokin-alpha Complex, and Uses Thereof
; FILE REFERENCE: 1488.1810002
; CURRENT APPLICATION NUMBER: US/10/742,634
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: US 60/435,262
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; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/467,198
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-742-634-9

Query Match      100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 24
US-10-626-914-6
; Sequence 6, Application US/10626914
; Publication No. US20050043516A1
; GENERAL INFORMATION:
; Patin Docket Preview
; APPLICANT: CHUNTHARAPAI, ANAN
; APPLICANT: GREWAL, Iqbal
; APPLICANT: KIM, KYUNG JIN
; APPLICANT: YAN, MINHONG
; TITLE OF INVENTION: TACI Antibodies and Uses Thereof
; FILE REFERENCE: P1942R1
; CURRENT APPLICATION NUMBER: US/10/626,914
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 60/398,530
; PRIOR FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 6
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-626-914-6

Query Match      100.0%; Score 201; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 25
US-10-485-489-6
; Sequence 6, Application US/10485489
; Publication No. US20050070689A1
; GENERAL INFORMATION:
; APPLICANT: Dixit, Vishva
; APPLICANT: Grewal, Iqbal
; APPLICANT: Ridgway, John
; APPLICANT: Yan, Minhong
; TITLE OF INVENTION: TACIs and BR3 Polypeptides and Uses Thereof
; FILE REFERENCE: 11669.175USWO
; CURRENT APPLICATION NUMBER: US/10/485,489
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: PCT/US02/23487
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US 60/310,114
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/377,171
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 19
; SEQ ID NO 6
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; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-489-6

Query Match      100.0%; Score 201; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 26
US-10-861-049-27
; Sequence 27, Application US/10861049
; Publication No. US20050095243A1
; GENERAL INFORMATION:
; APPLICANT: Andrew Chan
; APPLICANT: Qian Gong
; APPLICANT: Flavius Martin
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
; FILE REFERENCE: P2040R1US
; CURRENT APPLICATION NUMBER: US/10/861,049
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 27
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-861-049-27

Query Match      100.0%; Score 201; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 27
US-10-989-826-46
; Sequence 46, Application US/10989826
; Publication No. US20050238650A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Crowley, Craig
; APPLICANT: De Sauvage, Frederic J.
; APPLICANT: Eaton, Daniel L.
; APPLICANT: Ebens, Allen
; APPLICANT: Polson, Andrew
; APPLICANT: Smith, Victoria
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Tumor of
; FILE REFERENCE: P5105R1US
; CURRENT APPLICATION NUMBER: US/10/989,826
; CURRENT FILING DATE: 2004-11-16
; PRIOR APPLICATION NUMBER: US 60/520,842
; PRIOR FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: US 60/532,426
; PRIOR FILING DATE: 2003-12-24
; NUMBER OF SEQ ID NOS: 75
; SEQ ID NO 46
; LENGTH: 184
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-989-826-46

Query Match      100.0%; Score 201; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 28
US-10-742-634-9
; Sequence 9, Application US/10742634
; Publication No. US20050249671A9
; GENERAL INFORMATION:
; APPLICANT: Parmelee, David
; APPLICANT: Yeh, Ren-Hwa
; APPLICANT: Galperina, Olga
; APPLICANT: Hilbert, David
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Neurokine-alpha Conjugate, Neurokine-alpha Complex, and Uses The
; FILE REFERENCE: 1488.1810002
; CURRENT APPLICATION NUMBER: US/10/742,634
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: US 60/435,262
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/467,198
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-742-634-9

Query Match      100.0%; Score 201; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 29
US-10-967-527A-8
; Sequence 8, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-967-527A-8

Query Match      100.0%; Score 201; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 41

RESULT 30
US-10-501-841-4
; Sequence 4, Application US/10501841
; Publication No. US20060084055A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Mannion, Jane
; APPLICANT: Algate, Paul A.
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordenez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis
; TITLE OF INVENTION: and Therapy of Hematological Malignancies
; FILE REFERENCE: 014058-014402PC
; CURRENT APPLICATION NUMBER: US/10/501,841
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 10/057,475
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: WO PCT/US03/02353
; PRIOR FILING DATE: 2003-01-22
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-501-841-4

Query Match 100.0%; Score 201; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 41

RESULT 31
US-11-021-874-27
; Sequence 27, Application US/11021874
; Publication No. US20050163775A1
; GENERAL INFORMATION:
; APPLICANT: Andrew Chan
; APPLICANT: Qian Gong
; APPLICANT: Flavius Martin
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
; FILE REFERENCE: P2040R1P1
; CURRENT APPLICATION NUMBER: US/11/021,874
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US 10/661,049
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 27
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-874-27

Query Match 100.0%; Score 201; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 41

RESULT 32
US-11-242-294-27
; Sequence 27, Application US/11242294
; Publication No. US20060034852A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/11/242,294
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US/10/152,363
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-242-294-27

Query Match 100.0%; Score 201; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 41

RESULT 33
US-11-200-992-8
; Sequence 8, Application US/11200992
; Publication No. US20060067933A1
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen
; APPLICANT: Yee, David P.
; TITLE OF INVENTION: SOLUBLE RECEPTOR BR43X2 AND METHODS OF USING
; FILE REFERENCE: 05558.0034.CNUS01
; CURRENT APPLICATION NUMBER: US/11/200,992
; CURRENT FILING DATE: 2005-08-10
; PRIOR APPLICATION NUMBER: 60/115,068
; PRIOR FILING DATE: 1999-01-07
; PRIOR APPLICATION NUMBER: 60/169,890
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/479,856
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-200-992-8

Query Match 100.0%; Score 201; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 41

RESULT 34
US-11-021-874-27
; Sequence 27, Application US/11021874
; Publication No. US20050163775A1
; GENERAL INFORMATION:
; APPLICANT: Andrew Chan
; APPLICANT: Qian Gong
; APPLICANT: Flavius Martin
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
; FILE REFERENCE: P2040R1P1
; CURRENT APPLICATION NUMBER: US/11/021,874
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US 10/661,049
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 27
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-874-27

Query Match 100.0%; Score 201; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Db 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41
|||||

RESULT 34
US-11-069-473-4
; Sequence 4, Application US/11069473
; Publication No. US20060073146A1
; GENERAL INFORMATION:
; APPLICANT: AVI J. ASHKENAZI
; APPLICANT: KELLY H. DODGE
; APPLICANT: IQBAL GREWAL
; APPLICANT: KYUNG JIN KIM
; APPLICANT: SCOT A. MARSTERS
; APPLICANT: ROBERT M. PITTI
; APPLICANT: MINHONG YAN
; TITLE OF INVENTION: USES OF AGONISTS AND ANTAGONISTS TO MODULATE ACTIVITY
; TITLE OF INVENTION: OF TNF-RELATED MOLECULES
; FILE REFERENCE: P1805R1
; CURRENT APPLICATION NUMBER: US/11/069,473
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US/09/724,341
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/182,938
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: US 60/226,986
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 4
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-069-473-4

Query Match 100.0%; Score 201; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
|||||

Db 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41
|||||

RESULT 35
US-09-854-864-9
; Sequence 9, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-9

Query Match 100.0%; Score 201; DB 3; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.8e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
|||||

Db 5 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 38

RESULT 36
US-09-855-158-9
; Sequence 9, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL1
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-9

Query Match 100.0%; Score 201; DB 3; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.8e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
|||||

Db 5 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 38
|||||

RESULT 37
US-10-469-469-120
; Sequence 120, Application US/10469469
; Publication No. US20060079493A1
; GENERAL INFORMATION:
; APPLICANT: FRITZ, LAWRENCE C.
; APPLICANT: BURROWS, FRANCIS J.
; TITLE OF INVENTION: METHODS FOR TREATING GENETICALLY-DEFINED PROLIFERATIVE
; FILE REFERENCE: DISORDERS WITH HSP90 INHIBITORS
; CURRENT APPLICATION NUMBER: US/10/469,469
; CURRENT FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: PCT/US02/06518
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: 60/272,751
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 120
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-469-469-120

Query Match 100.0%; Score 201; DB 5; Length 288;
Best Local Similarity 100.0%; Pred. No. 1.8e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
|||||

Db 112 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 145
|||||

RESULT 38
US-10-115-192-12
; Sequence 12, Application US/10115192
; Publication No. US20030082175A1


```
; GENERAL INFORMATION:
; APPLICANT: Apotech R & D S.A.
; APPLICANT: Biogen, Inc.
; TITLE OF INVENTION: April Receptor (BCMA) and Uses Thereof
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/115,192
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 60/215688
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/181807
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/157933
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 302
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-115-192-12

Query Match          100.0%; Score 201; DB 4; Length 302;
Best Local Similarity 100.0%; Pred. No. 1.9e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSNTTPTLTCORYC 34
   |||||
Db 31 CSQNEYFDSLHACIPCOLRCSNTTPTLTCORYC 64
   |||||

RESULT 39
US-10-077-438-3
; Sequence 3, Application US/10077438
; Publication No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-3

Query Match          90.0%; Score 181; DB 4; Length 207;
Best Local Similarity 63.0%; Pred. No. 3.7e-14;
Matches 34; Conservative 0; Mismatches 0; Indels 20; Gaps 1;

QY 1 CSQNEYFDSLHACIPCOLRCSNTTPTLTCORYC 34
   |||||
Db 46 CSQNEYFDSLHACIPCOLRCSNTTPTLTCORYC 99
   |||||

RESULT 40
US-10-077-137-3
; Sequence 3, Application US/10077137
; Publication No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-3

Query Match          90.0%; Score 181; DB 4; Length 207;
Best Local Similarity 63.0%; Pred. No. 3.7e-14;
Matches 34; Conservative 0; Mismatches 0; Indels 20; Gaps 1;

QY 1 CSQNEYFDSLHACIPCOLRCSNTTPTLTCORYC 34
   |||||
Db 46 CSQNEYFDSLHACIPCOLRCSNTTPTLTCORYC 99
   |||||

RESULT 41
US-09-854-864-11
; Sequence 11, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Murine
US-09-854-864-11

Query Match          67.7%; Score 136; DB 3; Length 185;
Best Local Similarity 70.6%; Pred. No. 1.1e-08;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 CSQNEYFDSLHACIPCOLRCSNTTPTLTCORYC 34
   |||||
Db 5 CPHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36
   |||||

RESULT 42
US-10-077-137-3
; Sequence 3, Application US/10077137
; Publication No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/115,192
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 60/215688
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/181807
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/157933
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 302
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-115-192-12

Query Match          100.0%; Score 201; DB 4; Length 302;
Best Local Similarity 100.0%; Pred. No. 1.9e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSNTTPTLTCORYC 34
   |||||
Db 31 CSQNEYFDSLHACIPCOLRCSNTTPTLTCORYC 64
   |||||

RESULT 39
US-10-077-438-3
; Sequence 3, Application US/10077438
; Publication No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-3

Query Match          90.0%; Score 181; DB 4; Length 207;
Best Local Similarity 63.0%; Pred. No. 3.7e-14;
Matches 34; Conservative 0; Mismatches 0; Indels 20; Gaps 1;

QY 1 CSQNEYFDSLHACIPCOLRCSNTTPTLTCORYC 34
   |||||
Db 46 CSQNEYFDSLHACIPCOLRCSNTTPTLTCORYC 99
   |||||

RESULT 40
US-10-077-137-3
; Sequence 3, Application US/10077137
; Publication No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-3

Query Match          90.0%; Score 181; DB 4; Length 207;
Best Local Similarity 63.0%; Pred. No. 3.7e-14;
Matches 34; Conservative 0; Mismatches 0; Indels 20; Gaps 1;

QY 1 CSQNEYFDSLHACIPCOLRCSNTTPTLTCORYC 34
   |||||
Db 46 CSQNEYFDSLHACIPCOLRCSNTTPTLTCORYC 99
   |||||

RESULT 41
US-09-854-864-11
; Sequence 11, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Murine
US-09-854-864-11

Query Match          67.7%; Score 136; DB 3; Length 185;
Best Local Similarity 70.6%; Pred. No. 1.1e-08;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 CSQNEYFDSLHACIPCOLRCSNTTPTLTCORYC 34
   |||||
Db 5 CPHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36
   |||||

RESULT 42
US-10-077-137-3
```

US-09-855-158-11
; Sequence 11, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; TITLE OF INVENTION: 3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Murine
US-09-855-158-11

Query Match 67.7%; Score 136; DB 3; Length 185;
Best Local Similarity 70.6%; Pred. No. 1.1e-08;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

Qy 1 CSONEYFDSLHACIPCOLRCSSTPPLTCQRYC 34
| : ||||| ||||| ||||| : ||||| |||||
Db 5 CFHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36

RESULT 43

US-10-216-074-17
; Sequence 17, Application US/10216074
; Publication No. US20030148445A1
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/10/216,074
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-216-074-17

Query Match 67.7%; Score 136; DB 4; Length 185;
Best Local Similarity 70.6%; Pred. No. 1.1e-08;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

Qy 1 CSONEYFDSLHACIPCOLRCSSTPPLTCQRYC 34
| : ||||| ||||| ||||| : ||||| |||||
Db 5 CFHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36

RESULT 44

US-10-967-527A-10
; Sequence 10, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.

; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; TITLE OF INVENTION: Receptor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 185
; TYPE: PRT
; ORGANISM: mus musculus
US-10-967-527A-10

Query Match 67.7%; Score 136; DB 5; Length 185;
Best Local Similarity 70.6%; Pred. No. 1.1e-08;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

Qy 1 CSONEYFDSLHACIPCOLRCSSTPPLTCQRYC 34
| : ||||| ||||| ||||| : ||||| |||||
Db 5 CFHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36

RESULT 45

US-09-854-864-10
; Sequence 10, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-854-864-10

Query Match 67.7%; Score 136; DB 3; Length 281;
Best Local Similarity 70.6%; Pred. No. 1.1e-08;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

Qy 1 CSONEYFDSLHACIPCOLRCSSTPPLTCQRYC 34
| : ||||| ||||| ||||| : ||||| |||||
Db 5 CFHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36

RESULT 46

US-09-855-158-10
; Sequence 10, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; TITLE OF INVENTION: 3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039

RESULT 48
US-09-854-864-12
; Sequence 12, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCES: A-686B
; CURRENT APPLICATION NUMBER: US/09/854, 864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PR1
; ORGANISM: human-murine Consensus
US-09-854-864-12

```

; Publication No. US20030093824A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; TITLE OF INVENTION: SPC6 SERINE PROTEASE GENE DISRUPTIONS,
; FILE REFERENCE: R-720
; CURRENT APPLICATION NUMBER: US/10/180,903
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/300,978
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/324,820
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1548
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-180-903-2

Query Match      33.6%; Score 67.5; DB 4; Length 1548;
Best Local Similarity 37.8%; Pred. No. 19;
Matches 14; Conservative 4; Mismatches 14; Indels 5; Gaps 1;

Qy      1 CSQNEYFDSLHACIPQCLRCSSNTTPP-----LTCOR 32
Db      1152 CAAVEWDEGSHRCQCHKKKSCFSGPSEDOCYTCPR 1188

RESULT 54
US-09-779-050A-45
; Sequence 45, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-45

Query Match      33.1%; Score 66.5; DB 3; Length 37;
Best Local Similarity 32.4%; Pred. No. 0.71;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy      1 CSQNEYFDSLHACIPQCLRCSSNTTPPLTCORYC 34
Db      2 CPREEQWDPILGTCMSCKTICNHQS-QRTCAAF 34

RESULT 55
US-10-967-527A-20
; Sequence 20, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; SEQ ID NO 21
; LENGTH: 249
; TYPE: PRT
; ORGANISM: mus musculus
US-10-967-527A-21

Query Match      35.6%; Score 71.5; DB 5; Length 249;
Best Local Similarity 35.3%; Pred. No. 1.1;
Matches 12; Conservative 8; Mismatches 13; Indels 1; Gaps 1;

Qy      1 CSQNEYFDSLHACIPQCLRCSSNTTPPLTCORYC 34
Db      6 CPKQYWDSSRKSCVSCALTCSQRS-QRTCTDFC 38

RESULT 52
US-11-200-992-20
; Sequence 20, Application US/11200992
; Publication No. US20060067933A1
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen
; APPLICANT: Yee, David P.
; TITLE OF INVENTION: SOLUBLE RECEPTOR BR43X2 AND METHODS OF USING
; FILE REFERENCE: 05558.0034.CNUS01
; CURRENT APPLICATION NUMBER: US/11/200,992
; CURRENT FILING DATE: 2005-08-10
; PRIOR APPLICATION NUMBER: 60/115,068
; PRIOR FILING DATE: 1999-01-07
; PRIOR APPLICATION NUMBER: 60/169,890
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/479,856
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-200-992-20

Query Match      35.3%; Score 71.5; DB 6; Length 249;
Best Local Similarity 35.3%; Pred. No. 1.1;
Matches 12; Conservative 8; Mismatches 13; Indels 1; Gaps 1;

Qy      1 CSQNEYFDSLHACIPQCLRCSSNTTPPLTCORYC 34
Db      6 CPKQYWDSSRKSCVSCALTCSQRS-QRTCTDFC 38

RESULT 53
US-10-180-903-2
; Sequence 2, Application US/10180903
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; TITLE OF INVENTION: SPC6 SERINE PROTEASE GENE DISRUPTIONS,
; FILE REFERENCE: R-720
; CURRENT APPLICATION NUMBER: US/10/180,903
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/300,978
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/324,820
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1548
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-180-903-2
```



```
Best Local Similarity 32.4%; Pred. No. 1.3;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSONEYFDSLHACIPQLRCSSNTPPLTCQRYC 34
Db 1 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAF 33

RESULT 60
US-09-854-864-15
; Sequence 15, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TAC1
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-15

Query Match 33.1%; Score 66.5; DB 3; Length 166;
Best Local Similarity 32.4%; Pred. No. 3;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSONEYFDSLHACIPQLRCSSNTPPLTCQRYC 34
Db 34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAF 66

RESULT 61
US-09-855-158-15
; Sequence 15, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-15

Query Match 33.1%; Score 66.5; DB 3; Length 166;
Best Local Similarity 32.4%; Pred. No. 3;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSONEYFDSLHACIPQLRCSSNTPPLTCQRYC 34
Db 34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAF 66
```

```
RESULT 62
US-10-293-816-6
; Sequence 6, Application US/10293816
; Publication No. US20030082173A1
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: Von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; FILE REFERENCE: 44158/254623
; CURRENT APPLICATION NUMBER: US/10/293,816
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 09/782,857
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/290,333
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US 08/810,572
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-816-6

Query Match 33.1%; Score 66.5; DB 4; Length 166;
Best Local Similarity 32.4%; Pred. No. 3;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSONEYFDSLHACIPQLRCSSNTPPLTCQRYC 34
Db 34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAF 66

RESULT 63
US-11-079-418-6
; Sequence 6, Application US/11079418
; Publication No. US20050183148A1
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: Von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; FILE REFERENCE: 44158/254623
; CURRENT APPLICATION NUMBER: US/11/079,418
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US/10/293,816
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 09/782,857
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/290,333
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US 08/810,572
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-079-418-6

Query Match 33.1%; Score 66.5; DB 6; Length 166;
Best Local Similarity 32.4%; Pred. No. 3;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSONEYFDSLHACIPQLRCSSNTPPLTCQRYC 34
Db 34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAF 66
```

RESULT 66

```
; FILE REFERENCE: P2040R1US
; CURRENT APPLICATION NUMBER: US/10/861,049
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 36
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-861-049-36

Query Match 33.1%; Score 66.5; DB 5; Length 265;
Best Local Similarity 32.4%; Pred. No. 4.7;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 34 CPBEQYWDPLLGTCTMSCKTICNHQS-QRTCAAF 66

RESULT 69
US-11-021-874-36
; Sequence 36, Application US/11021874
; Publication No. US20050163775A1
; GENERAL INFORMATION:
; APPLICANT: Andrew Chan
; APPLICANT: Qian Gong
; APPLICANT: Flavien Martin
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
; FILE REFERENCE: P2040R1P1
; CURRENT APPLICATION NUMBER: US/11/021,874
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US 10/861,049
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 36
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-021-874-36

Query Match 33.1%; Score 66.5; DB 6; Length 265;
Best Local Similarity 32.4%; Pred. No. 4.7;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 34 CPBEQYWDPLLGTCTMSCKTICNHQS-QRTCAAF 66

RESULT 70
US-11-069-473-9
; Sequence 9, Application US/11069473
; Publication No. US20060073146A1
; GENERAL INFORMATION:
; APPLICANT: AVI J. ASHKENAZI
; APPLICANT: KELLY H. DODGE
; APPLICANT: IQBAL GREWAL
; APPLICANT: KYUNG JIN KIM
; APPLICANT: SCOT A. MARSTERS
; APPLICANT: ROBERT M. PITTI
; APPLICANT: MINHONG YAN

; TITLE OF INVENTION: USES OF AGONISTS AND ANTAGONISTS TO MODULATE ACTIVITY
; FILE REFERENCE: P1805R1
; CURRENT APPLICATION NUMBER: US/11/069,473
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US/09/724,341
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/182,938
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: US 60/226,986
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 9
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-069-473-9

Query Match 33.1%; Score 66.5; DB 6; Length 265;
Best Local Similarity 32.4%; Pred. No. 4.7;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 34 CPBEQYWDPLLGTCTMSCKTICNHQS-QRTCAAF 66

RESULT 71
US-09-779-050A-43
; Sequence 43, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-779-050A-43

Query Match 33.1%; Score 66.5; DB 3; Length 291;
Best Local Similarity 32.4%; Pred. No. 5.1;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 34 CPBEQYWDPLLGTCTMSCKTICNHQS-QRTCAAF 66

RESULT 72
US-10-967-527A-19
; Sequence 19, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
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; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 19

; LENGTH: 292

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-967-527A-19

Query Match

Best Local Similarity 33.1%; Score 66.5; DB 5; Length 292;

Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSQNEFYDLSLLHACIPCOLRCSSNTTPTLCQRYC 34

Db 34 CPEQYWDPLLGTGCMCKTICNHQS-QRTCAAF 66

RESULT 73

US-09-879-919-22

; Sequence 22, Application US/09879919

; Patent No. US20020064829A1

; GENERAL INFORMATION:

; APPLICANT: YU, Guo-Liang, et al.

; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon

; FILE REFERENCE: PF253P1

; CURRENT APPLICATION NUMBER: US/09/879,919

; CURRENT FILING DATE: 2001-06-14

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/277,978

; PRIOR FILING DATE: 2001-03-23

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/254,875

; PRIOR FILING DATE: 2000-12-13

; PRIOR APPLICATION NUMBER: 60/241,952

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/211,537

; PRIOR FILING DATE: 2000-06-15

; PRIOR APPLICATION NUMBER: 08/815,783

; PRIOR FILING DATE: 1997-03-12

; PRIOR APPLICATION NUMBER: 60/016,812

; PRIOR FILING DATE: 1996-03-14

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 22

; LENGTH: 293

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-879-919-22

Query Match

Best Local Similarity 33.1%; Score 66.5; DB 3; Length 293;

Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSQNEFYDLSLLHACIPCOLRCSSNTTPTLCQRYC 34

Db 34 CPEQYWDPLLGTGCMCKTICNHQS-QRTCAAF 66

RESULT 74

US-09-854-864-14

; Sequence 14, Application US/09854864

; Patent No. US20020081296A1

; GENERAL INFORMATION:

; APPLICANT: THEILL, LARS EYDE

; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

; FILE REFERENCE: A-686B

; CURRENT APPLICATION NUMBER: US/09/854,864

; CURRENT FILING DATE: 2001-09-11

; PRIOR APPLICATION NUMBER: US 60/204,039

; PRIOR FILING DATE: 2000-05-12

; PRIOR APPLICATION NUMBER: US 60/214,591

; PRIOR FILING DATE: 2000-06-27

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 14

; LENGTH: 293

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-854-864-14

Query Match

Best Local Similarity 33.1%; Score 66.5; DB 3; Length 293;

Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSQNEFYDLSLLHACIPCOLRCSSNTTPTLCQRYC 34

Db 34 CPEQYWDPLLGTGCMCKTICNHQS-QRTCAAF 66

RESULT 75

US-09-855-158-14

; Sequence 14, Application US/09855158

; Publication No. US20020086018A1

; GENERAL INFORMATION:

; APPLICANT: THEILL, LARS EYDE

; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL

; FILE REFERENCE: A-686A

; CURRENT APPLICATION NUMBER: US/09/855,158

; CURRENT FILING DATE: 2001-09-11

; PRIOR APPLICATION NUMBER: US 60/214,591

; PRIOR FILING DATE: 2000-06-27

; PRIOR APPLICATION NUMBER: US 60/204,039

; PRIOR FILING DATE: 2000-05-12

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 14

; LENGTH: 293

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-855-158-14

Query Match

Best Local Similarity 33.1%; Score 66.5; DB 3; Length 293;

Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSQNEFYDLSLLHACIPCOLRCSSNTTPTLCQRYC 34

Db 34 CPEQYWDPLLGTGCMCKTICNHQS-QRTCAAF 66

RESULT 76

US-09-961-376-2

; Sequence 2, Application US/09961376

; Patent No. US20020106736A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR17

; FILE REFERENCE: PF524P1

; CURRENT APPLICATION NUMBER: US/09/961,376

; CURRENT FILING DATE: 2001-09-25

; PRIOR APPLICATION NUMBER: 60/254,874

; PRIOR FILING DATE: 2000-12-13

; PRIOR APPLICATION NUMBER: 60/235,991

; PRIOR FILING DATE: 2000-09-26

; PRIOR APPLICATION NUMBER: 09/533,822

; PRIOR FILING DATE: 2000-03-24

; PRIOR APPLICATION NUMBER: 60/188,208

; PRIOR FILING DATE: 2000-03-10

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

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; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-961-376-2

Query Match      33.1%; Score 66.5; DB 3; Length 293;
Best Local Similarity 32.4%; Pred. No. 5.1;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCORYC 34
Db 34 CPSEQYWDPLLGTCMSCKTICNHQS-QRTCAAFC 66

RESULT 77
US-09-779-050A-42
; Sequence 42, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: HSU, HAILIANG
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-42

Query Match      33.1%; Score 66.5; DB 3; Length 293;
Best Local Similarity 32.4%; Pred. No. 5.1;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCORYC 34
Db 34 CPSEQYWDPLLGTCMSCKTICNHQS-QRTCAAFC 66

RESULT 78
US-09-302-863-2
; Sequence 2, Application US/09302863
; Publication No. US2003002233A1
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G
; APPLICANT: Din, Wanwan S.
; TITLE OF INVENTION: METHODS OF USE OF THE TACI/TACI-L INTERACTION
; FILE REFERENCE: 2519
; CURRENT APPLICATION NUMBER: US/09/302,863
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Human
US-09-302-863-2

Query Match      33.1%; Score 66.5; DB 3; Length 293;
Best Local Similarity 32.4%; Pred. No. 5.1;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCORYC 34
Db 34 CPSEQYWDPLLGTCMSCKTICNHQS-QRTCAAFC 66

RESULT 79
US-09-302-863-2
; Sequence 2, Application US/09302863
; Publication No. US2003002233A1
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G
; APPLICANT: Din, Wanwan S.
; TITLE OF INVENTION: METHODS OF USE OF THE TACI/TACI-L INTERACTION
; FILE REFERENCE: 2519
; CURRENT APPLICATION NUMBER: US/09/302,863
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Human
US-09-302-863-2

Query Match      33.1%; Score 66.5; DB 3; Length 293;
Best Local Similarity 32.4%; Pred. No. 5.1;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCORYC 34
Db 34 CPSEQYWDPLLGTCMSCKTICNHQS-QRTCAAFC 66

RESULT 80
US-10-087-192-1650
; Sequence 1650, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1650
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-192-1650

Query Match      33.1%; Score 66.5; DB 4; Length 293;
Best Local Similarity 32.4%; Pred. No. 5.1;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCORYC 34
Db 34 CPSEQYWDPLLGTCMSCKTICNHQS-QRTCAAFC 66

RESULT 81
US-10-084-971-2
; Sequence 2, Application US/10084971
; Publication No. US20020187526A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Neurokine-alpha Binding Proteins and Methods Based Thereon
; FILE REFERENCE: PF524PCT
; CURRENT APPLICATION NUMBER: US/10/084,971
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/533,822
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RESULT 86
US-10-152-363A-2
; Sequence 2, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-152-363A-2

Query Match          33.1%; Score 66.5; DB 4; Length 293;
Best Local Similarity 32.4%; Pred. No. 5.1;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSQNEYFDSLHACIPCOLRCSSNPTPLTCORYC 34
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Db 34 CPSEQYWDPLLTGCMSCKTCICNHQS-QRTCAAFC 66

RESULT 87
US-10-268-951-22
; Sequence 22, Application US/10268951
; Publication No. US20030166864A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PF253P2
; CURRENT APPLICATION NUMBER: US/10/268,951
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 10/082,260
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/879,919
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/328,401
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/293,812
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-268-951-22

Query Match          33.1%; Score 66.5; DB 4; Length 293;
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; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-489-3

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Best Local Similarity 32.4%; Pred. No. 5.1;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSONEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 34 CPEEQYWDPLLGTGCMSCCKTICNHQS-ORTCAAF 66

RESULT 95
US-10-861-049-25
; Sequence 25, Application US/10861049
; Publication No. US20050095243A1
; GENERAL INFORMATION:
; APPLICANT: Andrew Chan
; APPLICANT: Qian Gong
; APPLICANT: Flavius Martin
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
; FILE REFERENCE: P2040R1P1
; CURRENT APPLICATION NUMBER: US/10/861,049
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 145
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; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-861-049-25

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Db 34 CPEEQYWDPLLGTGCMSCCKTICNHQS-ORTCAAF 66

RESULT 96
US-10-742-634-7
; Sequence 7, Application US/10742634
; Publication No. US20050249671A9
; GENERAL INFORMATION:
; APPLICANT: Parmelee, David
; APPLICANT: Yeh, Ren-Hwa
; APPLICANT: Galperina, Olga
; APPLICANT: Hilbert, David
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Neutrokin-alpha Conjugate, Neutrokin-alpha Complex, and Uses Th
; FILE REFERENCE: 1488.181002
; CURRENT APPLICATION NUMBER: US/10/742,634
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: US 60/435,262
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/467,198
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 7
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-742-634-7
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Best Local Similarity 32.4%; Pred. No. 5.1;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

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Db 34 CPEEQYWDPLLGTGCMSCCKTICNHQS-ORTCAAF 66

RESULT 97
US-11-021-874-25
; Sequence 25, Application US/11021874
; Publication No. US20050163775A1
; GENERAL INFORMATION:
; APPLICANT: Andrew Chan
; APPLICANT: Qian Gong
; APPLICANT: Flavius Martin
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
; FILE REFERENCE: P2040R1P1
; CURRENT APPLICATION NUMBER: US/11/021,874
; PRIOR FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US 10/861,049
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 25
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-874-25

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Best Local Similarity 32.4%; Pred. No. 5.1;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSONEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 34 CPEEQYWDPLLGTGCMSCCKTICNHQS-ORTCAAF 66

RESULT 98
US-11-079-418-2
; Sequence 2, Application US/11079418
; Publication No. US20050183148A1
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: Von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML AND METHODS OF USE THEREOF
; FILE REFERENCE: 44158/254623
; CURRENT APPLICATION NUMBER: US/11/079,418
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US/10/293,816
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 09/782,857
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/290,333
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US 08/810,572
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-079-418-2
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Search completed: July 10, 2006, 16:43:51
Job time : 35.6 secs

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RESULT 99
US-11-221-849-2
; Sequence 2, Application US/11221849
; Publication No. US2006003380A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR11
; FILE REFERENCE: PF524PlD1
; CURRENT APPLICATION NUMBER: US/11/221,849
; CURRENT FILING DATE: 2005-09-09
; PRIOR APPLICATION NUMBER: 09/961,376
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/254,874
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/235,991
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/533,822
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/188,208
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-221-849-2

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Query Match      33.1%; Score 66.5; DB 6; Length 293;
Best Local Similarity 32.4%; Pred. No. 5.1;
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Db       34 CPEEOYWDPLGLTGMCKKTCINHS-ORTCAAF 66

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RESULT 100
US-11-242-294-2
; Sequence 2, Application US/11242294
; Publication No. US20060034852A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; APPLICANT: Groess, Jane A.
; TITLE OF INVENTION: TAC1-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/11/242,294
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US/10/152,363
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-242-294-2

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Query Match 33.1%; Score 66.5; DB 6; Length 293;
Best Local Similarity 32.4%; Pred. No. 5.1;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

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GenCore version 5.1.9

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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:41:19 ; Search time 10.4 Seconds
(without alignments)
314.555 Million cell updates/sec

Title: US-10-077-137A-1_COPY_8_41

Perfect score: 201

Sequence: 1 CSQNYFDSLHLHACIPQLRCSSTPPLTCQRYC 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1000 summaries

Database :

PIR 80:*

1: Pirl:*

2: Pirl:*

3: Pirl:*

4: Pirl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 67.5 | 33.6 | 1548 | 2 S34583 | serine proteinase |
| 3 | 64.5 | 32.1 | 5376 | 2 T42215 | zonadhesin - mouse |
| 4 | 61 | 30.3 | 1101 | 2 T16840 | hypothetical prote |
| 5 | 59 | 29.4 | 758 | 2 T15577 | hypothetical prote |
| 6 | 58 | 28.9 | 1299 | 2 T43251 | furin (EC 3.4.21.7 |
| 7 | 57.5 | 28.6 | 63 | 2 S07127 | chymotrypsin/elast |
| 8 | 57.5 | 28.6 | 1680 | 2 A43434 | furin (EC 3.4.21.7 |
| 9 | 57 | 28.4 | 1717 | 1 A45558 | epidermal growth f |
| 10 | 56 | 27.9 | 2476 | 2 T34022 | zonadhesin - pig |
| 11 | 55.5 | 27.6 | 989 | 2 T01519 | hypothetical prote |
| 12 | 55 | 27.4 | 330 | 2 T25169 | hypothetical prote |
| 13 | 55 | 27.4 | 1513 | 2 T23681 | hypothetical prote |
| 14 | 54.5 | 27.1 | 2155 | 2 T30197 | alpha tectorin - m |
| 15 | 54 | 26.9 | 1980 | 2 S54307 | myosin heavy chain |
| 16 | 54 | 26.9 | 2022 | 2 A59256 | myosin-IXb [simila |
| 17 | 53.5 | 26.6 | 758 | 2 S46625 | finger protein YUL |
| 18 | 53 | 26.4 | 1574 | 2 T13954 | MEGF6 protein - ra |
| 19 | 53 | 26.4 | 2824 | 2 T22759 | hypothetical prote |
| 20 | 52.5 | 26.1 | 118 | 2 S61051 | hypothetical prote |
| 21 | 52 | 25.9 | 255 | 2 A84544 | hypothetical prote |
| 22 | 52 | 25.9 | 294 | 2 T23682 | hypothetical prote |
| 23 | 52 | 25.9 | 547 | 2 T34318 | hypothetical prote |
| 24 | 52 | 25.9 | 1474 | 2 D86550 | protein ZC84.6 [im |
| 25 | 52 | 25.9 | 2844 | 2 S28291 | hypothetical prote |
| 26 | 51.5 | 25.6 | 63 | 2 S57816 | antimicrobial pept |
| 27 | 51.5 | 25.6 | 282 | 2 I48763 | siab-1A protein |
| 28 | 51.5 | 25.6 | 282 | 2 S35754 | siab-1B protein - |
| 29 | 51.5 | 25.6 | 497 | 2 T27827 | hypothetical prote |

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| 30 | 51.5 | 25.6 | 915 | 2 | T21773 | hypothetical prote |
| 31 | 51.5 | 25.6 | 927 | 2 | T21772 | hypothetical prote |
| 32 | 51.5 | 25.6 | 999 | 2 | T19275 | alpha tectorin - c |
| 33 | 51.5 | 25.6 | 2120 | 2 | T30243 | probable transcrip |
| 34 | 51 | 25.4 | 641 | 2 | E96612 | hypothetical prote |
| 35 | 51 | 25.4 | 653 | 2 | G96675 | hypothetical prote |
| 36 | 51 | 25.4 | 746 | 2 | G84605 | hypothetical prote |
| 37 | 50.5 | 25.1 | 610 | 1 | I46001 | chymotrypsin/elast |
| 38 | 50 | 24.9 | 63 | 2 | S08572 | ubiquitin / riboso |
| 39 | 50 | 24.9 | 74 | 2 | S10332 | hypothetical prote |
| 40 | 50 | 24.9 | 342 | 2 | T30370 | probable aminotran |
| 41 | 50 | 24.9 | 376 | 2 | C81272 | tumor necrosis fac |
| 42 | 50 | 24.9 | 455 | 1 | GQHUT1 | hypothetical prote |
| 43 | 50 | 24.9 | 561 | 2 | T27318 | hypothetical prote |
| 44 | 50 | 24.9 | 626 | 2 | T27319 | hypothetical prote |
| 45 | 50 | 24.9 | 922 | 2 | T23573 | hypothetical prote |
| 46 | 50 | 24.9 | 1360 | 2 | F96596 | hypothetical prote |
| 47 | 49.5 | 24.6 | 216 | 2 | G83398 | probable two-compo |
| 48 | 49.5 | 24.6 | 392 | 2 | T27303 | hypothetical prote |
| 49 | 49.5 | 24.6 | 1847 | 2 | T30558 | resistance protein |
| 50 | 49 | 24.4 | 189 | 2 | T48828 | hypothetical prote |
| 51 | 49 | 24.4 | 283 | 2 | T72272 | hypothetical prote |
| 52 | 49 | 24.4 | 306 | 2 | B71439 | hypothetical prote |
| 53 | 49 | 24.4 | 321 | 1 | S28390 | homeotic protein m |
| 54 | 49 | 24.4 | 346 | 2 | T20458 | hypothetical prote |
| 55 | 49 | 24.4 | 350 | 2 | JC5828 | paired-box-contain |
| 56 | 49 | 24.4 | 447 | 2 | A96639 | protein TIF9.18 [i |
| 57 | 49 | 24.4 | 461 | 2 | JC4302 | tumor necrosis fac |
| 58 | 49 | 24.4 | 602 | 2 | T47794 | hypothetical prote |
| 59 | 49 | 24.4 | 654 | 2 | T30136 | hypothetical prote |
| 60 | 49 | 24.4 | 1483 | 2 | S30015 | hypothetical prote |
| 61 | 49 | 24.4 | 1620 | 2 | T12783 | hypothetical prote |
| 62 | 49 | 24.4 | 1984 | 2 | T13171 | probable vitelloge |
| 63 | 49 | 24.4 | 2531 | 2 | A46019 | notch-1 protein - |
| 64 | 49 | 24.4 | 3635 | 2 | T10053 | laminin alpha 5 ch |
| 65 | 48.5 | 24.1 | 474 | 2 | T27297 | hypothetical prote |
| 66 | 48.5 | 24.1 | 608 | 1 | ABONS1 | serum albumin 1 pr |
| 67 | 48.5 | 24.1 | 608 | 1 | ABONS2 | serum albumin 2 pr |
| 68 | 48.5 | 24.1 | 1846 | 2 | T33079 | hypothetical prote |
| 69 | 48.5 | 24.1 | 3034 | 2 | T14119 | seven-pass transme |
| 70 | 48 | 23.9 | 56 | 2 | JN0380 | trypsin inhibitor |
| 71 | 48 | 23.9 | 98 | 2 | C89046 | protein C10G8.4 [i |
| 72 | 48 | 23.9 | 304 | 1 | JC2264 | tissue factor path |
| 73 | 48 | 23.9 | 314 | 2 | T27686 | hypothetical prote |
| 74 | 48 | 23.9 | 450 | 1 | TVFVMR | protein kinase (EC |
| 75 | 48 | 23.9 | 513 | 2 | D88991 | protein apx-1 [imp |
| 76 | 48 | 23.9 | 539 | 2 | T01513 | CTP synthase [EC 6 |
| 77 | 48 | 23.9 | 596 | 2 | F88188 | protein C18H9.7 [i |
| 78 | 48 | 23.9 | 597 | 2 | T08681 | adenosylhomocystei |
| 79 | 48 | 23.9 | 661 | 2 | E71427 | hypothetical prote |
| 80 | 48 | 23.9 | 666 | 2 | T30098 | hypothetical prote |
| 81 | 48 | 23.9 | 681 | 2 | B53542 | brefeldin A-sensit |
| 82 | 48 | 23.9 | 689 | 2 | T52060 | protein MEDEA [imp |
| 83 | 48 | 23.9 | 962 | 2 | JC5571 | subtilisin-like pr |
| 84 | 48 | 23.9 | 969 | 1 | A39490 | subtilisin-like pr |
| 85 | 48 | 23.9 | 975 | 2 | JC5570 | subtilisin-like pr |
| 86 | 48 | 23.9 | 1034 | 2 | JC5598 | mucin - rat |
| 87 | 48 | 23.9 | 1079 | 1 | TVFVMI | gag-Rml-env poly |
| 88 | 48 | 23.9 | 1203 | 2 | A49175 | Motch B protein - |
| 89 | 48 | 23.9 | 1797 | 2 | A55677 | laminin beta-2 cha |
| 90 | 47.5 | 23.6 | 249 | 2 | T35643 | hypothetical prote |
| 91 | 47.5 | 23.6 | 275 | 2 | T51437 | hypothetical prote |
| 92 | 47.5 | 23.6 | 355 | 1 | S22181 | gamma-1-microglobu |
| 93 | 47.5 | 23.6 | 546 | 2 | S67292 | probable membrane |
| 94 | 47.5 | 23.6 | 837 | 2 | S43656 | furin (EC 3.4.21.7 |
| 95 | 47.5 | 23.6 | 1188 | 2 | D86236 | protein F14N23.5 [i |
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| 97 | 47.5 | 23.6 | 2180 | 2 | T25764 | hypothetical prote |
| 98 | 47.5 | 23.6 | 2823 | 2 | F87908 | protein T22A3.8 [i |
| 99 | 47.5 | 23.6 | 2823 | 2 | T23064 | hypothetical prote |
| 100 | 47.5 | 23.6 | 3102 | 2 | T43291 | laminin alpha chai |
| 101 | 47 | 23.4 | 105 | 2 | T00232 | hypothetical 11.7K |
| 102 | 47 | 23.4 | 345 | 2 | T04016 | hypothetical prote |

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|-----|------|------|------|---|--------|--------------------|-----|------|------|------|---|--------|--------------------|
| 103 | 47 | 23.4 | 348 | 2 | T28623 | hypothetical prote | 176 | 45 | 22.4 | 102 | 2 | S26409 | protein 108 precu |
| 104 | 47 | 23.4 | 349 | 2 | D36858 | gene G4R protein - | 177 | 45 | 22.4 | 104 | 2 | G71202 | hypothetical prote |
| 105 | 47 | 23.4 | 349 | 2 | D72175 | G2R protein - vari | 178 | 45 | 22.4 | 182 | 2 | T28390 | ORF MSV229 leucine |
| 106 | 47 | 23.4 | 601 | 2 | C89451 | protein T04G9.6 [i | 179 | 45 | 22.4 | 187 | 2 | G87521 | RNA endonuclease f |
| 107 | 47 | 23.4 | 664 | 2 | AB1136 | NADH flavin oxidor | 180 | 45 | 22.4 | 320 | 1 | A39479 | homeotic protein m |
| 108 | 47 | 23.4 | 664 | 2 | AD1494 | NADH flavin oxidor | 181 | 45 | 22.4 | 334 | 2 | T24819 | hypothetical prote |
| 109 | 47 | 23.4 | 701 | 2 | S62460 | hypothetical prote | 182 | 45 | 22.4 | 364 | 2 | JC4249 | recf protein - Azo |
| 110 | 47 | 23.4 | 877 | 2 | T41794 | RNA polymerase LEF | 183 | 45 | 22.4 | 370 | 2 | T37282 | probable cathepsin |
| 111 | 47 | 23.4 | 932 | 2 | I52527 | PACE4A - mouse (fr | 184 | 45 | 22.4 | 384 | 2 | S25771 | gas1 protein - mou |
| 112 | 47 | 23.4 | 937 | 2 | I53282 | gene PACE4 protein | 185 | 45 | 22.4 | 396 | 2 | S53325 | tissue factor path |
| 113 | 47 | 23.4 | 1650 | 2 | S53457 | dominant autoantig | 186 | 45 | 22.4 | 420 | 2 | T30507 | probable alkaline |
| 114 | 47 | 23.4 | 2616 | 2 | A57096 | nudel protein prec | 187 | 45 | 22.4 | 431 | 2 | G75305 | hypothetical prote |
| 115 | 47 | 23.4 | 4660 | 2 | T42737 | gp130 protein prec | 188 | 45 | 22.4 | 450 | 2 | B97297 | hydrogenase chain |
| 116 | 47 | 23.4 | 4753 | 1 | A47437 | LDL-receptor-relat | 189 | 45 | 22.4 | 464 | 2 | T24011 | hypothetical prote |
| 117 | 46.5 | 23.1 | 63 | 1 | T1NP82 | proteinase inhibit | 190 | 45 | 22.4 | 479 | 2 | AF2146 | deoxyribopyrimidin |
| 118 | 46.5 | 23.1 | 135 | 2 | AD2688 | transcription regu | 191 | 45 | 22.4 | 511 | 2 | JC7682 | spermatogenesis as |
| 119 | 46.5 | 23.1 | 135 | 2 | G97469 | hypothetical prote | 192 | 45 | 22.4 | 557 | 2 | A48434 | variant-specific s |
| 120 | 46.5 | 23.1 | 186 | 2 | A45910 | ultra-high-sulfur | 193 | 45 | 22.4 | 661 | 2 | G97717 | hypothetical prote |
| 121 | 46.5 | 23.1 | 202 | 2 | T22237 | hypothetical prote | 194 | 45 | 22.4 | 672 | 2 | G71719 | hypothetical prote |
| 122 | 46.5 | 23.1 | 202 | 2 | T34078 | hypothetical prote | 195 | 45 | 22.4 | 702 | 2 | T21148 | hypothetical prote |
| 123 | 46.5 | 23.1 | 278 | 2 | T05774 | hypothetical prote | 196 | 45 | 22.4 | 763 | 2 | S51300 | probable membrane |
| 124 | 46.5 | 23.1 | 389 | 2 | T29488 | hypothetical prote | 197 | 45 | 22.4 | 964 | 2 | T30455 | hypothetical prote |
| 125 | 46.5 | 23.1 | 413 | 2 | G82422 | anaerobic glycerol | 198 | 45 | 22.4 | 1397 | 2 | T46354 | hypothetical prote |
| 126 | 46.5 | 23.1 | 419 | 2 | S69207 | vascular endotheli | 199 | 45 | 22.4 | 1839 | 1 | RRWP8M | genome polyprotein |
| 127 | 46.5 | 23.1 | 425 | 2 | T18592 | hypothetical prote | 200 | 45 | 22.4 | 2548 | 2 | ES9435 | myosin IXA import |
| 128 | 46.5 | 23.1 | 461 | 2 | B88953 | protein P16B4.8 [i | 201 | 45 | 22.4 | 2626 | 2 | T31099 | myosin-RhoGAP prot |
| 129 | 46.5 | 23.1 | 461 | 2 | T32663 | hypothetical prote | 202 | 45 | 22.4 | 4543 | 1 | A53102 | alpha-2-macroglobu |
| 130 | 46.5 | 23.1 | 600 | 2 | T18593 | hypothetical prote | 203 | 45 | 22.4 | 4544 | 1 | S02392 | alpha-2-macroglobu |
| 131 | 46.5 | 23.1 | 802 | 2 | T24293 | hypothetical prote | 204 | 45 | 22.4 | 4545 | 1 | S25111 | alpha-2-macroglobu |
| 132 | 46.5 | 23.1 | 874 | 2 | JO0893 | genome polyprotein | 205 | 44.5 | 22.1 | 142 | 2 | I51063 | MHC class II beta |
| 133 | 46.5 | 23.1 | 949 | 2 | T24294 | hypothetical prote | 206 | 44.5 | 22.1 | 175 | 2 | S37649 | high-sulfur kerati |
| 134 | 46.5 | 23.1 | 1124 | 1 | S58388 | protein-tyrosine k | 207 | 44.5 | 22.1 | 180 | 2 | PC1305 | MHC class II beta |
| 135 | 46.5 | 23.1 | 1365 | 2 | S14871 | suppressor two of | 208 | 44.5 | 22.1 | 217 | 2 | I51062 | hypothetical prote |
| 136 | 46.5 | 23.1 | 1597 | 2 | S68420 | citron - mouse | 209 | 44.5 | 22.1 | 251 | 2 | S23821 | vif protein - feli |
| 137 | 46.5 | 23.1 | 1935 | 2 | T39411 | RNA helicase - fis | 210 | 44.5 | 22.1 | 283 | 1 | ASLJFP | conserved hypotnet |
| 138 | 46.5 | 23.1 | 2111 | 2 | T15390 | hypothetical prote | 211 | 44.5 | 22.1 | 298 | 2 | B69532 | anaerobic sulfate |
| 139 | 46.5 | 23.1 | 3033 | 1 | GNWU8 | genome polyprotein | 212 | 44.5 | 22.1 | 347 | 2 | AC0825 | hypothetical prote |
| 140 | 46 | 22.9 | 99 | 2 | S60231 | gibberellin-regula | 213 | 44.5 | 22.1 | 357 | 2 | T21152 | hypothetical prote |
| 141 | 46 | 22.9 | 232 | 2 | S40738 | hypothetical prote | 214 | 44.5 | 22.1 | 368 | 1 | H81059 | phosphoserine amin |
| 142 | 46 | 22.9 | 311 | 2 | B64332 | hypothetical prote | 215 | 44.5 | 22.1 | 396 | 1 | JH0633 | cellular tumor ant |
| 143 | 46 | 22.9 | 335 | 2 | I72789 | interleukin 12 p40 | 216 | 44.5 | 22.1 | 400 | 2 | F81432 | probable transamin |
| 144 | 46 | 22.9 | 366 | 2 | T15895 | hypothetical prote | 217 | 44.5 | 22.1 | 481 | 2 | A56429 | i-kappa-B-related |
| 145 | 46 | 22.9 | 369 | 2 | S21471 | genome polyprotein | 218 | 44.5 | 22.1 | 493 | 2 | JC5486 | membrane glycoprot |
| 146 | 46 | 22.9 | 404 | 2 | C96549 | hypothetical prote | 219 | 44.5 | 22.1 | 592 | 1 | A30314 | protein kinase C (|
| 147 | 46 | 22.9 | 430 | 2 | AB0811 | probable transcrip | 220 | 44.5 | 22.1 | 592 | 1 | JC1480 | protein kinase C (|
| 148 | 46 | 22.9 | 439 | 2 | T23627 | hypothetical prote | 221 | 44.5 | 22.1 | 597 | 1 | S53711 | C4BP alpha chain p |
| 149 | 46 | 22.9 | 440 | 2 | T41766 | ARF-1 orf20/21 - | 222 | 44.5 | 22.1 | 654 | 2 | C96782 | unknown protein F2 |
| 150 | 46 | 22.9 | 458 | 2 | S61974 | SSU1 protein - yea | 223 | 44.5 | 22.1 | 949 | 2 | S54020 | probable membrane |
| 151 | 46 | 22.9 | 528 | 2 | S14944 | regulatory protein | 224 | 44.5 | 22.1 | 1115 | 2 | S40241 | G protein-coupled |
| 152 | 46 | 22.9 | 593 | 2 | I51213 | drebrin - chicken | 225 | 44.5 | 22.1 | 1126 | 2 | S49208 | transmembrane prot |
| 153 | 46 | 22.9 | 782 | 2 | S18031 | genome polyprotein | 226 | 44.5 | 22.1 | 1171 | 2 | A42916 | metabotropic gluta |
| 154 | 46 | 22.9 | 783 | 2 | A41627 | furin (EC 3.4.21.7 | 227 | 44.5 | 22.1 | 1180 | 2 | JC2132 | metabotropic gluta |
| 155 | 46 | 22.9 | 876 | 2 | B72856 | late expression fa | 228 | 44.5 | 22.1 | 1212 | 2 | JC2131 | metabotropic gluta |
| 156 | 46 | 22.9 | 1747 | 2 | T43182 | vitellogenin - gyp | 229 | 44.5 | 22.1 | 1297 | 2 | T52065 | probable myb-relat |
| 157 | 46 | 22.9 | 1753 | 2 | T00350 | hypothetical prote | 230 | 44.5 | 22.1 | 1661 | 2 | T31330 | head-activator bin |
| 158 | 46 | 22.9 | 2135 | 2 | T14602 | variant-specific s | 231 | 44.5 | 22.1 | 1791 | 2 | T02345 | hypothetical prote |
| 159 | 46 | 22.9 | 2910 | 2 | T42214 | otogelin - mouse | 232 | 44.5 | 22.1 | 2150 | 2 | T32497 | hypothetical prote |
| 160 | 46 | 22.9 | 3084 | 1 | MMWSA | laminin alpha-1 ch | 233 | 44.5 | 22.1 | 2471 | 2 | A49128 | cell-fate determin |
| 161 | 45.5 | 22.6 | 131 | 2 | S55390 | Norrie disease pro | 234 | 44 | 21.9 | 72 | 2 | B27725 | small proline-rich |
| 162 | 45.5 | 22.6 | 133 | 2 | A57005 | Norrie disease can | 235 | 44 | 21.9 | 93 | 2 | JE0159 | gibberellin-stimul |
| 163 | 45.5 | 22.6 | 155 | 2 | D82755 | conserved hypotnet | 236 | 44 | 21.9 | 114 | 2 | D75422 | hypothetical prote |
| 164 | 45.5 | 22.6 | 201 | 2 | D71190 | hypothetical prote | 237 | 44 | 21.9 | 118 | 2 | T49515 | hypothetical prote |
| 165 | 45.5 | 22.6 | 209 | 2 | A88104 | protein W10G11.3 [| 238 | 44 | 21.9 | 128 | 2 | T22276 | hypothetical prote |
| 166 | 45.5 | 22.6 | 225 | 2 | S57810 | hypothetical prote | 239 | 44 | 21.9 | 165 | 2 | S74697 | hypothetical prote |
| 167 | 45.5 | 22.6 | 318 | 2 | A45522 | variant surface gl | 240 | 44 | 21.9 | 165 | 2 | AB2113 | hypothetical prote |
| 168 | 45.5 | 22.6 | 386 | 2 | A41950 | retrovirus-related | 241 | 44 | 21.9 | 166 | 2 | H89044 | protein B0238.12 [|
| 169 | 45.5 | 22.6 | 392 | 2 | T29519 | hypothetical prote | 242 | 44 | 21.9 | 167 | 2 | H72579 | hypothetical prote |
| 170 | 45.5 | 22.6 | 697 | 2 | E56752 | hypothetical prote | 243 | 44 | 21.9 | 185 | 2 | AI2991 | conserved hypotnet |
| 171 | 45.5 | 22.6 | 704 | 2 | T50303 | hypothetical prote | 244 | 44 | 21.9 | 185 | 2 | A99292 | hypothetical prote |
| 172 | 45.5 | 22.6 | 749 | 2 | S13518 | transposase Tam3 - | 245 | 44 | 21.9 | 191 | 2 | I46412 | keratin KAP5.4 - s |
| 173 | 45.5 | 22.6 | 1077 | 2 | T41146 | probable cysteine- | 246 | 44 | 21.9 | 199 | 2 | B86288 | F9U1.31 protein - |
| 174 | 45.5 | 22.6 | 1171 | 2 | T13065 | Pip82 protein - fr | 247 | 44 | 21.9 | 224 | 2 | C81417 | probable transcrip |
| 175 | 45 | 22.4 | 99 | 2 | S40012 | fill protein - gar | 248 | 44 | 21.9 | 242 | 2 | T29699 | hypothetical prote |

| | | | | | | | | | | | | | |
|-----|------|------|------|---|--------|---------------------|-----|------|------|------|---|--------|--------------------|
| 249 | 44 | 21.9 | 304 | 1 | TIHUCK | tissue factor path | 322 | 43 | 21.4 | 141 | 1 | UTRTB | lutropin beta chai |
| 250 | 44 | 21.9 | 319 | 2 | E72852 | actin rearrangemen | 323 | 43 | 21.4 | 145 | 2 | S03298 | Ig alpha chain C r |
| 251 | 44 | 21.9 | 324 | 2 | E44221 | orf5 protein - Aut | 324 | 43 | 21.4 | 147 | 2 | AF0711 | conserved hypotet |
| 252 | 44 | 21.9 | 338 | 2 | T18715 | hypothetical prote | 325 | 43 | 21.4 | 158 | 2 | S57452 | ferredoxin 2[4Fe-4 |
| 253 | 44 | 21.9 | 340 | 2 | S58770 | cathepsin B (EC 3. | 326 | 43 | 21.4 | 169 | 2 | T41898 | hypothetical prote |
| 254 | 44 | 21.9 | 361 | 2 | B84827 | probable GDSL-moti | 327 | 43 | 21.4 | 214 | 2 | I49758 | hypoxanthine phosp |
| 255 | 44 | 21.9 | 405 | 2 | T42992 | cyclin D - Caenorh | 328 | 43 | 21.4 | 218 | 1 | RTHUG | hypoxanthine phosp |
| 256 | 44 | 21.9 | 405 | 2 | T26578 | hypothetical prote | 329 | 43 | 21.4 | 218 | 1 | RTMSG | hypoxanthine phosp |
| 257 | 44 | 21.9 | 418 | 2 | A64508 | hypothetical prote | 330 | 43 | 21.4 | 218 | 1 | T10288 | hypoxanthine phosp |
| 258 | 44 | 21.9 | 441 | 2 | S12707 | hypothetical prote | 331 | 43 | 21.4 | 298 | 2 | UN0265 | genome polyprotein |
| 259 | 44 | 21.9 | 455 | 2 | E90316 | genome polyprotein | 332 | 43 | 21.4 | 322 | 2 | JN0265 | genome polyprotein |
| 260 | 44 | 21.9 | 469 | 2 | E86421 | oxidoreductase [im | 333 | 43 | 21.4 | 337 | 1 | B71052 | hypothetical prote |
| 261 | 44 | 21.9 | 502 | 2 | T20130 | hypothetical prote | 334 | 43 | 21.4 | 338 | 2 | T29179 | hypothetical prote |
| 262 | 44 | 21.9 | 548 | 2 | T16642 | hypothetical prote | 335 | 43 | 21.4 | 395 | 2 | A46031 | hypothetical prote |
| 263 | 44 | 21.9 | 601 | 2 | B36346 | hypothetical prote | 336 | 43 | 21.4 | 401 | 2 | AC2207 | immobilization sur |
| 264 | 44 | 21.9 | 659 | 2 | T01520 | fibulin 1 precursor | 337 | 43 | 21.4 | 415 | 2 | PC4407 | L-cysteine/cystine |
| 265 | 44 | 21.9 | 661 | 2 | B96596 | hypothetical prote | 338 | 43 | 21.4 | 424 | 2 | T10400 | alkaline exonuclea |
| 266 | 44 | 21.9 | 667 | 2 | T01999 | hypothetical prote | 339 | 43 | 21.4 | 424 | 2 | E30857 | hypothetical prote |
| 267 | 44 | 21.9 | 669 | 2 | T06702 | hypothetical prote | 340 | 43 | 21.4 | 434 | 2 | F84605 | hypothetical prote |
| 268 | 44 | 21.9 | 683 | 2 | C36346 | hypothetical prote | 341 | 43 | 21.4 | 468 | 2 | T33857 | hypothetical prote |
| 269 | 44 | 21.9 | 685 | 2 | S78040 | fibulin 1 precursor | 342 | 43 | 21.4 | 472 | 1 | A35327 | vitamin D-binding |
| 270 | 44 | 21.9 | 705 | 2 | S34968 | fibulin, splice fo | 343 | 43 | 21.4 | 474 | 1 | VYHUD | probable oxidoredu |
| 271 | 44 | 21.9 | 761 | 2 | H65083 | glycolate oxidase | 344 | 43 | 21.4 | 475 | 2 | T35799 | apoptosis inhibito |
| 272 | 44 | 21.9 | 776 | 2 | A82787 | TonB-dependent rec | 345 | 43 | 21.4 | 497 | 2 | S69544 | hypothetical prote |
| 273 | 44 | 21.9 | 780 | 2 | A34102 | von Willebrand fac | 346 | 43 | 21.4 | 503 | 2 | T16920 | hypothetical prote |
| 274 | 44 | 21.9 | 780 | 2 | T31548 | hypothetical prote | 347 | 43 | 21.4 | 513 | 2 | S28358 | prespore vesicle p |
| 275 | 44 | 21.9 | 782 | 2 | S19876 | genome polyprotein | 348 | 43 | 21.4 | 524 | 2 | S47143 | A mating type prot |
| 276 | 44 | 21.9 | 838 | 2 | T20125 | hypothetical prote | 349 | 43 | 21.4 | 533 | 2 | D97480 | probable heat-shoc |
| 277 | 44 | 21.9 | 862 | 1 | QRMSLD | LDL receptor precu | 350 | 43 | 21.4 | 534 | 2 | T27054 | hypothetical prote |
| 278 | 44 | 21.9 | 879 | 2 | C90879 | hypothetical prote | 351 | 43 | 21.4 | 536 | 2 | D81700 | CTP synthase TC045 |
| 279 | 44 | 21.9 | 879 | 2 | H64888 | membrane protein y | 352 | 43 | 21.4 | 539 | 2 | H71545 | probable ctp synth |
| 280 | 44 | 21.9 | 879 | 2 | G85739 | hypothetical prote | 353 | 43 | 21.4 | 572 | 2 | T29880 | hypothetical prote |
| 281 | 44 | 21.9 | 915 | 1 | A48225 | subtilisin-like pr | 354 | 43 | 21.4 | 656 | 2 | S76505 | hypothetical prote |
| 282 | 44 | 21.9 | 1111 | 2 | T26972 | hypothetical prote | 355 | 43 | 21.4 | 677 | 2 | C42125 | trophozoite cystei |
| 283 | 44 | 21.9 | 1166 | 1 | S06142 | protein-tyrosine k | 356 | 43 | 21.4 | 697 | 2 | T21567 | hypothetical prote |
| 284 | 44 | 21.9 | 1221 | 2 | T23472 | hypothetical prote | 357 | 43 | 21.4 | 782 | 2 | T1FCHE | ovotransferrin pre |
| 285 | 44 | 21.9 | 1255 | 1 | A24571 | protein-tyrosine k | 358 | 43 | 21.4 | 783 | 2 | S18032 | genome polyprotein |
| 286 | 44 | 21.9 | 3075 | 2 | S14458 | laminin alpha-1 ch | 359 | 43 | 21.4 | 798 | 2 | T48304 | hypothetical prote |
| 287 | 43.5 | 21.6 | 61 | 2 | S57815 | antimicrobial pept | 360 | 43 | 21.4 | 856 | 2 | T52415 | polycomb protein E |
| 288 | 43.5 | 21.6 | 155 | 2 | B32669 | vasotocin 2 / neur | 361 | 43 | 21.4 | 859 | 2 | T05470 | hypothetical prote |
| 289 | 43.5 | 21.6 | 247 | 2 | I51060 | MHC class II beta | 362 | 43 | 21.4 | 869 | 2 | S49844 | probable membrane |
| 290 | 43.5 | 21.6 | 292 | 2 | B42822 | cyclin D3 - human | 363 | 43 | 21.4 | 877 | 2 | T43449 | hypothetical prote |
| 291 | 43.5 | 21.6 | 312 | 2 | T32379 | hypothetical prote | 364 | 43 | 21.4 | 888 | 2 | A54280 | cell differentiat |
| 292 | 43.5 | 21.6 | 339 | 1 | KHRTB | cathepsin B (EC 3. | 365 | 43 | 21.4 | 895 | 2 | T49010 | hypothetical prote |
| 293 | 43.5 | 21.6 | 347 | 2 | A38453 | anaerobic sulfite | 366 | 43 | 21.4 | 898 | 2 | T01503 | hypothetical prote |
| 294 | 43.5 | 21.6 | 352 | 2 | S11926 | cellulose 1,4-beta | 367 | 43 | 21.4 | 902 | 2 | T01127 | curly leaf protein |
| 295 | 43.5 | 21.6 | 356 | 2 | G88968 | G-protein signalin | 368 | 43 | 21.4 | 915 | 2 | B48225 | probable propotei |
| 296 | 43.5 | 21.6 | 481 | 2 | S62427 | metalloproteinase- | 369 | 43 | 21.4 | 942 | 2 | JC7316 | testicular zinc fi |
| 297 | 43.5 | 21.6 | 484 | 2 | JC9020 | protein kinase C (| 370 | 43 | 21.4 | 966 | 2 | D89042 | protein F14F9.6 [i |
| 298 | 43.5 | 21.6 | 592 | 2 | JN0877 | beta-transducin - | 371 | 43 | 21.4 | 1023 | 2 | T31669 | neural zinc finger |
| 299 | 43.5 | 21.6 | 595 | 2 | T39228 | probable transcrip | 372 | 43 | 21.4 | 1032 | 2 | T14124 | neural zinc finger |
| 300 | 43.5 | 21.6 | 625 | 2 | T37604 | protein kinase hom | 373 | 43 | 21.4 | 1051 | 2 | A40021 | integrin alpha-3 c |
| 301 | 43.5 | 21.6 | 799 | 2 | T02456 | carbon-monoxide de | 374 | 43 | 21.4 | 1193 | 2 | A44018 | laminin B2t chain |
| 302 | 43.5 | 21.6 | 805 | 2 | A39764 | p95 orf83 - Bombyx | 375 | 43 | 21.4 | 1817 | 2 | T34249 | hypothetical prote |
| 303 | 43.5 | 21.6 | 839 | 2 | T41826 | viral capsid assoc | 376 | 43 | 21.4 | 2219 | 2 | T27684 | hypothetical prote |
| 304 | 43.5 | 21.6 | 847 | 2 | D72860 | infected cell prot | 377 | 43 | 21.4 | 2588 | 2 | T14342 | NSD1 protein - mou |
| 305 | 43.5 | 21.6 | 850 | 1 | WNBE56 | probable transcrip | 378 | 43 | 21.4 | 3010 | 1 | S18030 | genome polyprotein |
| 306 | 43.5 | 21.6 | 857 | 2 | T40824 | hypothetical prote | 379 | 43 | 21.4 | 3672 | 2 | T23433 | hypothetical prote |
| 307 | 43.5 | 21.6 | 925 | 2 | T19361 | hypothetical prote | 380 | 43 | 21.4 | 3704 | 2 | T37316 | probable laminin a |
| 308 | 43.5 | 21.6 | 1036 | 2 | E84620 | RNA-dependent RNA | 381 | 42.5 | 21.1 | 99 | 2 | S60230 | gibberellin-regula |
| 309 | 43.5 | 21.6 | 1057 | 4 | B47521 | gastric mucin MUC5 | 382 | 42.5 | 21.1 | 137 | 2 | C72648 | hypothetical prote |
| 310 | 43.5 | 21.6 | 1373 | 2 | JR0095 | laminin alpha-4 ch | 383 | 42.5 | 21.1 | 181 | 2 | T05301 | hypothetical prote |
| 311 | 43.5 | 21.6 | 1816 | 1 | S68960 | gag-pol-like fusio | 384 | 42.5 | 21.1 | 198 | 2 | JC6547 | high sulfur protei |
| 312 | 43.5 | 21.6 | 1870 | 2 | C47521 | testicular luteini | 385 | 42.5 | 21.1 | 198 | 2 | T24476 | hypothetical prote |
| 313 | 43 | 21.4 | 80 | 2 | I65235 | hypothetical prote | 386 | 42.5 | 21.1 | 252 | 1 | A54677 | homeotic protein g |
| 314 | 43 | 21.4 | 108 | 2 | H69834 | hypothetical prote | 387 | 42.5 | 21.1 | 256 | 1 | A42768 | homeotic protein g |
| 315 | 43 | 21.4 | 114 | 2 | C90766 | phospholipase A2 h | 388 | 42.5 | 21.1 | 263 | 2 | S76994 | hypothetical prote |
| 316 | 43 | 21.4 | 118 | 2 | S01141 | lutropin beta chai | 389 | 42.5 | 21.1 | 288 | 2 | T21158 | hypothetical prote |
| 317 | 43 | 21.4 | 118 | 2 | PN0141 | lutropin beta chai | 390 | 42.5 | 21.1 | 315 | 2 | T21907 | hypothetical prote |
| 318 | 43 | 21.4 | 118 | 2 | PN0139 | type IV pilin prot | 391 | 42.5 | 21.1 | 323 | 2 | T28951 | hypothetical prote |
| 319 | 43 | 21.4 | 129 | 2 | A81187 | hypothetical prote | 392 | 42.5 | 21.1 | 328 | 2 | C86351 | hypothetical prote |
| 320 | 43 | 21.4 | 130 | 2 | C81154 | hypothetical prote | 393 | 42.5 | 21.1 | 332 | 2 | T21458 | hypothetical prote |
| 321 | 43 | 21.4 | 139 | 2 | I52320 | testicular luteini | 394 | 42.5 | 21.1 | 343 | 2 | S09272 | Ig alpha chain C r |

lutropin beta chai
Ig alpha chain C r
conserved hypotet
ferredoxin 2[4Fe-4
hypothetical prote
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alkaline exonuclea
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vitamin D-binding
probable oxidoredu
apoptosis inhibito
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probable ctp synth
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genome polyprotein
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|-----|------|------|------|---|---------|---------------------|-----|------|------|------|---|---------|---------------------|
| 395 | 42.5 | 21.1 | 352 | 2 | T21909 | hypotheical prote | 468 | 42 | 20.9 | 727 | 2 | T08920 | hypotheical prote |
| 396 | 42.5 | 21.1 | 379 | 2 | T37274 | probable cathepsin | 469 | 42 | 20.9 | 728 | 2 | T20561 | hypotheical prote |
| 397 | 42.5 | 21.1 | 389 | 2 | T47323 | hypotheical prote | 470 | 42 | 20.9 | 757 | 2 | T05688 | hypotheical prote |
| 398 | 42.5 | 21.1 | 397 | 2 | F72072 | probable transamin | 471 | 42 | 20.9 | 757 | 2 | T07693 | hypotheical prote |
| 399 | 42.5 | 21.1 | 397 | 2 | C86552 | aspartate aminotra | 472 | 42 | 20.9 | 776 | 2 | S28258 | androgen-regulated |
| 400 | 42.5 | 21.1 | 403 | 2 | S70676 | glycosyltransferas | 473 | 42 | 20.9 | 794 | 2 | S158376 | hypotheical prote |
| 401 | 42.5 | 21.1 | 415 | 1 | T7VHUSA | transforming prote | 474 | 42 | 20.9 | 853 | 2 | T23697 | hypotheical prote |
| 402 | 42.5 | 21.1 | 423 | 2 | T21570 | hypotheical prote | 475 | 42 | 20.9 | 923 | 2 | G81253 | probable oxidoredu |
| 403 | 42.5 | 21.1 | 438 | 2 | S55631 | virion protein kin | 476 | 42 | 20.9 | 963 | 2 | T09478 | ubiquitin thiolest |
| 404 | 42.5 | 21.1 | 439 | 2 | S86168 | hypotheical prote | 477 | 42 | 20.9 | 984 | 2 | C84781 | hypotheical prote |
| 405 | 42.5 | 21.1 | 440 | 2 | T21568 | hypotheical prote | 478 | 42 | 20.9 | 1104 | 2 | L38869 | transcription fact |
| 406 | 42.5 | 21.1 | 509 | 2 | AC2217 | hypotheical prote | 479 | 42 | 20.9 | 1107 | 2 | T15884 | hypotheical prote |
| 407 | 42.5 | 21.1 | 511 | 2 | T17298 | hypotheical prote | 480 | 42 | 20.9 | 1137 | 2 | T18625 | atrial natriuretic |
| 408 | 42.5 | 21.1 | 650 | 2 | T16077 | hypotheical prote | 481 | 42 | 20.9 | 1158 | 2 | E86327 | protein F18014.19 |
| 409 | 42.5 | 21.1 | 655 | 2 | G70900 | probable priA prot | 482 | 42 | 20.9 | 1210 | 2 | D88013 | hypotheical prote |
| 410 | 42.5 | 21.1 | 682 | 2 | D84579 | probable tail-like | 483 | 42 | 20.9 | 1264 | 2 | H96498 | hypotheical prote |
| 411 | 42.5 | 21.1 | 755 | 2 | A44315 | cartilage oligomer | 484 | 42 | 20.9 | 1428 | 2 | T08852 | lustin A - Califo |
| 412 | 42.5 | 21.1 | 769 | 2 | G83183 | probable chemotaxi | 485 | 42 | 20.9 | 1557 | 2 | T28811 | hypotheical prote |
| 413 | 42.5 | 21.1 | 1009 | 1 | DJBEM2 | DNA-directed DNA p | 486 | 42 | 20.9 | 1599 | 2 | T15854 | hypotheical prote |
| 414 | 42.5 | 21.1 | 1256 | 2 | C71436 | probable resistance | 487 | 42 | 20.9 | 1721 | 2 | T21214 | LR11 protein - mou |
| 415 | 42.5 | 21.1 | 1304 | 2 | G85188 | disease resistance | 488 | 42 | 20.9 | 2215 | 2 | T00348 | von Willebrand fac |
| 416 | 42.5 | 21.1 | 1317 | 2 | B85189 | disease resistance | 489 | 42 | 20.9 | 2813 | 1 | VWU | chitobiase-related |
| 417 | 42.5 | 21.1 | 1407 | 2 | B42239 | adenylate cyclase | 490 | 41.5 | 20.6 | 51 | 2 | A42243 | GRF-binding regula |
| 418 | 42.5 | 21.1 | 1422 | 2 | B71437 | probable resistanc | 491 | 41.5 | 20.6 | 68 | 2 | B42243 | gibberellin-regula |
| 419 | 42.5 | 21.1 | 1876 | 2 | T28627 | vitellogenin - Rip | 492 | 41.5 | 20.6 | 96 | 2 | S43910 | hypotheical prote |
| 420 | 42.5 | 21.1 | 2088 | 2 | E71436 | hypotheical prote | 493 | 41.5 | 20.6 | 127 | 2 | S61582 | hypotheical prote |
| 421 | 42.5 | 21.1 | 2467 | 2 | D71437 | probable resistance | 494 | 41.5 | 20.6 | 133 | 1 | PSOXG | phospholipase A2 (|
| 422 | 42.5 | 21.1 | 2643 | 2 | T29149 | hypotheical prote | 495 | 41.5 | 20.6 | 142 | 2 | S15061 | MHC class II beta |
| 423 | 42.5 | 21.1 | 4868 | 2 | B54161 | ryanodine-binding | 496 | 41.5 | 20.6 | 177 | 2 | S37650 | high-sulfur kerati |
| 424 | 42 | 20.9 | 50 | 2 | B64035 | hypotheical prote | 497 | 41.5 | 20.6 | 211 | 2 | S04927 | wound-induced prot |
| 425 | 42 | 20.9 | 87 | 2 | T00562 | gibberellin-regula | 498 | 41.5 | 20.6 | 233 | 1 | C48560 | UL56 protein - hum |
| 426 | 42 | 20.9 | 153 | 1 | S15621 | E6 protein - human | 499 | 41.5 | 20.6 | 237 | 2 | C40035 | cyclin-like protei |
| 427 | 42 | 20.9 | 169 | 2 | T15611 | hypotheical prote | 500 | 41.5 | 20.6 | 239 | 2 | T41837 | BRO-b - Bombyx mor |
| 428 | 42 | 20.9 | 177 | 2 | S32743 | genome polyprotein | 501 | 41.5 | 20.6 | 245 | 1 | A47539 | homeotic protein g |
| 429 | 42 | 20.9 | 180 | 2 | J00257 | trappin-11 - hippo | 502 | 41.5 | 20.6 | 253 | 2 | T00838 | hypotheical prote |
| 430 | 42 | 20.9 | 200 | 2 | S04926 | wound-induced prot | 503 | 41.5 | 20.6 | 280 | 2 | T09504 | ULM-protein FHL3, (|
| 431 | 42 | 20.9 | 210 | 2 | T15105 | hypotheical prote | 504 | 41.5 | 20.6 | 281 | 2 | D88637 | protein W09G12.1 (|
| 432 | 42 | 20.9 | 217 | 2 | S23244 | hypotheical prote | 505 | 41.5 | 20.6 | 293 | 2 | JC4012 | cyclin D3 - rat |
| 433 | 42 | 20.9 | 218 | 1 | RPHYG | hypoxanthine phosph | 506 | 41.5 | 20.6 | 312 | 2 | G84472 | hypotheical prote |
| 434 | 42 | 20.9 | 218 | 2 | S14474 | hypoxanthine phosph | 507 | 41.5 | 20.6 | 339 | 1 | KHMSB | cathepsin B (EC 3. |
| 435 | 42 | 20.9 | 218 | 2 | S43043 | hypoxanthine (guan | 508 | 41.5 | 20.6 | 363 | 2 | S42386 | hypotheical prote |
| 436 | 42 | 20.9 | 240 | 2 | H87149 | superoxide dismuta | 509 | 41.5 | 20.6 | 370 | 2 | B40605 | transmembrane redo |
| 437 | 42 | 20.9 | 253 | 2 | T00967 | hypotheical prote | 510 | 41.5 | 20.6 | 391 | 1 | S02192 | cellular tumor ant |
| 438 | 42 | 20.9 | 269 | 2 | T21407 | hypotheical prote | 511 | 41.5 | 20.6 | 393 | 2 | JC6176 | tumor suppressor p |
| 439 | 42 | 20.9 | 274 | 2 | F86276 | FI417.2 protein - | 512 | 41.5 | 20.6 | 399 | 2 | T49934 | carboxypeptidase-1 |
| 440 | 42 | 20.9 | 281 | 2 | S39495 | u-plasminogen acti | 513 | 41.5 | 20.6 | 400 | 2 | AB2922 | conserved hypotet |
| 441 | 42 | 20.9 | 295 | 1 | S29399 | homeotic protein m | 514 | 41.5 | 20.6 | 425 | 2 | C97696 | ITS beta (AF105057 |
| 442 | 42 | 20.9 | 297 | 1 | YXUNTP | thymidylate synthet | 515 | 41.5 | 20.6 | 437 | 2 | C35147 | integrase homolog |
| 443 | 42 | 20.9 | 324 | 1 | LURT3 | annexin III - rat | 516 | 41.5 | 20.6 | 450 | 2 | AF1884 | glycolate oxidase |
| 444 | 42 | 20.9 | 325 | 2 | T16709 | hypotheical prote | 517 | 41.5 | 20.6 | 507 | 2 | T151658 | terminal deoxynucl |
| 445 | 42 | 20.9 | 326 | 1 | GOVZML | T2 protein - myxom | 518 | 41.5 | 20.6 | 536 | 2 | B70973 | probable TRANSKETO |
| 446 | 42 | 20.9 | 329 | 2 | G86472 | probable hyoscyami | 519 | 41.5 | 20.6 | 536 | 2 | E84428 | hypotheical prote |
| 447 | 42 | 20.9 | 335 | 2 | S09275 | ig alpha chain C r | 520 | 41.5 | 20.6 | 593 | 2 | A71361 | probable thiamin A |
| 448 | 42 | 20.9 | 335 | 2 | A39743 | u-plasminogen acti | 521 | 41.5 | 20.6 | 622 | 2 | D71078 | aldehyde-ferridoxi |
| 449 | 42 | 20.9 | 340 | 2 | D71371 | conserved hypotet | 522 | 41.5 | 20.6 | 650 | 2 | T33350 | hypotheical prote |
| 450 | 42 | 20.9 | 388 | 2 | A88949 | protein R09B5.5 (i | 523 | 41.5 | 20.6 | 700 | 2 | C86296 | hypotheical prote |
| 451 | 42 | 20.9 | 399 | 2 | T32126 | hypotheical prote | 524 | 41.5 | 20.6 | 716 | 2 | T21516 | hypotheical prote |
| 452 | 42 | 20.9 | 417 | 2 | G84276 | imidazole-5-prop | 525 | 41.5 | 20.6 | 747 | 2 | T33746 | integrin beta-3 su |
| 453 | 42 | 20.9 | 426 | 2 | G96528 | protein F27J15.2 (| 526 | 41.5 | 20.6 | 788 | 2 | T15130 | infected cell prot |
| 454 | 42 | 20.9 | 461 | 1 | A35356 | tumor necrosis fac | 527 | 41.5 | 20.6 | 798 | 1 | B44051 | env polyprotein E |
| 455 | 42 | 20.9 | 461 | 2 | T24012 | hypotheical prote | 528 | 41.5 | 20.6 | 857 | 2 | T16235 | hypotheical prote |
| 456 | 42 | 20.9 | 475 | 2 | AD2698 | molecular chaperon | 529 | 41.5 | 20.6 | 925 | 2 | T16235 | 113.9K hypotheica |
| 457 | 42 | 20.9 | 499 | 2 | JC6141 | beta 1,3-glucanase | 530 | 41.5 | 20.6 | 1028 | 2 | B86473 | hypotheical prote |
| 458 | 42 | 20.9 | 545 | 2 | B70374 | conserved hypotet | 531 | 41.5 | 20.6 | 1043 | 2 | T15191 | hypotheical prote |
| 459 | 42 | 20.9 | 555 | 2 | AB3010 | microcystin synthe | 532 | 41.5 | 20.6 | 1442 | 2 | T27408 | transcription acti |
| 460 | 42 | 20.9 | 555 | 2 | D98274 | hypotheical prote | 533 | 41.5 | 20.6 | 1607 | 1 | MMMS2 | laminin gamma-1 ch |
| 461 | 42 | 20.9 | 560 | 2 | S53382 | protein YKR029c ho | 534 | 41.5 | 20.6 | 1639 | 1 | MMFFB2 | laminin gamma-1 ch |
| 462 | 42 | 20.9 | 579 | 4 | D40201 | artifac-warnin s | 535 | 41.5 | 20.6 | 2787 | 2 | S45416 | TEU protein - yea |
| 463 | 42 | 20.9 | 580 | 2 | B84554 | hypotheical prote | 536 | 41.5 | 20.6 | 53 | 2 | S23202 | kappa-casein - bov |
| 464 | 42 | 20.9 | 594 | 2 | T02129 | hypotheical prote | 537 | 41 | 20.4 | 88 | 2 | B84564 | similar to gibbere |
| 465 | 42 | 20.9 | 617 | 2 | T23952 | hypotheical prote | 538 | 41 | 20.4 | 97 | 2 | T18173 | hypotheical prote |
| 466 | 42 | 20.9 | 633 | 2 | T47524 | hypotheical prote | 539 | 41 | 20.4 | 120 | 2 | T10318 | hypotheical prote |
| 467 | 42 | 20.9 | 646 | 2 | T33346 | hypotheical prote | 540 | 41 | 20.4 | | | | |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|--------|--------------------|-----|------|------|------|---|--------|--------------------|
| 541 | 41 | 20.4 | 123 | 2 | T07886 | protein kinase (EC | 614 | 41 | 20.4 | 650 | 2 | D56612 | hypothetical prote |
| 542 | 41 | 20.4 | 126 | 2 | S77781 | probable glucosam | 615 | 41 | 20.4 | 689 | 2 | T08918 | hypothetical prote |
| 543 | 41 | 20.4 | 134 | 2 | T22275 | hypothetical prote | 616 | 41 | 20.4 | 747 | 2 | F69332 | heterodisulfide re |
| 544 | 41 | 20.4 | 137 | 2 | T15609 | hypothetical prote | 617 | 41 | 20.4 | 762 | 2 | H83415 | cis/trans isomeras |
| 545 | 41 | 20.4 | 146 | 2 | D64445 | ferredoxin 2[4Fe-4 | 618 | 41 | 20.4 | 768 | 2 | I53821 | p-selectin - rat |
| 546 | 41 | 20.4 | 152 | 2 | A32669 | vasotocin 1 / neur | 619 | 41 | 20.4 | 787 | 2 | P80677 | hypothetical prote |
| 547 | 41 | 20.4 | 153 | 2 | AE1883 | hypothetical prote | 620 | 41 | 20.4 | 861 | 2 | A48825 | Notch homolog MRC |
| 548 | 41 | 20.4 | 159 | 2 | T10921 | 3C3.12 protein - S | 621 | 41 | 20.4 | 871 | 1 | I48696 | protein-tyrosine k |
| 549 | 41 | 20.4 | 160 | 2 | I84444 | eosinophil-derived | 622 | 41 | 20.4 | 881 | 1 | I48697 | protein-tyrosine k |
| 550 | 41 | 20.4 | 177 | 2 | S32749 | genome polypeptide | 623 | 41 | 20.4 | 899 | 2 | G02428 | subtilisin-like pr |
| 551 | 41 | 20.4 | 177 | 2 | S62037 | hypothetical prote | 624 | 41 | 20.4 | 915 | 2 | JC6148 | subtilisin-like pr |
| 552 | 41 | 20.4 | 190 | 2 | A13299 | 5-methylcytosine-s | 625 | 41 | 20.4 | 920 | 2 | JC7313 | aryl hydrocarbon r |
| 553 | 41 | 20.4 | 197 | 2 | A07050 | hypothetical prote | 626 | 41 | 20.4 | 922 | 2 | T18878 | hypothetical prote |
| 554 | 41 | 20.4 | 198 | 2 | S25656 | T-cell surface gly | 627 | 41 | 20.4 | 927 | 2 | T38518 | ribonuclease II RN |
| 555 | 41 | 20.4 | 210 | 2 | T16744 | hypothetical prote | 628 | 41 | 20.4 | 1039 | 2 | T22982 | hypothetical prote |
| 556 | 41 | 20.4 | 223 | 2 | B38346 | ultra-high-sulfur | 629 | 41 | 20.4 | 1073 | 2 | F89467 | protein R09H3.1 (i |
| 557 | 41 | 20.4 | 230 | 2 | A38346 | ultra-high-sulfur | 630 | 41 | 20.4 | 1119 | 2 | A88481 | protein C16A3.6 (i |
| 558 | 41 | 20.4 | 232 | 2 | D96663 | unknown protein, 5 | 631 | 41 | 20.4 | 1119 | 2 | T16720 | hypothetical prote |
| 559 | 41 | 20.4 | 235 | 1 | RWHUT8 | T-cell surface gly | 632 | 41 | 20.4 | 1192 | 2 | H88293 | protein F59B10.1 (|
| 560 | 41 | 20.4 | 237 | 2 | B71424 | hypothetical prote | 633 | 41 | 20.4 | 1245 | 1 | MMMSND | nidogen precursor |
| 561 | 41 | 20.4 | 240 | 2 | AG2085 | hypothetical prote | 634 | 41 | 20.4 | 1254 | 2 | I48161 | p-185 precursor - |
| 562 | 41 | 20.4 | 266 | 2 | T46314 | hypothetical prote | 635 | 41 | 20.4 | 1260 | 1 | TVRTNU | protein-tyrosine k |
| 563 | 41 | 20.4 | 267 | 2 | E75269 | WD-repeat family p | 636 | 41 | 20.4 | 1357 | 2 | T16860 | hypothetical prote |
| 564 | 41 | 20.4 | 268 | 1 | UHMS2 | interleukin-2 rece | 637 | 41 | 20.4 | 1357 | 2 | B96696 | protein FIN21.4 (i |
| 565 | 41 | 20.4 | 273 | 2 | T16246 | hypothetical prote | 638 | 41 | 20.4 | 1610 | 2 | D89451 | protein T04G9.1 (i |
| 566 | 41 | 20.4 | 277 | 2 | T05539 | hypothetical prote | 639 | 41 | 20.4 | 1713 | 2 | A53347 | adhesive ligand ep |
| 567 | 41 | 20.4 | 282 | 2 | A48516 | surfactant protein | 640 | 41 | 20.4 | 2124 | 2 | T28658 | polyketide synthas |
| 568 | 41 | 20.4 | 295 | 2 | S35293 | hypothetical prote | 641 | 41 | 20.4 | 2533 | 2 | T28675 | alpha-51D immobili |
| 569 | 41 | 20.4 | 297 | 2 | JQ1209 | attachment protein | 642 | 41 | 20.4 | 2533 | 2 | T28674 | alpha-51D-immobili |
| 570 | 41 | 20.4 | 301 | 2 | F82446 | transcription regu | 643 | 41 | 20.4 | 3010 | 1 | GNWVCJ | genome polypeptide |
| 571 | 41 | 20.4 | 302 | 2 | T10810 | chitinase (EC 3.2. | 644 | 41 | 20.4 | 3010 | 1 | GNWVTW | genome polypeptide |
| 572 | 41 | 20.4 | 308 | 2 | A99993 | hypothetical prote | 645 | 41 | 20.4 | 3106 | 1 | S33868 | laminin alpha-2 ch |
| 573 | 41 | 20.4 | 313 | 2 | T06440 | probable transcrip | 646 | 40.5 | 20.1 | 102 | 2 | A36192 | inhibin beta-A cha |
| 574 | 41 | 20.4 | 315 | 2 | PS0011 | envelope glycoprot | 647 | 40.5 | 20.1 | 118 | 2 | S01801 | phospholipase A2 (|
| 575 | 41 | 20.4 | 315 | 2 | PN0164 | chitinase (EC 3.2. | 648 | 40.5 | 20.1 | 133 | 2 | AE2302 | hypothetical prote |
| 576 | 41 | 20.4 | 324 | 2 | T10802 | hypothetical prote | 649 | 40.5 | 20.1 | 149 | 2 | A41132 | collagen-related p |
| 577 | 41 | 20.4 | 335 | 2 | T31561 | hypothetical prote | 650 | 40.5 | 20.1 | 155 | 2 | D72761 | hypothetical prote |
| 578 | 41 | 20.4 | 335 | 2 | T31559 | hypothetical prote | 651 | 40.5 | 20.1 | 180 | 2 | PC1303 | genome polypeptide |
| 579 | 41 | 20.4 | 335 | 2 | T31560 | hypothetical prote | 652 | 40.5 | 20.1 | 203 | 2 | S57141 | probable membrane |
| 580 | 41 | 20.4 | 358 | 2 | T23802 | hypothetical prote | 653 | 40.5 | 20.1 | 213 | 2 | A98289 | transcription elon |
| 581 | 41 | 20.4 | 365 | 1 | W2WLHS | E2 protein - human | 654 | 40.5 | 20.1 | 226 | 2 | C71860 | hypothetical prote |
| 582 | 41 | 20.4 | 365 | 2 | E81704 | conserved hypotet | 655 | 40.5 | 20.1 | 229 | 2 | A46049 | dihydrofolate redu |
| 583 | 41 | 20.4 | 371 | 2 | T22652 | hypothetical prote | 656 | 40.5 | 20.1 | 241 | 2 | T41893 | BRO-e - Bombyx mor |
| 584 | 41 | 20.4 | 375 | 2 | T01468 | hypothetical prote | 657 | 40.5 | 20.1 | 258 | 2 | A71282 | conserved hypotet |
| 585 | 41 | 20.4 | 378 | 2 | B89588 | protein R09F10.7 (| 658 | 40.5 | 20.1 | 259 | 2 | T28483 | probable DNA-direc |
| 586 | 41 | 20.4 | 382 | 2 | G81879 | hypothetical prote | 659 | 40.5 | 20.1 | 259 | 2 | C72156 | C4L protein - vari |
| 587 | 41 | 20.4 | 407 | 2 | T37888 | hypothetical prote | 660 | 40.5 | 20.1 | 259 | 2 | G36841 | E4L protein - vari |
| 588 | 41 | 20.4 | 420 | 2 | A84864 | hypothetical prote | 661 | 40.5 | 20.1 | 283 | 2 | C23660 | calcium channel pr |
| 589 | 41 | 20.4 | 421 | 2 | T41577 | pombe specific con | 662 | 40.5 | 20.1 | 294 | 2 | A23660 | calcium channel pr |
| 590 | 41 | 20.4 | 440 | 2 | H71106 | hypothetical prote | 663 | 40.5 | 20.1 | 294 | 2 | B23660 | hypothetical prote |
| 591 | 41 | 20.4 | 442 | 2 | F75054 | hypothetical prote | 664 | 40.5 | 20.1 | 324 | 2 | T18790 | VSG expression sit |
| 592 | 41 | 20.4 | 458 | 2 | A96776 | F25A4.34 (imported | 665 | 40.5 | 20.1 | 325 | 1 | VMUT17 | mlo2 protein - fis |
| 593 | 41 | 20.4 | 476 | 1 | VVRTD | vitamin D-binding | 666 | 40.5 | 20.1 | 329 | 2 | T40419 | glucanase - vari |
| 594 | 41 | 20.4 | 483 | 2 | T24856 | hypothetical prote | 667 | 40.5 | 20.1 | 352 | 2 | S05500 | Ig alpha-1 chain C |
| 595 | 41 | 20.4 | 484 | 2 | D81422 | flagellar biosynth | 668 | 40.5 | 20.1 | 368 | 2 | F81816 | phosphoserine tran |
| 596 | 41 | 20.4 | 485 | 2 | D84475 | probable Athila re | 669 | 40.5 | 20.1 | 369 | 2 | F82333 | iron-sulfur Cluste |
| 597 | 41 | 20.4 | 485 | 2 | T49237 | hypothetical prote | 670 | 40.5 | 20.1 | 396 | 2 | E96911 | glucanase - vari |
| 598 | 41 | 20.4 | 487 | 2 | F84727 | hypothetical prote | 671 | 40.5 | 20.1 | 411 | 2 | T29475 | glucanase - vari |
| 599 | 41 | 20.4 | 495 | 2 | G95147 | polysaccharide bio | 672 | 40.5 | 20.1 | 411 | 2 | PC2061 | hypothetical prote |
| 600 | 41 | 20.4 | 495 | 2 | E98015 | conserved hypotet | 673 | 40.5 | 20.1 | 425 | 1 | A26431 | genome polypeptide |
| 601 | 41 | 20.4 | 509 | 2 | T00793 | hypothetical prote | 674 | 40.5 | 20.1 | 433 | 2 | S69999 | nerve growth facto |
| 602 | 41 | 20.4 | 513 | 2 | PC1284 | genome polypeptide | 675 | 40.5 | 20.1 | 438 | 2 | T02804 | sterigmatocystin s |
| 603 | 41 | 20.4 | 517 | 1 | T37831 | phenol 2-monooxyge | 676 | 40.5 | 20.1 | 477 | 2 | AG0765 | hypothetical prote |
| 604 | 41 | 20.4 | 520 | 2 | G88846 | protein T12A7.2 (i | 677 | 40.5 | 20.1 | 477 | 2 | SL5313 | phosphomannomutase |
| 605 | 41 | 20.4 | 540 | 2 | S70403 | zona pellucida gly | 678 | 40.5 | 20.1 | 492 | 2 | S41288 | genome polypeptide |
| 606 | 41 | 20.4 | 581 | 2 | C96538 | hypothetical prote | 679 | 40.5 | 20.1 | 494 | 2 | SL1301 | cytochrome P450 c1 |
| 607 | 41 | 20.4 | 589 | 2 | A10684 | hypothetical prote | 680 | 40.5 | 20.1 | 494 | 2 | A45888 | cytochrome P450 ar |
| 608 | 41 | 20.4 | 618 | 2 | I48914 | protein-tyrosine k | 681 | 40.5 | 20.1 | 512 | 2 | E71641 | ATP synthase alpha |
| 609 | 41 | 20.4 | 621 | 2 | I38467 | low density lipopr | 682 | 40.5 | 20.1 | 533 | 2 | E97854 | H+-transporting tw |
| 610 | 41 | 20.4 | 623 | 2 | S55652 | transcription cont | 683 | 40.5 | 20.1 | 534 | 2 | T41081 | hypothetical prote |
| 611 | 41 | 20.4 | 641 | 2 | AC1354 | NADH oxidase homol | 684 | 40.5 | 20.1 | 554 | 2 | T08976 | 2-amino-4-hydroxy- |
| 612 | 41 | 20.4 | 641 | 2 | AD1724 | NADH oxidase homol | 685 | 40.5 | 20.1 | 557 | 2 | T50788 | ubiquitin specific |
| 613 | 41 | 20.4 | 644 | 2 | A36325 | epidermal growth f | 686 | 40.5 | 20.1 | 608 | 1 | ABXL68 | 68K serum albumin |

| | | | | | | |
|-----|------|------|------|---|--------|---------------------|
| 687 | 40.5 | 20.1 | 608 | 2 | S54360 | reverse transcript |
| 688 | 40.5 | 20.1 | 627 | 2 | F95867 | conserved hypotet |
| 689 | 40.5 | 20.1 | 640 | 2 | J01584 | genome polyprotein |
| 690 | 40.5 | 20.1 | 649 | 2 | T46500 | hypothetical prote |
| 691 | 40.5 | 20.1 | 655 | 1 | A46688 | hepatocyte growth |
| 692 | 40.5 | 20.1 | 656 | 2 | T48254 | hypothetical prote |
| 693 | 40.5 | 20.1 | 682 | 2 | T12968 | hypothetical prote |
| 694 | 40.5 | 20.1 | 698 | 2 | S25409 | transcription fact |
| 695 | 40.5 | 20.1 | 721 | 2 | T41942 | hypothetical prote |
| 696 | 40.5 | 20.1 | 751 | 2 | T21967 | hypothetical prote |
| 697 | 40.5 | 20.1 | 794 | 2 | S26668 | finger protein 2FY |
| 698 | 40.5 | 20.1 | 794 | 2 | S59068 | Z13 protein - mous |
| 699 | 40.5 | 20.1 | 819 | 2 | T10355 | hypothetical prote |
| 700 | 40.5 | 20.1 | 855 | 1 | JQ2003 | env polyprotein - |
| 701 | 40.5 | 20.1 | 865 | 2 | A25762 | regulatory protein |
| 702 | 40.5 | 20.1 | 895 | 2 | A86410 | protein F3M18.22 (|
| 703 | 40.5 | 20.1 | 905 | 2 | T23229 | hypothetical prote |
| 704 | 40.5 | 20.1 | 965 | 2 | S62935 | hypothetical prote |
| 705 | 40.5 | 20.1 | 1020 | 2 | JN0124 | glycine dehydrogen |
| 706 | 40.5 | 20.1 | 1151 | 2 | T38424 | hypothetical prote |
| 707 | 40.5 | 20.1 | 1192 | 2 | S69000 | laminin gamma 2 ch |
| 708 | 40.5 | 20.1 | 1222 | 2 | T41835 | DNA helicase P143 |
| 709 | 40.5 | 20.1 | 1230 | 2 | S53974 | hypothetical prote |
| 710 | 40.5 | 20.1 | 1243 | 2 | JC5615 | membrane-associate |
| 711 | 40.5 | 20.1 | 1251 | 2 | A57293 | latent transformin |
| 712 | 40.5 | 20.1 | 1331 | 2 | S05031 | calcium channel al |
| 713 | 40.5 | 20.1 | 1371 | 2 | S77521 | sensory transducti |
| 714 | 40.5 | 20.1 | 1430 | 2 | T21910 | hypothetical prote |
| 715 | 40.5 | 20.1 | 1609 | 1 | MMHUB2 | laminin gamma-1 ch |
| 716 | 40.5 | 20.1 | 1700 | 2 | S08167 | Balbiani ring 3 pr |
| 717 | 40.5 | 20.1 | 1737 | 2 | T00209 | MEGF8 protein - hu |
| 718 | 40.5 | 20.1 | 2139 | 2 | A44467 | voltage-dependent |
| 719 | 40.5 | 20.1 | 2143 | 2 | JH0427 | calcium channel pr |
| 720 | 40.5 | 20.1 | 2166 | 2 | S11339 | calcium channel al |
| 721 | 40.5 | 20.1 | 2171 | 2 | S05034 | calcium channel pr |
| 722 | 40.5 | 20.1 | 2220 | 2 | A45290 | calcium channel pr |
| 723 | 40.5 | 20.1 | 4391 | 2 | A38096 | perlecan precursor |
| 724 | 40.5 | 20.1 | 52 | 2 | C60232 | T-cell surface gly |
| 725 | 40.5 | 20.1 | 71 | 2 | A83316 | hypothetical prote |
| 726 | 40.5 | 20.1 | 90 | 2 | C97046 | hypothetical prote |
| 727 | 40.5 | 20.1 | 91 | 2 | C82657 | hypothetical prote |
| 728 | 40.5 | 20.1 | 92 | 2 | T30364 | hypothetical prote |
| 729 | 40.5 | 20.1 | 97 | 2 | S71371 | gibberellin-regula |
| 730 | 40.5 | 20.1 | 98 | 2 | S60229 | gibberellin-regula |
| 731 | 40.5 | 20.1 | 103 | 2 | A42523 | As3R protein - vac |
| 732 | 40.5 | 20.1 | 103 | 2 | J01791 | SalF16R protein - |
| 733 | 40.5 | 20.1 | 110 | 2 | T51963 | GAS45-like protein |
| 734 | 40.5 | 20.1 | 118 | 2 | C35913 | hypothetical membr |
| 735 | 40.5 | 20.1 | 126 | 2 | B69320 | conserved hypotet |
| 736 | 40.5 | 20.1 | 129 | 2 | A96787 | protein F10A5.6 [1 |
| 737 | 40.5 | 20.1 | 129 | 2 | T47863 | hypothetical prote |
| 738 | 40.5 | 20.1 | 135 | 2 | T35853 | probable oxidoredu |
| 739 | 40.5 | 20.1 | 135 | 2 | E82578 | hypothetical prote |
| 740 | 40.5 | 20.1 | 137 | 1 | B46938 | hypothetical prote |
| 741 | 40.5 | 20.1 | 137 | 2 | G90939 | hypothetical prote |
| 742 | 40.5 | 20.1 | 137 | 2 | C85788 | hypothetical prote |
| 743 | 40.5 | 20.1 | 137 | 2 | AB0263 | conserved hypotet |
| 744 | 40.5 | 20.1 | 141 | 1 | UTPGB | lutropin beta chai |
| 745 | 40.5 | 20.1 | 144 | 2 | A29101 | vasopressin / neur |
| 746 | 40.5 | 20.1 | 146 | 2 | E82251 | hypothetical prote |
| 747 | 40.5 | 20.1 | 147 | 2 | B82131 | PlIB-related prote |
| 748 | 40.5 | 20.1 | 159 | 2 | B29879 | vasotocin / neurop |
| 749 | 40.5 | 20.1 | 161 | 2 | E69305 | conserved hypotet |
| 750 | 40.5 | 20.1 | 164 | 2 | H64803 | ybfp protein - Esc |
| 751 | 40.5 | 20.1 | 172 | 2 | A69944 | phage-related prote |
| 752 | 40.5 | 20.1 | 174 | 2 | T15176 | hypothetical prote |
| 753 | 40.5 | 20.1 | 192 | 2 | JC4663 | l-cell receptor CD |
| 754 | 40.5 | 20.1 | 195 | 2 | T28803 | hypothetical prote |
| 755 | 40.5 | 20.1 | 197 | 2 | T10081 | sperm mitochondria |
| 756 | 40.5 | 20.1 | 216 | 2 | PQ0299 | hypothetical prote |
| 757 | 40.5 | 20.1 | 224 | 2 | A60032 | cerebellin-like gl |
| 758 | 40.5 | 20.1 | 235 | 2 | T26489 | hypothetical prote |
| 759 | 40.5 | 20.1 | 243 | 2 | T31144 | hypothetical prote |

| | | | | | | |
|-----|----|------|-----|---|--------|---------------------|
| 760 | 40 | 19.9 | 250 | 2 | JQ2165 | glycoprotein gL pr |
| 761 | 40 | 19.9 | 250 | 2 | T30124 | hypothetical prote |
| 762 | 40 | 19.9 | 252 | 2 | F39534 | floral homeotic pr |
| 763 | 40 | 19.9 | 285 | 1 | H64151 | hydroxyethylthiaz |
| 764 | 40 | 19.9 | 280 | 2 | B95931 | probable amino aci |
| 765 | 40 | 19.9 | 282 | 2 | A10721 | hydrogenase-1 oper |
| 766 | 40 | 19.9 | 284 | 2 | H70369 | hydrogenase small |
| 767 | 40 | 19.9 | 293 | 2 | A96946 | N-dimethylarginine |
| 768 | 40 | 19.9 | 299 | 2 | I46937 | tissue factor path |
| 769 | 40 | 19.9 | 300 | 2 | SL2143 | lipoprotein-associ |
| 770 | 40 | 19.9 | 307 | 1 | MMNW38 | PE-38 protein - Org |
| 771 | 40 | 19.9 | 307 | 1 | T10421 | protein PE38 - Org |
| 772 | 40 | 19.9 | 319 | 2 | S10154 | catechol 2,3-dioxy |
| 773 | 40 | 19.9 | 319 | 2 | A53502 | follicstatin - Afri |
| 774 | 40 | 19.9 | 321 | 2 | S04253 | guinate 5-dehydrog |
| 775 | 40 | 19.9 | 322 | 2 | T03686 | peroxidase [EC 1.1 |
| 776 | 40 | 19.9 | 328 | 2 | G89152 | protein C24B5.5 [1 |
| 777 | 40 | 19.9 | 329 | 2 | T32115 | hypothetical prote |
| 778 | 40 | 19.9 | 335 | 2 | B75091 | pyruvate formate-1 |
| 779 | 40 | 19.9 | 337 | 2 | I47079 | follicstatin - shee |
| 780 | 40 | 19.9 | 341 | 2 | AE1824 | permease protein o |
| 781 | 40 | 19.9 | 343 | 2 | S55369 | follicstatin - chic |
| 782 | 40 | 19.9 | 343 | 2 | S45321 | follicstatin - mous |
| 783 | 40 | 19.9 | 343 | 2 | A81423 | hypothetical prote |
| 784 | 40 | 19.9 | 344 | 1 | A27701 | follicstatin precu |
| 785 | 40 | 19.9 | 344 | 2 | A32141 | follicstatin 1 prec |
| 786 | 40 | 19.9 | 344 | 2 | I45894 | follicstatin - bovi |
| 787 | 40 | 19.9 | 344 | 2 | I57698 | follicstatin - rat |
| 788 | 40 | 19.9 | 356 | 2 | T21881 | hypothetical prote |
| 789 | 40 | 19.9 | 370 | 2 | T49246 | hypothetical prote |
| 790 | 40 | 19.9 | 379 | 2 | T16213 | APX-1 protein homo |
| 791 | 40 | 19.9 | 395 | 2 | H72222 | conserved hypotet |
| 792 | 40 | 19.9 | 403 | 2 | T06762 | hypothetical prote |
| 793 | 40 | 19.9 | 406 | 2 | T16520 | hypothetical prote |
| 794 | 40 | 19.9 | 409 | 2 | C87538 | conserved hypotet |
| 795 | 40 | 19.9 | 409 | 2 | C86402 | protein T22C5.21 (|
| 796 | 40 | 19.9 | 423 | 2 | S38953 | carboxypeptidase D |
| 797 | 40 | 19.9 | 423 | 2 | F75635 | hypothetical prote |
| 798 | 40 | 19.9 | 427 | 1 | GQHUN | nerve growth facto |
| 799 | 40 | 19.9 | 427 | 2 | I38909 | damage-specific DN |
| 800 | 40 | 19.9 | 432 | 2 | I56934 | fibrinogen-like pr |
| 801 | 40 | 19.9 | 432 | 2 | A27447 | cytotoxic T-lympho |
| 802 | 40 | 19.9 | 434 | 2 | A38282 | p58 galactosyltran |
| 803 | 40 | 19.9 | 435 | 2 | H96556 | auxin conjugate hy |
| 804 | 40 | 19.9 | 437 | 2 | T40653 | aspartate transami |
| 805 | 40 | 19.9 | 439 | 2 | I37391 | fibrinogen-like pr |
| 806 | 40 | 19.9 | 440 | 2 | JC8032 | PU.1-binding prote |
| 807 | 40 | 19.9 | 468 | 2 | T00794 | hypothetical prote |
| 808 | 40 | 19.9 | 470 | 2 | S71466 | homeotic protein S |
| 809 | 40 | 19.9 | 472 | 1 | A26730 | ovoinhibitor precu |
| 810 | 40 | 19.9 | 473 | 2 | A86442 | hypothetical prote |
| 811 | 40 | 19.9 | 488 | 1 | VCLJCN | env polyprotein - |
| 812 | 40 | 19.9 | 488 | 1 | VCLJMT | env polyprotein - |
| 813 | 40 | 19.9 | 488 | 1 | VCVWH | env polyprotein - |
| 814 | 40 | 19.9 | 488 | 2 | SL4605 | envelope glycoprot |
| 815 | 40 | 19.9 | 488 | 2 | A45714 | envelope glycoprot |
| 816 | 40 | 19.9 | 488 | 2 | B61547 | env polyprotein - |
| 817 | 40 | 19.9 | 490 | 2 | B28516 | cytochrome P450 2C |
| 818 | 40 | 19.9 | 525 | 2 | T10574 | hypothetical prote |
| 819 | 40 | 19.9 | 526 | 2 | S49641 | L-galactonolactone |
| 820 | 40 | 19.9 | 526 | 2 | T13484 | frizzled protein h |
| 821 | 40 | 19.9 | 527 | 1 | S01302 | adenosylhomocyste |
| 822 | 40 | 19.9 | 539 | 2 | B56447 | crp synthetase hom |
| 823 | 40 | 19.9 | 545 | 1 | A39193 | cytochrome c3 pre |
| 824 | 40 | 19.9 | 552 | 2 | T27424 | hypothetical prote |
| 825 | 40 | 19.9 | 565 | 1 | HNN2C1 | hemagglutinin-neur |
| 826 | 40 | 19.9 | 565 | 1 | HNN2C2 | hemagglutinin-neur |
| 827 | 40 | 19.9 | 565 | 1 | HNN2C3 | hemagglutinin-neur |
| 828 | 40 | 19.9 | 565 | 1 | HNN2SV | hemagglutinin G - s |
| 829 | 40 | 19.9 | 593 | 2 | S49525 | hypothetical prote |
| 830 | 40 | 19.9 | 600 | 2 | D84588 | hypothetical prote |
| 831 | 40 | 19.9 | 620 | 2 | F72395 | hypothetical prote |
| 832 | 40 | 19.9 | 647 | 2 | A35648 | B-cell adhesion pr |

| | | | | | | | | | | | | | |
|-----|------|------|------|---|--------|---------------------|-----|------|------|-----|---|--------|----------------------|
| 833 | 40 | 19.9 | 662 | 2 | T23271 | hypothetical prote | 906 | 39.5 | 19.7 | 172 | 1 | KRSHHA | keratin high-sulfu |
| 834 | 40 | 19.9 | 668 | 2 | C71868 | hypothetical prote | 907 | 39.5 | 19.7 | 182 | 2 | I47105 | high-sulfur wool m |
| 835 | 40 | 19.9 | 671 | 2 | A35912 | homeotic protein o | 908 | 39.5 | 19.7 | 210 | 2 | AI0031 | probable two-compo |
| 836 | 40 | 19.9 | 714 | 2 | S56208 | hypothetical prote | 909 | 39.5 | 19.7 | 237 | 2 | S08073 | cyclic nucleotide |
| 837 | 40 | 19.9 | 717 | 2 | AD0627 | probable membrane | 910 | 39.5 | 19.7 | 240 | 2 | T33698 | hypothetical prote |
| 838 | 40 | 19.9 | 720 | 2 | T02734 | hypothetical prote | 911 | 39.5 | 19.7 | 244 | 2 | S29982 | class II histocomp |
| 839 | 40 | 19.9 | 722 | 2 | B71376 | hypothetical prote | 912 | 39.5 | 19.7 | 247 | 2 | IS1059 | MHC class II beta |
| 840 | 40 | 19.9 | 728 | 2 | S71467 | hypothetical prote | 913 | 39.5 | 19.7 | 249 | 2 | S68684 | cysteine-rich secr |
| 841 | 40 | 19.9 | 739 | 2 | A54808 | diacylglycerol kin | 914 | 39.5 | 19.7 | 252 | 2 | F64503 | hypothetical prote |
| 842 | 40 | 19.9 | 745 | 1 | I49101 | conserved helix-lo | 915 | 39.5 | 19.7 | 259 | 1 | RNV230 | DNA-directed RNA p |
| 843 | 40 | 19.9 | 766 | 2 | E82445 | fatty acid cis/tra | 916 | 39.5 | 19.7 | 259 | 2 | T30797 | DNA-directed RNA p |
| 844 | 40 | 19.9 | 768 | 2 | A42755 | p-selectin precurs | 917 | 39.5 | 19.7 | 259 | 2 | H42508 | E4L protein - vacc |
| 845 | 40 | 19.9 | 782 | 2 | S19875 | genome polyprotein | 918 | 39.5 | 19.7 | 267 | 2 | T30007 | hypothetical prote |
| 846 | 40 | 19.9 | 786 | 2 | S22155 | oncogene 1 (tre-2 | 919 | 39.5 | 19.7 | 283 | 2 | E88597 | protein Y47D3B.6 l |
| 847 | 40 | 19.9 | 793 | 2 | T40285 | hypothetical prote | 920 | 39.5 | 19.7 | 295 | 2 | A08048 | probable AraC-famI |
| 848 | 40 | 19.9 | 805 | 2 | A46266 | aryl hydrocarbon r | 921 | 39.5 | 19.7 | 300 | 2 | A32837 | transcription acti |
| 849 | 40 | 19.9 | 810 | 2 | S65226 | probable membrane | 922 | 39.5 | 19.7 | 302 | 2 | D91266 | regulator of melib |
| 850 | 40 | 19.9 | 811 | 2 | JC7619 | hypoxia-inducible | 923 | 39.5 | 19.7 | 302 | 2 | A86107 | regulator of melib |
| 851 | 40 | 19.9 | 817 | 2 | T25674 | hypothetical prote | 924 | 39.5 | 19.7 | 342 | 2 | T16857 | hypothetical prote |
| 852 | 40 | 19.9 | 837 | 2 | D84428 | hypothetical prote | 925 | 39.5 | 19.7 | 366 | 2 | H87332 | articularin, probabl |
| 853 | 40 | 19.9 | 843 | 2 | A27131 | epidermal growth f | 926 | 39.5 | 19.7 | 374 | 2 | A31382 | DNA-binding protei |
| 854 | 40 | 19.9 | 846 | 2 | JC7721 | aryl hydrocarbon r | 927 | 39.5 | 19.7 | 379 | 2 | A59180 | wnt inhibitory fac |
| 855 | 40 | 19.9 | 860 | 1 | QRHULD | LDL receptor precu | 928 | 39.5 | 19.7 | 388 | 2 | T31887 | hypothetical prote |
| 856 | 40 | 19.9 | 879 | 2 | B70014 | antibiotic synthet | 929 | 39.5 | 19.7 | 388 | 2 | T31888 | hypothetical prote |
| 857 | 40 | 19.9 | 909 | 2 | T33749 | hypothetical prote | 930 | 39.5 | 19.7 | 392 | 2 | PC1144 | finger protein Zinc |
| 858 | 40 | 19.9 | 991 | 2 | T03377 | hypothetical prote | 931 | 39.5 | 19.7 | 394 | 2 | A60392 | zinc finger protei |
| 859 | 40 | 19.9 | 1017 | 2 | T42384 | hypothetical prote | 932 | 39.5 | 19.7 | 397 | 2 | T46223 | probable enzyme si |
| 860 | 40 | 19.9 | 1042 | 2 | S76045 | inositol-1,4,5-tri | 933 | 39.5 | 19.7 | 400 | 2 | D95928 | hypothetical prote |
| 861 | 40 | 19.9 | 1089 | 2 | S22158 | transforming prote | 934 | 39.5 | 19.7 | 405 | 2 | E64995 | hypothetical prote |
| 862 | 40 | 19.9 | 1098 | 2 | T50364 | hypothetical prote | 935 | 39.5 | 19.7 | 413 | 2 | JC4862 | activin beta-A cha |
| 863 | 40 | 19.9 | 1106 | 2 | T44598 | hypothetical prote | 936 | 39.5 | 19.7 | 422 | 2 | AD2191 | hypothetical prote |
| 864 | 40 | 19.9 | 1106 | 2 | T19338 | gene shuttles craft | 937 | 39.5 | 19.7 | 438 | 2 | T31898 | hypothetical prote |
| 865 | 40 | 19.9 | 1117 | 2 | C85018 | hypothetical prote | 938 | 39.5 | 19.7 | 445 | 2 | T31899 | hypothetical prote |
| 866 | 40 | 19.9 | 1170 | 2 | S52525 | probable membrane | 939 | 39.5 | 19.7 | 467 | 2 | D86237 | protein F14N23.21 |
| 867 | 40 | 19.9 | 1324 | 2 | T17468 | peptide-synthetase | 940 | 39.5 | 19.7 | 479 | 2 | S60924 | hypothetical prote |
| 868 | 40 | 19.9 | 1330 | 1 | GQFFE | epidermal growth f | 941 | 39.5 | 19.7 | 485 | 2 | C86143 | hypothetical prote |
| 869 | 40 | 19.9 | 1404 | 2 | T19277 | hypothetical prote | 942 | 39.5 | 19.7 | 501 | 1 | F64462 | polyferredoxin 2 - |
| 870 | 40 | 19.9 | 1435 | 2 | A37793 | erythrocyte-bindin | 943 | 39.5 | 19.7 | 527 | 2 | T41047 | hypothetical prote |
| 871 | 40 | 19.9 | 1451 | 2 | T33083 | hypothetical prote | 944 | 39.5 | 19.7 | 536 | 2 | T19488 | hypothetical prote |
| 872 | 40 | 19.9 | 1474 | 2 | T18281 | hypothetical prote | 945 | 39.5 | 19.7 | 546 | 2 | F84647 | hypothetical prote |
| 873 | 40 | 19.9 | 1490 | 2 | F88311 | protein T06D8.10 l | 946 | 39.5 | 19.7 | 560 | 1 | JC4795 | plasma hyaluronan- |
| 874 | 40 | 19.9 | 1490 | 2 | T24502 | hypothetical prote | 947 | 39.5 | 19.7 | 572 | 2 | S42866 | serine/threonine p |
| 875 | 40 | 19.9 | 1786 | 1 | MMWSB1 | laminin beta-1 cha | 948 | 39.5 | 19.7 | 597 | 1 | NBHUC4 | C4b-binding protei |
| 876 | 40 | 19.9 | 1829 | 2 | T24580 | hypothetical prote | 949 | 39.5 | 19.7 | 604 | 2 | JC7252 | transcription acti |
| 877 | 40 | 19.9 | 1964 | 2 | T09059 | notch4 - mouse | 950 | 39.5 | 19.7 | 604 | 2 | S68449 | apoptosis inhibito |
| 878 | 40 | 19.9 | 2052 | 2 | T37711 | probable n-end-rec | 951 | 39.5 | 19.7 | 607 | 1 | ABXL72 | 74K albumin precur |
| 879 | 40 | 19.9 | 2150 | 1 | S27802 | zinc finger protei | 952 | 39.5 | 19.7 | 607 | 1 | S63395 | probable starch sy |
| 880 | 40 | 19.9 | 2150 | 2 | T19450 | hypothetical prote | 953 | 39.5 | 19.7 | 610 | 2 | T06280 | probable membrane |
| 881 | 40 | 19.9 | 2195 | 2 | T34264 | hypothetical prote | 954 | 39.5 | 19.7 | 612 | 2 | S29318 | lysophospholipase |
| 882 | 40 | 19.9 | 2437 | 2 | S42612 | transmembrane prot | 955 | 39.5 | 19.7 | 650 | 2 | H81708 | hypothetical prote |
| 883 | 40 | 19.9 | 2504 | 1 | A57788 | enoyl-lacyl-carrie | 956 | 39.5 | 19.7 | 654 | 2 | T19785 | hypothetical prote |
| 884 | 40 | 19.9 | 2509 | 2 | G01880 | fatty-acid synthas | 957 | 39.5 | 19.7 | 679 | 2 | C71413 | hypothetical prote |
| 885 | 40 | 19.9 | 2664 | 2 | T28626 | variant-specific s | 958 | 39.5 | 19.7 | 692 | 2 | T32980 | hypothetical prote |
| 886 | 40 | 19.9 | 2769 | 1 | UIBO | throglobulin prec | 959 | 39.5 | 19.7 | 700 | 1 | HVHUMB | meprin A (EC 3.4.2 |
| 887 | 40 | 19.9 | 3011 | 1 | S40770 | genome polyprotein | 960 | 39.5 | 19.7 | 700 | 2 | B84125 | iron-sulphur-bindi |
| 888 | 40 | 19.9 | 3014 | 1 | SC5620 | genome polyprotein | 961 | 39.5 | 19.7 | 705 | 2 | S55420 | conserved hypotet |
| 889 | 40 | 19.9 | 3133 | 2 | S52093 | hemocytin - silkw | 962 | 39.5 | 19.7 | 710 | 1 | I51283 | hepatocyte growth |
| 890 | 40 | 19.9 | 3712 | 2 | S18253 | laminin alpha-1 ch | 963 | 39.5 | 19.7 | 742 | 2 | S12533 | zfa protein - mous |
| 891 | 40 | 19.9 | 3951 | 1 | VF1HB1 | F1 protein - avian | 964 | 39.5 | 19.7 | 746 | 2 | E64701 | conserved hypotet |
| 892 | 40 | 19.9 | 4967 | 2 | T92269 | ryanodine receptor | 965 | 39.5 | 19.7 | 764 | 1 | BBHU | complement factor |
| 893 | 40 | 19.9 | 4969 | 2 | A37113 | metallothionein - | 966 | 39.5 | 19.7 | 799 | 2 | A34729 | sex-determining pr |
| 894 | 39.5 | 19.7 | 75 | 2 | S17156 | hypothetical prote | 967 | 39.5 | 19.7 | 801 | 2 | A33630 | zinc finger protei |
| 895 | 39.5 | 19.7 | 95 | 2 | D69121 | hypothetical prote | 968 | 39.5 | 19.7 | 805 | 2 | B35047 | zinc finger protei |
| 896 | 39.5 | 19.7 | 104 | 2 | G84607 | hypothetical prote | 969 | 39.5 | 19.7 | 815 | 1 | T05754 | S-receptor kinase |
| 897 | 39.5 | 19.7 | 112 | 2 | S22151 | gibberellin-regula | 970 | 39.5 | 19.7 | 851 | 2 | A46160 | interferon alpha-1 |
| 898 | 39.5 | 19.7 | 120 | 1 | J01280 | lipid transfer pro | 971 | 39.5 | 19.7 | 852 | 2 | A85041 | probable receptor |
| 899 | 39.5 | 19.7 | 123 | 2 | AC3280 | hypothetical prote | 972 | 39.5 | 19.7 | 869 | 1 | JC4858 | VLDL receptor prec |
| 900 | 39.5 | 19.7 | 126 | 2 | T49488 | hypothetical prote | 973 | 39.5 | 19.7 | 884 | 2 | T20405 | hypothetical prote |
| 901 | 39.5 | 19.7 | 134 | 1 | WYMS | whcy acidic protei | 974 | 39.5 | 19.7 | 894 | 2 | D96713 | probable menaquin |
| 902 | 39.5 | 19.7 | 148 | 2 | S38660 | finger protein ZFX | 975 | 39.5 | 19.7 | 909 | 1 | QRXLL1 | LDL receptor 1 pre |
| 903 | 39.5 | 19.7 | 152 | 2 | I47109 | high-sulfur wool m | 976 | 39.5 | 19.7 | 923 | 2 | A53054 | lipoxigenase (EC 1 |
| 904 | 39.5 | 19.7 | 152 | 2 | I47112 | high-sulfur wool m | 977 | 39.5 | 19.7 | 938 | 2 | C84480 | hypothetical prote |
| 905 | 39.5 | 19.7 | 162 | 2 | I47107 | high-sulfur wool m | 978 | 39.5 | 19.7 | 941 | 2 | T37626 | DNA mismatch repai |

S07127
chymotrypsin/elastase inhibitor - common roundworm
C:Species: Ascaris lumbricoides (common roundworm)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S07127
R:Babin, D.R.; Peanasky, R.J.; Goos, S.M.
Arch. Biochem. Biophys.: 232, 143-161, 1984
A>Title: The isoforms of chymotrypsin/elastase from Ascaris lumbricoides: the primary structure of the major isoform
A:Reference number: S07127; MUID:84255715; PMID:6564898
A:Accession: S07127
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-63 <BAB>
A:Cross-references: UNIPARC:UPI000012D146
C:Superfamily: roundworm trypsin inhibitor

Query Match 28.6%; Score 57.5; DB 2; Length 63;
Best Local Similarity 37.1%; Pred. No. 2.5;
Matches 13; Conservative 5; Mismatches 10; Indels 7; Gaps 3;

QY 1 CSONEYFDSLHACIPQLRC--SSNTP-PLTCQR 32
DB 5 CGPNEVWTE----CTGCEMKCGPDENTCPLEMCRR 35
||| : ||| : ||| : ||| : ||| :
||| : ||| : ||| : ||| : ||| :

RESULT 8
A43434
furin (EC 3.4.21.75) 2 - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A43434
R:Roelbreck, A.J.; Creemers, J.W.; Pauli, I.G.; Kurzik-Dumke, U.; Rentrop, M.; Gateff, E.F.
J. Biol. Chem. 267, 17208-17215, 1992
A>Title: Cloning and functional expression of Dfurin2, a subtilisin-like proprotein processing enzyme from *Drosophila melanogaster*
A:Reference number: A43434; MUID:92381036; PMID:1512259
A:Accession: A43434
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1680 <ROE>
A:Cross-references: UNIPROT:P30432; UNIPARC:UPI000016BC03; GB:M94375; NID:g157461; PID:g157461; NCBI:P11934
A>Note: sequence extracted from NCBI backbone (NCBIN:111933, NCBIP:111934)
C:Genetics:
A:Gene: FlyBase:Fur2
A:Cross-references: FlyBase:FBgn0004598
C:Keywords: hydrolase; serine proteinase; transmembrane protein
F:409-652/Domain: subtilisin homology <SBT>
F:418,457,638/Active site: Asp, His, Ser #status predicted

Query Match 28.6%; Score 57.5; DB 2; Length 1680;
Best Local Similarity 34.3%; Pred. No. 41;
Matches 12; Conservative 5; Mismatches 17; Indels 1; Gaps 1;

QY 1 CSONEYFDSLHACIPQLRCSS--NTPLT-CQRYC 34
DB 1199 CSSSEFFVSVEGQCPCPCSCGSGNGADTSCTSC 1233
||||| : ||| : ||| : ||| : ||| :
||||| : ||| : ||| : ||| : ||| :

RESULT 9
A45558
epidermal growth factor receptor homolog precursor - fluke (*Schistosoma mansoni*)
N:Contains: protein-tyrosine kinase (EC 2.7.1.112)
C:Species: *Schistosoma mansoni*
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A45558; S27836
R:Shoenmaker, C.B.; Ramachandran, H.; Landa, A.; dos Reis, M.G.; Stein, L.D.
Mol. Biochem. Parasitol. 53, 17-32, 1992
A>Title: Alternative splicing of the *Schistosoma mansoni* gene encoding a homologue of epidermal growth factor receptor tyrosine kinase
A:Reference number: A45558; MUID:92365727; PMID:1501637
A:Accession: A45558
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1717 <SHO>
A:Cross-references: UNIPROT:Q26566; UNIPARC:UPI000007DCD7; EMBL:M86396; NID:g160957; PID:

A;Note: sequence extracted from NCBI backbone (NCBIP:111129)
C;Genetics:
A;Gene: SER
C;Superfamily: fluke epidermal growth factor receptor homolog 1; protein kinase homology
F;1-19/Domain: alternative splicing; ATP; autophosphorylation; glycoprotein; phosphoprotein
F;20-1717/Product: signal sequence #status predicted <SIG>
F;1018-1323/Domain: epidermal growth factor receptor homolog 1 #status predicted <MAT>
F;1026-1034/Region: protein kinase homology <KIN>
F;1026-1034/Region: protein kinase ATP-binding motif

Query Match 28.4%; Score 57; DB 1; Length 1717;
Best Local Similarity 40.9%; Pred. No. 48;
Matches 9; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CSQNEFDSLHACIPCOLRCS 22
Db 646 CPRNTYIDPQTRHCLPCNCS 667

RESULT 10
zonadhesin - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C;Accession: T34022
R;Hardy, D.M.; Garbers, D.L.
J. Biol. Chem. 270, 26025-26028, 1995
A;Title: A sperm membrane protein that binds in a species-specific manner to the egg ext
A;Reference number: 221464; MUID:96064658; PMID:7592795
A;Accession: T34022
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-2476 <HAR>
A;Cross-references: UNIPROT:Q28983; UNIPARC:UPI000013C373; EMBL:U40024; NID:gi066465; PI
A;Experimental source: strain Weishan; testis
C;Genetics:
A;Gene: Zan
C;Function:
A;Description: may be involved in sperm adhesion to the zona pellucida

Query Match 27.9%; Score 56; DB 2; Length 2476;
Best Local Similarity 31.6%; Pred. No. 87;
Matches 12; Conservative 8; Mismatches 14; Indels 4; Gaps 2;

Qy 1 CSQNEFDSLHACIP-CQ---LRCSNTPLTCQRYC 34
Db 1851 CSAHSVYTCVPSCLPSCQDPGQCTGAGAPSTCEGC 1888

RESULT 11
T01519
hypothetical protein T10M13.17.1 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01519
R;Johnson, A.F.; de la Bastide, M.; Lodhi, M.; Hoffman, J.; Hasegawa, A.; Gnoj, L.; Gott
Martienssen, R.; McCombie, W.
submitted to the EMBL Data Library, May 1997
A;Description: The sequence of the Arabidopsis thaliana T10M13 BAC.
A;Reference number: Z14346
A;Accession: T01519
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-989 <JOH>
A;Cross-references: UNIPROT:Q9ZU00; UNIPARC:UPI00000A0E3D; EMBL:AF001308; NID:g2104523;
A;Experimental source: cultivar Columbia
C;Genetics:
A;Map position: 4S
A;Introns: 31/3
A;Note: T10M13.17.1

Query Match 27.6%; Score 55.5; DB 2; Length 989;
Best Local Similarity 41.9%; Pred. No. 45;

Matches 13; Conservative 3; Mismatches 10; Indels 5; Gaps 2;

Qy 1 CSQNEFDSLHACIPC---QLRCSNTTP 27
Db 540 CARN-IDDRLFYHCSPCNFTLDRCLNPP 569

RESULT 12
T25169
hypothetical protein T23F1.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25169
R;Wilkinson, J.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19990
A;Accession: T25169
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-330 <WIL>
A;Cross-references: UNIPROT:O18118; UNIPARC:UPI000006118C; EMBL:Z81129; PIDN:CAB03405.1;
A;Experimental source: clone T23F1
C;Genetics:
A;Gene: CESP:T23F1.6
A;Map position: 5
A;Introns: 16/3
C;Superfamily: gliadin

Query Match 27.4%; Score 55; DB 2; Length 330;
Best Local Similarity 28.6%; Pred. No. 20;
Matches 12; Conservative 7; Mismatches 15; Indels 8; Gaps 2;

Qy 1 CSQNEFDSLHACIP-----COLRCSNTPL---TCQRYC 34
Db 59 CASSQYQLQTSQCMFACQSCSQCCOSNTNTQCTCQSC 100

RESULT 13
T23681
hypothetical protein M02G9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23681
R;Matthews, L.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19781
A;Accession: T23681
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1513 <WIL>
A;Cross-references: UNIPROT:O17970; UNIPARC:UPI0000076B6D; EMBL:Z81573; PIDN:CAB04625.1;
A;Experimental source: clone M02G9
C;Genetics:
A;Gene: CESP:M02G9.1
A;Map position: 2
A;Introns: 23/3; 71/3; 121/3; 183/1; 1083/3; 1141/3; 1408/1; 1449/1

Query Match 27.4%; Score 55; DB 2; Length 1513;
Best Local Similarity 44.8%; Pred. No. 75;
Matches 13; Conservative 3; Mismatches 11; Indels 2; Gaps 2;

Qy 8 DSLHAC-IPCQLRCS-SSNTPLPTCQRYC 34
Db 141 DSCQNVQNVCGACVCSQNSPPAVCQQT 169

RESULT 14
T30197
alpha tectorin - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30197
R;Legan, P.K.; Rau, A.; Keene, J.N.; Richardson, G.P.

J. Biol. Chem. 272, 8791-8801, 1997
A:Title: The mouse tectorins. Modular matrix proteins of the inner ear homologous to com
A:Reference number: Z20771; MUID:97236843; PMID:9079715
A:Accession: T30197
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2155 <LEG>
A:Cross-references: UNIPROT:O08523; UNIPARC:UPI000002793C; EMBL:X99805; NID:g1915908; PI
A:Experimental source: strain CD1; whole cochlea
A:Note: non-collagenous protein only expressed in the inner ear, by cells both in and su

Query Match 27.1%; Score 54.5; DB 2; Length 2155;
Best Local Similarity 29.4%; Pred. No. 1.2e+02;
Matches 10; Conservative 6; Mismatches 15; Indels 3; Gaps 1;
QY 1 CSQNEYFDLLHACIPCLRCSSNTPLTTCQRYC 34
DB 1372 CPNSHYVSCVQCP--RCAIRLKSDQNYHC 1402

RESULT 15
S54307
A:Title: myosin heavy chain - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S54307
R:Reinhard, J.; Scheel, A.A.; Diekmann, D.; Hall, A.; Ruppert, C.; Baehler, M.
EMBO J. 14, 697-704, 1995
A:Title: A novel type of myosin implicated in signalling by rho family GTPases.
A:Reference number: S54307; MUID:95188874; PMID:7882973
A:Accession: S54307
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1980 <REI>
A:Cross-references: UNIPROT:O63358; UNIPARC:UPI000012FAD6; EMBL:X77609; NID:g639998; PID
C:Superfamily: rat myosin heavy chain; myosin motor domain homology; protein kinase C z
C:Keywords: nucleotide binding; P-loop
F:149-942/Domain: myosin motor domain homology <MMOT>
F:239-246/Region: nucleotide-binding motif A (P-loop)
F:1593-1641/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match 26.9%; Score 54; DB 2; Length 1980;
Best Local Similarity 52.9%; Pred. No. 1.2e+02;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 16 PCQLRCSSNTPLTTCOR 32
DB 1812 PCLLRCPDNDPLTSMK 1828

RESULT 16
A59256
A:Title: myosin-IXb [similarity] - human
C:Species: Homo sapiens (man)
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 31-Dec-2004
C:Accession: A59256; I61700
R:Wirth, J.A.; Jensen, K.A.; Post, P.L.; Bement, W.M.; Mooseker, M.S.
J. Cell Sci. 109, 653-661, 1996
A:Title: Human myosin-IXb, an unconventional myosin with a chimerin-like rho/rac GTPase-
A:Reference number: A59256; MUID:97063843; PMID:8907710
A:Accession: A59256
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-2022 <WIR>
A:Cross-references: UNIPROT:Q14788; UNIPARC:UPI0000161189; GB:U42391; NID:g1147782; PIDN
R:Bement, W.M.; Hasson, T.; Wirth, J.A.; Cheney, R.E.; Mooseker, M.S.
Proc. Natl. Acad. Sci. U.S.A. 91, 6549-6553, 1994
A:Title: Identification and overlapping expression of multiple unconventional myosin gen
A:Reference number: A55758; MUID:94294418; PMID:8022818
A:Accession: I61700
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 234-322 <RES>

A:Cross-references: UNIPARC:UPI0000073918; GB:L29149; NID:g457257; PIDN:AAA20912.1; PID:9
C:Genetics:
A:Gene: GDB:MYO9B; OMIM:602129
A:Map position: 19p13.1
C:Superfamily: myosin motor domain homology; protein kinase C zinc-binding repeat homolo
C:Keywords: nucleotide binding; P-loop
F:149-941/Domain: myosin motor domain homology #status atypical <MMO>
F:239-246/Region: nucleotide-binding motif A (P-loop)

Query Match 26.9%; Score 54; DB 2; Length 2022;
Best Local Similarity 52.9%; Pred. No. 1.3e+02;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 16 PCQLRCSSNTPLTTCOR 32
DB 1852 PCLLRCPDNDPLTSMK 1868

RESULT 17
S46625
A:Title: finger protein YJL206C - yeast (Saccharomyces cerevisiae)
N:Alternate names: probable membrane protein YJL206C; protein J0316
C:Species: Saccharomyces cerevisiae
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Oct-2004
C:Accession: S46625; S56993
R:Purnelle, B.; Coster, F.; Goffeau, A.
Yeast 10, 1235-1249, 1994
A:Title: The sequence of a 36 kb segment on the left arm of yeast chromosome X identifies
ase gene ACO1 and two homologues to chromosome III genes.
A:Reference number: S46621; MUID:95274326; PMID:7754713
A:Accession: S46625
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-758 <PUR>
A:Cross-references: UNIPROT:P39529; UNIPARC:UPI000013B60A; EMBL:X77688; NID:g1183992; PI
R:Purnelle, B.; Coster, F.; Goffeau, A.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S56977
A:Accession: S56993
A:Molecule type: DNA
A:Residues: 1-758 <PUM>
A:Cross-references: UNIPARC:UPI000013B60A; EMBL:Z49481; NID:g1015584; PIDN:CAA89502.1; P
C:Genetics:
A:Map position: 10L
C:Keywords: DNA binding; nucleus; transcription regulation; transmembrane protein; zinc f
F:42-78/Domain: GAL4 zinc binuclear cluster homology <GAL4>

Query Match 26.6%; Score 53.5; DB 2; Length 758;
Best Local Similarity 50.0%; Pred. No. 63;
Matches 11; Conservative 2; Mismatches 6; Indels 3; Gaps 1;
QY 13 ACIPG---QLRCSSNTPLTTCQ 31
DB 46 ACIACRKRKVRCSGNIPCLCQ 67

RESULT 18
TI3954
A:Title: MEGF6 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: TI3954
R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A:Reference number: Z14126; MUID:98360089; PMID:9693030
A:Accession: TI3954
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1574 <NAK>
A:Cross-references: UNIPROT:O88281; UNIPARC:UPI0000043BEE; EMBL:AB011532; NID:g3449293; I
A:Experimental source: strain Sprague-Dawley; brain

C;Genetics:
A;Gene: F12K22.14
A;Map position: 1
C;Superfamily: Arabidopsis thaliana probable transcription factor F12K22.14; RING finger

Query Match 25.4%; Score 51; DB 2; Length 641;
Best Local Similarity 45.8%; Pred. No. 1.1e+02;
Matches 11; Conservative 2; Mismatches 3; Indels 8; Gaps 2;

QY 15 IPQ-----LRCSNTPP---LTC 30
:|| :||| ||| |||
Db 7 LPCDGDGVCRCCKSNPPPESLTC 30

RESULT 35
G96675
hypothetical protein T2JK8.9 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
R;Accession: G96675
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: G96675
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-653 <SPT>
A;Cross-references: UNIPROT:Q9SJU8; UNIPARC:UPI00000AAACE7; GB:AE005173; NID:g44646199; PII
C;Genetics:
A;Gene: T2JK8.9
A;Map position: 1

Query Match 25.4%; Score 51; DB 2; Length 653;
Best Local Similarity 42.3%; Pred. No. 1.1e+02;
Matches 11; Conservative 2; Mismatches 9; Indels 4; Gaps 1;

QY 7 FDSLLHACIFC----QLRCSNTPPL 28
|| : | | | | | | | |
Db 204 FDEMFFHCSCACFTLDLRVCSLPPL 229

RESULT 36
G84605
hypothetical protein At2g21840 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
R;Accession: G84605
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, I.
ature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: G84605
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-746 <STO>
A;Cross-references: UNIPROT:Q9SJU5; UNIPARC:UPI000009C804; GB:AE002093; NID:g4417278; PII
C;Genetics:
A;Gene: At2g21840
A;Map position: 2

Query Match 25.4%; Score 51; DB 2; Length 746;
Best Local Similarity 28.6%; Pred. No. 1.2e+02;
Matches 6; Conservative 5; Mismatches 10; Indels 0; Gaps 0;


```
Qy 1 CSQNEFDSLHACIPCOLRC 21
      |::|::|::|::|
Db 267 CKETVVDYDFYLCVECDLKC 287
      |::|::|::|::|

RESULT 37
146001
C4b-binding protein alpha chain - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: 146001; S43190
F:1-2/Product: ubiquitin (fragment) #status predicted <UBI>
F:3-74/Domain: ribosomal protein CEP52 #status predicted <RIB>
F:23-61/Region: zinc finger CCCC motif
F:68-74/Region: nuclear location signal
A:Title: Bovine C4b binding protein. Molecular cloning of the alpha- and beta-chains pro
A:Reference number: 146001; MUID:95015909; PMID:7930621
A:Accession: 146001
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-610 <HIL>
A:Cross-references: UNIPROT:Q28065; UNIPARC:UPI0000126C27; EMBL:Z31693; NID:9469117; PID
C:Superfamily: C4b-binding protein alpha chain; complement factor H repeat homology
F:50-107/Domain: complement factor H repeat homology <FH1>
F:112-169/Domain: complement factor H repeat homology <FH2>
F:174-234/Domain: complement factor H repeat homology <FH3>
F:239-294/Domain: complement factor H repeat homology <FH4>
F:299-362/Domain: complement factor H repeat homology <FH5>
F:366-425/Domain: complement factor H repeat homology <FH6>
F:429-483/Domain: complement factor H repeat homology <FH7>
F:487-541/Domain: complement factor H repeat homology <FH8>

Query Match 25.1%; Score 50.5; DB 1; Length 610;
Best Local Similarity 32.4%; Pred. No. 1.2e+02;
Matches 12; Conservative 5; Mismatches 9; Indels 11; Gaps 1;

Qy 6 YFDSLLHAC-----TPCQLRCSNTPPLTQC 31
      |::|::|::|::|
Db 259 YQQSIVTVACNKGFRLEGSLIHCEADNSWNPPTCE 295
      |::|::|::|::|

RESULT 38
S08572
chymotrypsin/elastase inhibitor - common roundworm
C:Species: Ascaris lumbricoides (common roundworm)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C:Accession: S08572
R:Babin, D.R.; Peanasky, R.J.; Goos, S.M.
Arch. Biochem. Biophys. 232, 143-161, 1984
A:Title: The isoforms of chymotrypsin/elastase from Ascaris lumbricoides: the prima
A:Reference number: S07127; MUID:84255715; PMID:6564898
A:Accession: S08572
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-83 <BAB>
A:Cross-references: UNIPARC:UPI0000176391
C:Superfamily: roundworm trypsin inhibitor

Query Match 24.9%; Score 50; DB 2; Length 63;
Best Local Similarity 30.8%; Pred. No. 20;
Matches 12; Conservative 6; Mismatches 9; Indels 12; Gaps 3;

Qy 1 CSQNEFDSLHACIPCOLRC--SSNTP-----PLTQC 31
      |::|::|::|::|
Db 4 CGKNEVWTE----CTGCELKCGQDENTPCALMCRPPSCE 38
      |::|::|::|::|

RESULT 39
S10332
ubiquitin / ribosomal protein CEP52 - common tobacco (fragment)
N:Alternate names: ubiquitin fusion protein
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C:Accession: S10332
```

```
R:Genschik, P.; Parmentier, Y.; Criqui, M.C.; Fleck, J.
Nucleic Acids Res. 18, 4007, 1990
A:Title: Sequence of a ubiquitin carboxyl extension protein of Nicotiana tabacum.
A:Reference number: S10332; MUID:90326543; PMID:2165257
A:Accession: S10332
A:Molecule type: DNA
A:Residues: 1-74 <GEN>
A:Cross-references: UNIPROT:P19379; UNIPARC:UPI000017715C; EMBL:X53011
C:Superfamily: ubiquitin/ribosomal protein CEP52; ribosomal protein CEP52 homology; ubiq
C:Keywords: DNA binding; protein biosynthesis; ribosome; zinc finger
F:1-2/Product: ubiquitin (fragment) #status predicted <UBI>
F:3-74/Product: ribosomal protein CEP52 #status predicted <RIB>
F:3-74/Domain: ribosomal protein CEP52 homology <CPH>
F:23-61/Region: zinc finger CCCC motif
F:68-74/Region: nuclear location signal

Query Match 24.9%; Score 50; DB 2; Length 74;
Best Local Similarity 44.4%; Pred. No. 23;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 14 CIPCOLRCSNTPPLTQC 31
      |::|::|::|::|
Db 22 CRKCYVRCPRRTPORTCR 39
      |::|::|::|::|

RESULT 40
T30370
hypothetical protein ORE23 - Lymantria dispar nuclear polyhedrosis virus
C:Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30370
R:Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohrn
Virology 251, 17-34, 1999
A:Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria di
A:Reference number: Z20836; MUID:99124785; PMID:9887315
A:Accession: T30370
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-342 <KUZ>
A:Cross-references: UNIPROT:Q9YMW1; UNIPARC:UPI00000F34B2; EMBL:AF081810; PIDN:AAC70208.1

Query Match 24.9%; Score 50; DB 2; Length 342;
Best Local Similarity 50.0%; Pred. No. 85;
Matches 10; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 13 ACIPCOLRCSNTPPLTQCR 32
      |::|::|::|::|
Db 270 ACIRCKSRFYKNPILYCSR 289
      |::|::|::|::|

RESULT 41
C81272
probable aminotransferase (degt family) Cj1294 [imported] - Campylobacter jejuni (strain
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: C81272
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A:Reference number: AB1250; MUID:20150912; PMID:10688204
A:Accession: C81272
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-376 <PAR>
A:Cross-references: UNIPROT:Q9PN05; UNIPARC:UPI00000C1EA5; GB:AL139078; GB:AL111168; NID:
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
C:Superfamily: erythromycin resistance protein

Query Match 24.9%; Score 50; DB 2; Length 376;
Best Local Similarity 52.6%; Pred. No. 92;
```


| Matches | 10; | Conservative | 3; | Mismatches | 6; | Indels | 0; | Gaps | 0; |
|---|-----|-------------------------|----|------------|----|--------|----|------|----|
| QY | 1 | CSQNEYFDLLHACIPQQL 19 | | | | | | | |
| Db | 294 | CQKEELFESLLHAGIGVQV 312 | | | | | | | |
| RESULT 42 | | | | | | | | | |
| GOHUT1 | | | | | | | | | |
| tumor necrosis factor receptor 1 precursor [validated] - human | | | | | | | | | |
| N:Alternate names: p55 tumor necrosis factor receptor; TNF receptor type 1 | | | | | | | | | |
| N:Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein | | | | | | | | | |
| C:Species: Homo sapiens (man) | | | | | | | | | |
| C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004 | | | | | | | | | |
| R:Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F. | | | | | | | | | |
| Genomics 13, 219-224, 1992 | | | | | | | | | |
| A:Title: Structure of the human TNF receptor 1 (p50) gene (TNFR1) and localization to ch | | | | | | | | | |
| A:Reference number: A38208; MUID:92250049; PMID:131517 | | | | | | | | | |
| A:Accession: A38208 | | | | | | | | | |
| A:Molecule type: DNA | | | | | | | | | |
| A:Residues: 1-455 <FUC> | | | | | | | | | |
| A:Cross-references: UNIPROT:P19438; UNIPARC:UPI000002CE11; GB:M75864; GB:M75865; GB:M758 | | | | | | | | | |
| R:Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lesslau | | | | | | | | | |
| Cell 61, 351-359, 1990 | | | | | | | | | |
| A:Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor recep | | | | | | | | | |
| A:Reference number: A34899; MUID:90235284; PMID:2158862 | | | | | | | | | |
| A:Accession: A34899 | | | | | | | | | |
| A:Molecule type: mRNA | | | | | | | | | |
| A:Residues: 1-455 <LOE> | | | | | | | | | |
| A:Cross-references: UNIPARC:UPI000002CE11; GB:M58286; GB:M33480; NID:g3339753; PIDN:AAA36 | | | | | | | | | |
| A:Experimental source: placenta | | | | | | | | | |
| A:Note: part of this sequence, including the amino end of the mature protein, confirmed | | | | | | | | | |
| R:Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T. | | | | | | | | | |
| Cell 61, 361-370, 1990 | | | | | | | | | |
| A:Title: Molecular cloning and expression of a receptor for human tumor necrosis factor. | | | | | | | | | |
| A:Reference number: A34900; MUID:90235285; PMID:2158863 | | | | | | | | | |
| A:Accession: A34900 | | | | | | | | | |
| A:Molecule type: mRNA | | | | | | | | | |
| A:Residues: 1-455 <SCH> | | | | | | | | | |
| A:Cross-references: UNIPARC:UPI000002CE11; GB:M33294; NID:g3339744; PIDN:AAA03210.1; PID: | | | | | | | | | |
| R:Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.; | | | | | | | | | |
| DNA Cell Biol. 9, 705-715, 1990 | | | | | | | | | |
| A:Title: Molecular cloning and expression of human and rat tumor necrosis factor recepto | | | | | | | | | |
| A:Reference number: A36555; MUID:91090841; PMID:1702293 | | | | | | | | | |
| A:Accession: A36555 | | | | | | | | | |
| A:Molecule type: mRNA | | | | | | | | | |
| A:Residues: 1-455 <HIM> | | | | | | | | | |
| A:Cross-references: UNIPARC:UPI000002CE11; GB:M63121; NID:g3339755; PIDN:AAA36754.1; PID: | | | | | | | | | |
| A:Accession: C36555 | | | | | | | | | |
| A:Molecule type: protein | | | | | | | | | |
| A:Residues: 30-38; 41-53, 'X', 55-79, 'XX', 82-94, 'NK', 'X', 100-104; 107-128; 162-167, 'X', 169-2 | | | | | | | | | |
| A:Cross-references: UNIPARC:UPI000002D398; UNIPARC:UPI000002D836; UNIPARC:UPI00001736DE; | | | | | | | | | |
| A:Note: the purified protein, called tumor necrosis factor binding protein, is a soluble | | | | | | | | | |
| R:Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M. | | | | | | | | | |
| Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990 | | | | | | | | | |
| A:Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of re | | | | | | | | | |
| A:Reference number: A38281; MUID:91017509; PMID:2170974 | | | | | | | | | |
| A:Accession: A38281 | | | | | | | | | |
| A:Molecule type: mRNA | | | | | | | | | |
| A:Residues: 1-455 <GRA> | | | | | | | | | |
| A:Cross-references: UNIPARC:UPI000002CE11; GB:M37764 | | | | | | | | | |
| A:Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372 | | | | | | | | | |
| R:Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann | | | | | | | | | |
| EMBO J. 9, 3269-3278, 1990 | | | | | | | | | |
| A:Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the typ | | | | | | | | | |
| le form of the receptor. | | | | | | | | | |
| A:Reference number: S12057; MUID:91006021; PMID:1698610 | | | | | | | | | |
| A:Accession: S12057 | | | | | | | | | |
| A:Molecule type: mRNA | | | | | | | | | |
| A:Residues: 1-455 <NOP> | | | | | | | | | |
| A:Cross-references: UNIPARC:UPI000002CE11; EMBL:X55313; NID:g37223; PIDN:CAA39021.1; PID | | | | | | | | | |
| A:Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, w | | | | | | | | | |

R:Kemper, O.; Wallach, D.
Gene 134, 209-216, 1993
A:Title: Cloning and partial characterization of the promoter for the human p55 tumor nec
A:Reference number: JT0758; MUID:94085779; PMID:8262379
A:Accession: JT0758
A:Molecule type: DNA
A:Residues: 1-13 <REM>
A:Cross-references: UNIPARC:UPI0000155CFB
R:Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.
Eur. J. Immunol. 20, 1167-1174, 1990
A:Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequence
A:Reference number: A60231; MUID:90292116; PMID:2113477
A:Accession: A60231
A:Molecule type: protein
A:Residues: 41-43, 'X', 45-53, 'X', 55-57 <SEC>
A:Cross-references: UNIPARC:UPI0000072FDB
R:Gatanaga, T.; Hwang, C.; Kohr, M.; Cappuccini, F.; Lucci III, J.A.; Jeffes, E.W.B.; Ler
Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
A:Title: Purification and characterization of an inhibitor (soluble tumor necrosis factor
tents.
A:Reference number: A38258; MUID:91062364; PMID:2174164
A:Accession: A38258
A:Molecule type: protein
A:Residues: 41-60 <GAT>
A:Cross-references: UNIPARC:UPI00001736E1
A:Experimental source: cancer patient serum
R:Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thyssell, H.; Grubb, A.; Adolf, G.
Eur. J. Haematol. 42, 270-275, 1989
A:Title: Isolation and characterization of a tumor necrosis factor binding protein from t
A:Reference number: A60594; MUID:89171156; PMID:2924890
A:Accession: A60594
A:Molecule type: protein
A:Residues: 41-43, 'X', 45-53, 'V', 55-57, 'XK', 60 <OLS>
A:Cross-references: UNIPARC:UPI00001736E2
A:Experimental source: renal failure patient urine
R:Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence f
A:Reference number: A35010; MUID:90110215; PMID:2153136
A:Accession: A35010
A:Molecule type: protein
A:Residues: 41-45 <ENG>
A:Cross-references: UNIPARC:UPI00001736E3
R:Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
Biochem. Biotechnol. 58, 2266-2268, 1994
A:Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified f
A:Reference number: JC2404; MUID:95128033; PMID:7765720
A:Accession: JC2404
A:Molecule type: protein
A:Residues: 41-53, 'X', 55-144, 'X', 146-150, 'X', 152-186, 'X', 188-201 <KAJ>
A:Cross-references: UNIPARC:UPI00001736E4
A:Experimental source: urine
C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
C:Genetics:
A:Gene: GDB:TNFR1
A:Cross-references: GDB:125913; OMIM:191190
A:Map position: 12p13.2-12p13.2
A:Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
A:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-455/Product: tumor necrosis factor receptor 1 #status predicted <MAT>
F:30-211/Domain: extracellular #status predicted <EXT>
F:41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status
F:44-82/Domain: NGF receptor repeat homology <NGI>
F:84-126/Domain: NGF receptor repeat homology <NG2>
F:127-167/Domain: NGF receptor repeat homology <NG3>
F:168-196/Domain: NGF receptor repeat homology <NG4>
F:212-234/Domain: transmembrane #status predicted <MEM>
F:235-455/Domain: intracellular #status predicted <INT>
F:54, 145, 151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 24.9%; Score 50; DB 1; Length 455;
Best Local Similarity 35.3%; Pred. No. 1.1e+02;
Matches 12; Conservative 5; Mismatches 13; Indels 2;
Gaps 2;

QY 1 CSQNE---YFDSLLHACIPQCRSSNTPPLTCQ 31
DB 127 CRKQYRHYWSNLFQCFNCSL-CLNGTVHLSQ 159

RESULT 43
T27318
hypothetical protein Y69H2.3a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T27318
R:McMurray, A.
submitted to the EMBL Data Library, August 1997
A:Reference number: Z20343
A:Accession: T27318
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-561 <WIL>
A:Cross-references: UNIPROT:Q9UIT6; UNIPARC:UPI0000164288; EMBL:Z98877; PIDN:CAB54472.1;
A:Experimental source: clone Y69H2
C:Genetics:
A:Gene: CESP:Y69H2.3a
A:Map position: 5
A:Introns: 183/1; 247/1; 288/1; 318/1; 364/1; 388/2; 457/1; 481/2; 521/3

Query Match 24.9%; Score 50; DB 2; Length 561;
Best Local Similarity 32.4%; Pred. No. 1.3e+02;
Matches 12; Conservative 3; Mismatches 12; Indels 10; Gaps 2;

QY 1 CSQNEYPDSLLHACIPQCRSS---NTPPLTCORYC 34
DB 499 CRSNEKFB-----PCKTVCSDTKCNEEPRFCQVC 528

RESULT 44
T27319
hypothetical protein Y69H2.3b - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T27319
R:McMurray, A.
submitted to the EMBL Data Library, August 1997
A:Reference number: Z20343
A:Accession: T27319
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-626 <WIL>
A:Cross-references: UNIPROT:Q9UIT5; UNIPARC:UPI0000164289; EMBL:Z98877; PIDN:CAB54473.1;
A:Experimental source: clone Y69H2
C:Genetics:
A:Gene: CESP:Y69H2.3b
A:Map position: 5
A:Introns: 183/1; 247/1; 312/1; 353/1; 383/1; 429/1; 453/2; 522/1; 546/2; 586/3

Query Match 24.9%; Score 50; DB 2; Length 626;
Best Local Similarity 32.4%; Pred. No. 1.4e+02;
Matches 12; Conservative 3; Mismatches 12; Indels 10; Gaps 2;

QY 1 CSQNEYPDSLLHACIPQCRSS---NTPPLTCORYC 34
DB 564 CRSNEKFB-----PCKTVCSDTKCNEEPRFCQVC 593

RESULT 45
T27373
hypothetical protein K10D3.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T27373

R:McMurray, A.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19762
A:Accession: T23573
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-922 <WIL>
A:Cross-references: UNIPROT:Q21418; UNIPARC:UPI00000762C2; EMBL:Z75545; PIDN:CAA99886.1;
A:Experimental source: clone K10D3
C:Genetics:
A:Gene: CESP:K10D3.4
A:Map position: 1
A:Introns: 60/1; 228/1; 278/1; 355/1; 743/1; 802/1; 885/2

Query Match 24.9%; Score 50; DB 2; Length 922;
Best Local Similarity 29.3%; Pred. No. 2e+02;
Matches 12; Conservative 7; Mismatches 14; Indels 8; Gaps 2;

QY 1 CSQNEYPDSLLHA--CIPQCRSSNTPP-----LTCORY 33
DB 68 CTQNRQCEAVWPGRAYCRSGECRCANNQPPFTRDGLVCLNY 108

RESULT 46
F96596
hypothetical protein TSA14.15 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: F96596
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
anssen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: F96596
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1360 <STO>
A:Cross-references: UNIPROT:Q9ZVU3; UNIPARC:UPI000009D265; GB:AE005173; NID:G4204269; PII
C:Genetics:
A:Gene: TSA14.15
A:Map position: 1

Query Match 24.9%; Score 50; DB 2; Length 1360;
Best Local Similarity 50.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 NEYFDSLLHACIPCOL 19
DB 947 NKOTDDLVAACLPCL 962

RESULT 47
G83398
probable two-component sensor PA1979 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: G83398
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bri
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathoc
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: G83398
A:Status: preliminary
A:Molecule type: DNA

T48828
hypothetical protein 68B2.120 [imported] - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 16-Feb-2001
C:Accession: T48828
E:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24541
A:Accession: T48828
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-189 <SCH>
A:Cross-references: UNIPARC:UPI0000179B99; EMBL:AL353821; GSPDB:GN00112; NCSP:68B2.120
A:Experimental source: cosmid contig 68B2; strain 74
C:Genetics:
A:Gene: NCSP:68B2.120
A:Map position: 2
C:Superfamily: Neurospora crassa hypothetical protein 68B2.120

Query Match 24.4%; Score 49; DB 2; Length 189;
Best Local Similarity 41.2%; Pred. No. 67;
Matches 7; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 14 CIPQCLRCSSNTPLTC 30
|:|:| :|:|:|
Db 117 CLPCDYNTTSKKPRLC 133

RESULT 51
C72272
hypothetical protein TM1292 - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: C72272
E:Neilson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.E.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.N.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequencing
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: C72272
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-283 <ARN>
A:Cross-references: UNIPROT:Q9X118; UNIPARC:UPI0000038D8; GB:AE001784; GB:AE000512; NID
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM1292
C:Superfamily: cell division inhibitor related protein; ferredoxin 2[4Fe-4S] homology

Query Match 24.4%; Score 49; DB 2; Length 283;
Best Local Similarity 44.4%; Pred. No. 95;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 7 FDSLHACIPQLRCSSN 24
|:|:| | | | | |
Db 95 FESLCHGCGACSIMCPVN 112

RESULT 52
B71439
hypothetical protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
A:Variety: Columbia
C:Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004
C:Accession: B71439
E:Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirks, P.; Wedler, K.; Wedler, E.; Wambutt, R.; Weitzenecker, T.; Pohl, T.M.; Terry, N.; Giele, avanagan, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Kieger, M.; Schaeffer, M.; Funk, B.
Nature 391, 485-488, 1998
A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech, erthof, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ansc, C.; Chlutzis, N.

A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thaliana
A;Reference number: A71400; MUID:98121113; PMID:9461215
A;Accession: B71439
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-306 <BEV>
A;Cross-References: UNIPROT:Q23551; UNIPARC:UPI00000A5737; GB:Z97342; NID:g2245031; PID:
C;Genetics:
C;Superfamily: Arabidopsis thaliana 33.5K hypothetical protein
Query Match 24.4%; Score 49; DB 2; Length 306;
Best Local Similarity 33.3%; Pred. No. 1.e+02;
Matches 9; Conservative 4; Mismatches 14; Indels 0; Gaps 0;
QY 7 FDSLHACIPQLRCSSNTPPLTCQRY 33
DB 115 FNSDGGCKACKVMCSGNDGFLCLDSW 141
RESULT 53
S28390
homeotic protein mec-3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: S28390; A27662
R;Xue, D.; Finney, M.; Ruvkun, G.; Chalfie, M.
EMBO J. 11, 4969-4979, 1992
A;Title: Regulation of the mec-3 gene by the C. elegans homeoproteins UNC-86 and MEC-3.
A;Reference number: S28390; MUID:93099872; PMID:1361171
A;Accession: S28390
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-321 <XUB>
A;Cross-References: UNIPROT:P09088; UNIPARC:UPI000012BEA8; EMBL:L02877; NID:gl56488; PID:
R;Way, J.C.; Chalfie, M.
Cell 54, 5-16, 1998
A;Title: mec-3, a homeobox-containing gene that specifies differentiation of the touch r
A;Reference number: A27662; MUID:88253425; PMID:2898300
A;Accession: A27662
A;Molecule type: DNA
A;Residues: 'MRLRHDWILLT', 20, 'DLLQSSS', 28, 'ITASSKNSSTIIYFQ', 44-321 <WAY>
A;Cross-References: UNIPARC:UPI000016B90E; GB:M20244; NID:gl56363; PIDN:AAA28108.1; PID:
C;Genetics:
A;Gene: mec-3
A;Introns: 82/3; 106/3; 190/3; 228/3; 300/1
C;Superfamily: homeotic protein mec-3; homeobox homology; LIM metal-binding repeat homol
C;Keywords: DNA binding; duplication; homeobox; nucleus; transcription regulation; zinc
F;29-79/Domain: LIM metal-binding repeat homology <LIM1>
F;89-145/Domain: LIM metal-binding repeat homology <LIM2>
F;218-274/Domain: homeobox homology <HOX>
Query Match 24.4%; Score 49; DB 1; Length 321;
Best Local Similarity 44.4%; Pred. No. 1.e+02;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 1 CSQNEYFDSLHACIPQC 18
DB 76 CSQHYKDHSHRCAGCK 93
RESULT 54
T20458
hypothetical protein F01D4.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Feb-2000
C;Accession: T20458
R;Wild, A.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19278
A;Accession: T20458
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA

A;Residues: 1-346 <WIL>
A;Cross-References: UNIPARC:UPI0000177DBC; EMBL:Z81054; PIDN:CAB02885.1; GSPDB:GN000022; C
A;Experimental source: clone F01D4
C;Genetics:
A;Gene: CESP:F01D4.6
A;Map position: 4
A;Introns: 26/3; 63/1; 107/2; 131/3; 215/3; 253/3; 325/1
C;Superfamily: homeotic protein mec-3; homeobox homology; LIM metal-binding repeat homol
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
Query Match 24.4%; Score 49; DB 2; Length 346;
Best Local Similarity 44.4%; Pred. No. 1.e+02;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 1 CSQNEYFDSLHACIPQC 18
DB 101 CSQHYKDHSHRCAGCK 118
RESULT 55
JC5828
paired-box-containing protein Pax-4 - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C;Accession: JC5828
R;Matsushita, T.; Yamaoka, T.; Otsuka, S.; Moritani, M.; Matsumoto, T.; Itakura, M.
Biochem. Biophys. Res. Commun. 242, 176-180, 1998
A;Title: Molecular cloning of mouse paired-box-containing gene (Pax)-4 from an islet bet
A;Reference number: JC5827; MUID:98102804; PMID:9439631
A;Accession: JC5828
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-350 <MAT>
A;Cross-References: UNIPROT:O43316; UNIPARC:UPI000013136A; DBJ:AB008913; NID:g2809074; I
C;Comment: This protein is involved in pancreatic islet development.
C;Superfamily: paired box transcription factor Pax-4; homeobox homology; paired box homol
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;5-129/Domain: paired box homology <PBH>
F;171-227/Domain: homeobox homology <HOX>
Query Match 24.4%; Score 49; DB 2; Length 350;
Best Local Similarity 53.3%; Pred. No. 1.e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 20 RCSNTPPLTCQRYC 34
DB 289 RCLSDTPPKACLKPC 303
RESULT 56
A96639
protein Tf9.18 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2004
C;Accession: A96639
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A96639
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-447 <STO>
A;Cross-References: UNIPROT:O64787; UNIPARC:UPI000009F9F6; GB:AE005173; NID:g3056597; PII
C;Genetics:
A;Gene: Tf9.18

A:Map position: 1
C:Superfamily: Arabidopsis thaliana hypothetical protein F17J16.30

Query Match 24.4%; Score 49; DB 2; Length 447;
Best Local Similarity 37.0%; Pred. No. 1.4e+02;
Matches 10; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 7 FDSLHACIPCOLRCSSNTPLTCQRY 33
DB 211 FKSLVVCMPNLLSIFLDAPTELCYKY 237

RESULT 57
JC4302
tumor necrosis factor receptor p55 precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C:Accession: JC4302; PC4093
R:Suter, B.; Pauli, U.
Gene 163, 263-266, 1995
A:Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.
A:Reference number: JC4302; MUID:96011645; PMID:7590278
A:Accession: JC4302
A:Molecule type: mRNA
A:Residues: 1-461 <SUT>
A:Cross-references: UNIPROT:P50555; UNIPARC:UPI00001372A9; GB:U19994; NID:g1141752; PIDN:JC4302
A:Experimental source: kidney cell line 15
C:Genetics:
C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog
C:Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-461/Product: tumor necrosis factor receptor p55 #status predicted <WAT>
F:44-194/Domain: extracellular cysteine rich #status predicted <EXT>
F:44-82/Domain: NGF receptor repeat homology <NG1>
F:84-126/Domain: NGF receptor repeat homology <NGP>
F:211-231/Domain: transmembrane #status predicted <TMW>
F:361-447/Domain: signal transduction #status predicted <SIT>
F:54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 24.4%; Score 49; DB 2; Length 461;
Best Local Similarity 33.3%; Pred. No. 1.4e+02;
Matches 11; Conservative 5; Mismatches 13; Indels 4; Gaps 2;

QY 1 CSQNE---YFDSLHACIPCOLRCSSNTPLTC 30
DB 127 CRKNQRYKYSETLFOCLNCSL-CPNGTVQLPC 158

RESULT 58
T47794
hypothetical protein F17J16.170 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T47794
R:D'Angelo, M.; Verzi, A.; Modesto, D.; Pigazzini, M.; Valle, G.; Mewes, H.W.; Rudd, S.; I
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24476
A:Accession: T47794
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-602 <DAN>
A:Cross-references: UNIPROT:Q9LYS4; UNIPARC:UPI000008A6194; EMBL:AL163527
A:Experimental source: cultivar Columbia; BAC clone F17J16
C:Genetics:
A:Map position: 3
A:Introns: 580/3
A:Note: F17J16.170

Query Match 24.4%; Score 49; DB 2; Length 602;
Best Local Similarity 37.5%; Pred. No. 1.8e+02;
Matches 12; Conservative 4; Mismatches 8; Indels 8; Gaps 2;

QY 4 NEYFDSLHACIPC---QLRCSSNTPLTCQ 31
DB 140 SEWF----YRCSICNFFLDFRCARNFPLTIQ 167

RESULT 59
T30136
hypothetical protein Cl4C11.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30136
R:Du, Z.; Gattung, S.
submitted to the EMBL Data Library, March 1996
A:Description: The sequence of C. elegans cosmid Cl4C11.
A:Reference number: Z20742
A:Accession: T30136
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-654 <DUZ>
A:Cross-references: UNIPROT:Q17982; UNIPARC:UPI000017B77E; EMBL:U53141; PIDN:AAA96110.1;
A:Experimental source: strain Bristol N2; clone Cl4C11
C:Genetics:
A:Gene: CESP:Cl4C11.8
A:Map position: 5
A:Introns: 50/3; 98/3; 155/3; 182/3; 229/3; 318/3; 365/3; 522/3; 543/3; 586/3

Query Match 24.4%; Score 49; DB 2; Length 654;
Best Local Similarity 42.9%; Pred. No. 1.9e+02;
Matches 12; Conservative 3; Mismatches 7; Indels 6; Gaps 2;

QY 13 ACIP-COLRCSSNTPLP-----TCORYC 34
DB 489 ACQPSQSSCGSNTQCVQACIPSCQQTCC 516

RESULT 60
S30015
hypothetical protein YKL010c - yeast (Saccharomyces cerevisiae)
A:Alternate names: hypothetical protein YKL162
C:Species: Saccharomyces cerevisiae
C:Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 09-Jul-2004
C:Accession: S30015; S37821
R:Pascalo, S.; Ghazvini, M.; Boyer, J.; Collea, L.; Thierry, A.; Dujon, B.
Yeast 8, 987-995, 1992
A:Title: The sequence of a 9.3 kb segment located on the left arm of the yeast chromosome
ribosomal protein L10.
A:Reference number: S30013; MUID:93127732; PMID:1481574
A:Accession: S30015
A:Molecule type: DNA
A:Residues: 1-1483 <PAS>
A:Cross-references: UNIPROT:P33202; UNIPARC:UPI0000137AD6; GB:S53418; NID:g263497; PIDN:Y
A:Experimental source: strain S288C
R:Boyer, J.; Pascolo, S.; Richard, G.F.; Ghazvini, M.; Collea, L.; Thierry, A.; Monnier
submitted to the Protein Sequence Database, March 1994
A:Reference number: S37813
A:Accession: S37821
A:Molecule type: DNA
A:Residues: 1-1483 <BOY>
A:Cross-references: UNIPARC:UPI0000137AD6; EMBL:Z28010; NID:g485992; PIDN:CAA81845.1; PI
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:UFD4
A:Cross-references: SGD:S0001493; MIPS:YKL010C
A:Map position: 111

Query Match 24.4%; Score 49; DB 2; Length 1483;
Best Local Similarity 34.4%; Pred. No. 3.9e+02;
Matches 11; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

```
Qy      2  SONEYFDSLHLHACIPCOLRCSSTNPPLTCORY 33
Db      499  SNQKGFSLVQCLIPILVEIYTNADFDVRY 530

RESULT 61
T27283
hypotheical protein Y64G10A.f - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T27283
R:Ainscough, R.
A:Title: Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of I
submitted to the EMBL Data Library, September 1999
A:Reference number: 220336
A:Accession: T27283
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1620 <WIL>
A:Cross-references: UNIPARC:UPI000017BCB4; EMBL:AL110498; NID:e1542303; PIDN:CAB54471.1;
A:Experimental source: clone Y64G10A
C:Genetics:
A:Gene: CESP:Y64G10A.f
A:Introns: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 625/1; 7
Query Match      24.4%; Score 49; DB 2; Length 1620;
Best Local Similarity 23.8%; Pred. No. 4.2e+02;
Matches 10; Conservative 7; Mismatches 17; Indels 8; Gaps 1;

Qy      1  CSONEYFDSLHLHACI-----PCQLRCSSTNPPLTCORYC 34
Db      1409  CENGVCDSSTGSCVCPGGYIGTRCEIACQSDRGPTCEKIC 1450

RESULT 62
T13171
probable vitellogenin receptor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: T13171
R:Schonbaum, C.P.; Lee, S.; Mahowald, A.P.
Proc. Natl. Acad. Sci. U.S.A. 92, 1485-1489, 1995
A:Title: The Drosophila yolkless gene encodes a vitellogenin receptor belonging to the 1
A:Reference number: 217627; MUID:95183490; PMID:7878005
A:Accession: T13171
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1984 <SCH>
A:Cross-references: UNIPROT:P98163; UNIPARC:UPI000013B879; EMBL:U13637; NID:G535345; PID
C:Genetics:
A:Gene: y1
A:Cross-references: FlyBase:FBgn0004649
A:Map position: 1
F:90-124/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F:123-166/Domain: LDL receptor ligand-binding repeat homology <LDL8>
F:184-220/Domain: LDL receptor ligand-binding repeat homology <LDL10>
F:227-262/Domain: LDL receptor ligand-binding repeat homology <LDL11>
F:266-304/Domain: LDL receptor ligand-binding repeat homology <LDL12>
F:1025-1062/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F:1074-1109/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F:1118-1152/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F:1158-1193/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F:1198-1232/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F:1243-1279/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F:1283-1318/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F:1340-1375/Domain: LDL receptor ligand-binding repeat homology <LDL9>
Query Match      24.4%; Score 49; DB 2; Length 1984;
Best Local Similarity 33.3%; Pred. No. 5e+02;
Matches 11; Conservative 7; Mismatches 11; Indels 4; Gaps 2;

Qy      1  CSONEY-FDSLHLHACIPCOLRCSSTNPPLTCOR 32
Db      1243  CAEDQYQTSNKLKCLPSAVRNGT---ECPR 1272
```

RESULT 63

```
A46019
notch-1 protein - mouse
N:Alternate names: notch protein
C:Species: Mus musculus (house mouse)
C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 05-Oct-2004
C:Accession: A46019; S25144; C49175; B46438; A46438; PH1569; S32109
R:del Amo, F.F.; Gendron-Maguire, M.; Swiatek, P.J.; Jenkins, N.A.; Copeland, N.G.; Gridl
Genomics 15, 259-264, 1993
A:Title: Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of I
A:Reference number: A46019; MUID:93194170; PMID:8449489
A:Accession: A46019
A:Status: not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-2531 <DEL>
A:Cross-references: UNIPROT:Q01705; UNIPARC:UPI000002922B; GB:Z11886; GB:S47228; NID:G286
A:Note: sequence extracted from NCBI backbone (NCBI:P127318)
R:Franco del Amo, F.; Smith, D.E.; Swiatek, P.J.; Gendron-Maguire, M.; Greenspan, R.J.; N
submitted to the EMBL Data Library, April 1992
A:Description: Expression pattern of Notch, a mouse homolog of Drosophila Notch, suggests
A:Reference number: S25144
A:Accession: S25144
A:Molecule type: mRNA
A:Residues: 1551-2108, 'Q', 2110-2114, 'ALP', 2118-2170 <FRA>
A:Cross-references: UNIPARC:UPI0000177461; EMBL:Z11886
R:Lardelli, M.; Lendahl, U.
Exp. Cell Res. 204, 364-372, 1993
A:Title: Notch A and Notch B-two mouse Notch homologues coexpressed in a wide variety of
A:Reference number: A49175; MUID:93178563; PMID:8440332
A:Accession: C49175
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1161-1547 <LAR>
A:Cross-references: UNIPARC:UPI0000177462; EMBL:X69278; NID:G287987; PIDN:CAA48339.1; PII
A:Experimental source: embryo
A:Note: sequence extracted from NCBI backbone (NCBI:P126159)
R:Kopan, R.; Weintraub, H.
J. Cell Biol. 121, 631-641, 1993
A:Title: Mouse notch: expression in hair follicles correlates with cell fate determinatic
A:Reference number: A46438; MUID:93252998; PMID:8486742
A:Accession: B46438
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1865-1932, 'RR', 1935-1937, 'L', 1938-1967, 'I', 1969-2044, 'IE', 2047-2052, 'S', 2054-
A:Cross-references: UNIPARC:UPI0000177463
A:Experimental source: embryo
A:Note: sequence extracted from NCBI backbone (NCBIN:131246, NCBI:P131247)
C:Comment: This protein has many EGF repeats and lin-12[1172]/Notch repeats.
C:Comment: This protein is one of the neurogenic proteins controlling the decision betwee
C:Genetics:
A:Gene: notch-1
A:Map position: 2
A:Note: proximal region of chromosome 2
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
F:106-138/Domain: EGF homology <EGF1>
F:144-175/Domain: EGF homology <EG01>
F:222-254/Domain: EGF homology <EGF2>
F:261-292/Domain: EGF homology <EG02>
F:339-370/Domain: EGF homology <EG03>
F:416-449/Domain: EGF homology <EGF3>
F:456-487/Domain: EGF homology <EG04>
F:494-525/Domain: EGF homology <EG05>
F:532-563/Domain: EGF homology <EG06>
F:607-638/Domain: EGF homology <EG07>
F:682-713/Domain: EGF homology <EG08>
F:757-788/Domain: EGF homology <EG09>
F:795-826/Domain: EGF homology <EG10>
F:873-904/Domain: EGF homology <EG11>
F:911-942/Domain: EGF homology <EG12>
F:949-980/Domain: EGF homology <EG13>
F:987-1018/Domain: EGF homology <EG14>
```

F:1025-1056/Domain: EGF homology <EG15>
F:1063-1094/Domain: EGF homology <EG16>
F:1149-1180/Domain: EGF homology <EG17>
F:1187-1218/Domain: EGF homology <EG18>
F:1233-1264/Domain: EGF homology <EGF4>
F:1352-1383/Domain: EGF homology <EG19>
F:1391-1425/Domain: EGF homology <EGF>
F:1917-1948/Domain: ankyrin repeat homology <AN1>
F:1949-1981/Domain: ankyrin repeat homology <AN2>
F:1983-2015/Domain: ankyrin repeat homology <AN3>
F:2016-2048/Domain: ankyrin repeat homology <AN4>
F:2049-2081/Domain: ankyrin repeat homology <AN5>

Query Match 24.4%; Score 49; DB 2; Length 2531;
Best Local Similarity 40.7%; Pred. No. 6.2e+02;
Matches 11; Conservative 4; Mismatches 10; Indels 2; Gaps 1;

OY 10 LKHACT--PCQLRCSSNTPLTCQRYC 34
DB 372 LKHACISNFCNCGSNDTPVNGKRIC 398

RESULT 64
T10053
laminin alpha 5 chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T10053
R:Miner, J.H.; Lewis, R.M.; Sanes, J.R.
Submitted to the EMBL Data Library, November 1997
A:Reference number: Z16923
A:Accession: T10053
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-3635 <MIN>
A:Cross-references: UNIPROT:Q61001; UNIPARC:UPI000004C5B8; EMBL:U37501; NID:g2599231; PID:10053

Query Match 24.4%; Score 49; DB 2; Length 3635;
Best Local Similarity 26.0%; Pred. No. 8.4e+02;
Matches 13; Conservative 5; Mismatches 14; Indels 18; Gaps 2;

OY 1 CSONEYFDS---LLHACIPQC-----LRCCSNTPLTCQRYC 32
DB 1763 CAPGYRDTKGLFLGRCVFCQCHGSHDRCLPGSGICVGCQHNTEGDQCR 1812

RESULT 65
T27297
hypothetical protein Y684A.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T27297
R:Steward, C.
Submitted to the EMBL Data Library, January 1998
A:Reference number: Z20340
A:Accession: T27297
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-474 <WIL>
A:Cross-references: UNIPROT:O5XX02; UNIPARC:UPI00000783D7; EMBL:AL021503; PIDN:CAA16417.
A:Experimental source: clone Y684A
C:Genetics:
A:Gene: CESP:Y684A.5
A:Map position: 5
A:Introns: 47/2; 80/3; 145/3; 181/2; 196/3; 238/2; 269/2; 306/3; 342/2; 357/3; 418/3

Query Match 24.1%; Score 48.5; DB 2; Length 474;
Best Local Similarity 42.9%; Pred. No. 1.7e+02;

Matches 9; Conservative 3; Mismatches 8; Indels 1; Gaps 1;

OY 14 CIPCOLRCSSNTPLTCQRYC 34
DB 357 CLPCQ-TCTSFDPGAAHASC 376

RESULT 66
ABONS1
serum albumin 1 precursor - Atlantic salmon
C:Species: Salmo salar (Atlantic salmon)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: A36238; S13079
R:Byrnes, L.; Gannon, F.
DNA Cell Biol. 9, 647-655, 1990
A:Title: Atlantic salmon (Salmo salar) serum albumin: cDNA sequence, evolution, and tissue
A:Reference number: A36238; MUID:91083837; PMID:2261082
A:Accession: A36238
A:Molecule type: mRNA
A:Residues: 1-608 <BYR>
A:Cross-references: UNIPROT:P21848; UNIPARC:UPI00001257B6; GB:X52397; NID:g64375; PIDN:CI
C:Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper, iron
mones (weak bonds with these hormones promote their transfer across the membranes), thyro
C:Superfamily: serum albumin; serum albumin repeat homology
C:Keywords: carrier protein; duplication; plasma
F:1-14/Domain: signal sequence #status predicted <SIG>
F:15-18/Domain: propeptide #status predicted <PRO>
F:19-608/Product: serum albumin #status predicted <MAT>
F:23-196/Domain: serum albumin repeat homology <SAL>
F:215-390/Domain: serum albumin repeat homology <SA2>
F:411-591/Domain: serum albumin repeat homology <SA3>
F:26-72, 71-80, 93-108, 107-118, 142-187, 186-195, 218-264, 263-271, 283-299, 298-309, 336-381, 380-

Query Match 24.1%; Score 48.5; DB 1; Length 608;
Best Local Similarity 34.4%; Pred. No. 2.1e+02;
Matches 11; Conservative 5; Mismatches 9; Indels 7; Gaps 1;

OY 8 DSSLHACIP-----COLRCSSNTPLTCQRYC 32
DB 51 DSTLGLVPLIAEALAMGVKCSGSDTPPEDCER 82

RESULT 67
ABONS2
serum albumin 2 precursor - Atlantic salmon
C:Species: Salmo salar (Atlantic salmon)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: A46757; S30594
R:Byrnes, L.
Submitted to the EMBL Data Library, June 1991
A:Reference number: A46757
A:Accession: A46757
A:Molecule type: mRNA
A:Residues: 1-608 <BYR>
A:Cross-references: UNIPROT:Q03156; UNIPARC:UPI00001257BB; EMBL:X60776; NID:g64349; PIDN:
R:Byrnes, L.; Gannon, F.
Gene 120, 319-320, 1992
A:Title: Sequence analysis of a second cDNA encoding Atlantic salmon (Salmo salar) serum
A:Reference number: S30594; MUID:93013056; PMID:1398147
A:Contents: annotation
A:Note: only a list of differences from sequence A36238 is shown
C:Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper, iron
mones (weak bonds with these hormones promote their transfer across the membranes), thyro
C:Superfamily: serum albumin; serum albumin repeat homology
C:Keywords: carrier protein; duplication; plasma
F:1-14/Domain: signal sequence #status predicted <SIG>
F:15-18/Domain: propeptide #status predicted <PRO>
F:19-608/Product: serum albumin #status predicted <MAT>
F:23-196/Domain: serum albumin repeat homology <SAL>
F:215-390/Domain: serum albumin repeat homology <SA2>
F:411-591/Domain: serum albumin repeat homology <SA3>
F:26-72, 71-80, 93-108, 107-118, 142-187, 186-195, 218-264, 263-271, 283-299, 298-309, 336-381, 380-

C:Comment: This protein inhibits the activities of factor Xa and tissue factor-factor VII
C:Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
C:Keywords: anticoagulant; glycoprotein; serine proteinase inhibitor
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-304/Product: tissue factor pathway inhibitor #status predicted <MAT>
F:54-104/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:125-175/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F:217-267/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F:54-104,63-87,79-100,125-175,134-158,150-171,217-267,226-250,242-263/Disulfide bonds: #
F:64/Inhibitory site: Lys (coagulation factor VII/tissue factor complex) #status predicted
F:135/Inhibitory site: Arg (coagulation factor X) #status predicted
F:145,195,256/Binding site: carboxylate (Asn) (covalent) #status predicted
F:227/Inhibitory site: Arg (unidentified proteinase) #status predicted

Query Match 23.9%; Score 48; DB 1; Length 304;
Best Local Similarity 31.6%; Pred. No. 1.3e+02;
Matches 12; Conservative 6; Mismatches 16; Indels 4; Gaps 2;

QY 1 CSQNE---YFSLHACIFCQLR-CSSNTPPLTCQRYC 34
DB 226 CRANENRFYNSVIGKCRPFKYSGCCGNNFTSKREC 263

RESULT 73
T27686
hypothetical protein ZK1067.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T27686
R:Thomas K.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z20404
A:Accession: T27686
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-314 <ML>
A:Cross-references: UNIPROT:Q23390; UNIPARC:UPI000007D293; EMBL:Z70039; PIDN:CAA93886.1;
A:Experimental source: clone ZK1067
C:Genetics:
A:Gene: CESP:ZK1067.7
A:Map position: 2
A:Introns: 30/3; 296/2
C:Superfamily: gliadin

Query Match 23.9%; Score 48; DB 2; Length 314;
Best Local Similarity 38.1%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 14 CIPCQLRCSNTPPLTCQRYC 34
DB 150 CGSCQSCQQTCTCNCQAC 170

RESULT 74
T27687
protein kinase (EC 2.7.1.37) R-mil - Rous-associated virus (type 1)
N:Alternate names: kinase-related transforming protein R-mil; R-mil proto-oncogene prote
C:Species: Rous-associated virus
A:Note: host Gallus gallus (chicken)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: A40341
R:Felder, M.P.; Eychens, A.; Barnier, J.V.; Calogeraki, I.; Calothy, G.; Marx, M.
J. Virol. 65, 3633-3640, 1991
A:Title: Common mechanism of retrovirus activation and transduction of c-mil and c-rmil
A:Reference number: A40341; MUID:91251215; PMID:1645786
A:Accession: A40341
A:Molecule type: DNA
A:Residues: 1-450 <PEL>
A:Cross-references: UNIPROT:P27966; UNIPARC:UPI00001342F7; GB:M62407; NID:G210080; PIDN:
C:Comment: This protein is translated as a mil-env polypeptide.
C:Genetics:
A:Gene: R-mil
C:Superfamily: kinase-related transforming protein; protein kinase homology

C:Keywords: ATP; oncogene; phosphotransferase; serine/threonine-specific protein kinase;
F:81-347/Domain: protein kinase homology <KIN>
F:89-97/Region: protein kinase ATP-binding motif
F:109/Active site: Lys #status predicted

Query Match 23.9%; Score 48; DB 1; Length 450;
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 10 LLHACIPCQLRCSSNT 25
DB 406 LLVCLPCLLCQVSSS 421

RESULT 75
DB8991
protein apx-1 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: DB8991
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_eleg
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: DB8991
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-513 <STO>
A:Cross-references: UNIPARC:UPI000017A664; GB:chr_V; PIDN:AAC69353.1; PID:G3808343; GSPD:
C:Genetics:
A:Gene: apx-1
A:Map position: 5

Query Match 23.9%; Score 48; DB 2; Length 513;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 11; Conservative 1; Mismatches 8; Indels 2; Gaps 1;

QY 15 IPCQLR--CSSNTPPLTCQRYC 34
DB 124 VTVQLRNLCSNHYGKRCNRYC 145

RESULT 76
T01513
CTP synthase (EC 6.3.4.2) T10M13.13 - Arabidopsis thaliana
N:Alternate names: CTP synthetase; UTP-ammonia ligase
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01513
R:Johnson, A.F.; de la Bastide, M.; Lodhi, M.; Hoffman, J.; Hasegawa, A.; Gnoj, L.; Gott
Martienssen, R.; McCombie, W.
submitted to the EMBL Data Library, May 1997
A:Description: The sequence of the Arabidopsis thaliana T10M13 BAC.
A:Reference number: Z14346
A:Accession: T01513
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-539 <JOH>
A:Cross-references: UNIPROT:O04952; UNIPARC:UPI00000AB89F; EMBL:AF001308; NID:G2104523; I
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 4S
A:Introns: 40/1; 66/3; 95/3; 152/1; 171/1; 192/3; 220/3; 237/3; 258/3; 293/3; 314/3; 344/
A:Note: T10M13.13
C:Superfamily: CTP synthase
C:Keywords: ligase; pyrimidine nucleotide biosynthesis

Query Match 23.9%; Score 48; DB 2; Length 539;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Query Match 23.9%; Score 48; DB 2; Length 681;
Best Local Similarity 31.4%; Pred. No. 2.7e+02;
Matches 11; Conservative 6; Mismatches 12; Indels 6; Gaps 1;

QY 5 EYFDLSLH-----ACIPQLRCSNTPITCORY 33
DB 514 EMFEVLIHOBIAQVSDVPKQYRWTKKSPPTHSKY 548

RESULT 82

T52060
protein MEDA [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C:Accession: T52060
R:Crossnuklaus, U.; Vielle-Calzada, J.P.; Hoepfner, M.A.; Gagliano, W.B.
Science 280, 446-450, 1998
A:Title: Maternal control of embryogenesis by MEDA, a polycomb group gene in Arabidopsis
A:Reference number: Z25927; PMID:98212068; PMID:9545225
A:Accession: T52060
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-689 <GRO>
A:Cross-references: UNIPROT:O65312; UNIPARC:UPI000003C2EE; EMBL:AF060485; PIDN:AA39446;
C:Genetics:
A:Gene: MEA

Query Match 23.9%; Score 48; DB 2; Length 689;
Best Local Similarity 36.4%; Pred. No. 2.7e+02;
Matches 8; Conservative 4; Mismatches 6; Indels 4; Gaps 1;

QY 17 COLRCSNTPPLT----CORRC 34
DB 452 CKSKCGQCPCLTHNCCCKYC 473

RESULT 83

JC5571
subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form E-II -
C:Species: Homo sapiens (man)
C:Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 09-Jul-2004
C:Accession: JC5571
R:Morit, K.; Kii, S.; Tsuji, A.; Nagahama, M.; Imamaki, A.; Hayashi, K.; Akamatsu, T.; Na
J. Biochem. 121, 941-948, 1997
A:Title: A novel human PACE4 isoform, PACE4E is an active processing protease containing
A:Reference number: JC5570; PMID:97335942; PMID:9192737
A:Accession: JC5571
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-962 <MOR>
A:Cross-references: UNIPROT:P29122; UNIPARC:UPI000002B06F; DDBJ:D87994; NID:G2330550; PI
A:Experimental source: brain cerebellum
C:Comment: This enzyme is a processing protease and responsible for processing of various
ch it is retained intracellularly.
C:Genetics:
A:Gene: GDB:PACE4

A:Cross-references: GDB:131390; OMIM:167405
A:Map position: 15q26-15q26
C:Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
C:Keywords: glycoprotein; hydrolase; serine proteinase
F:1-62/Domain: signal sequence #status predicted <SIG>
F:163-149/Domain: propeptide #status predicted <PRO>
F:196-434/Domain: subtilisin homology <SBT>
F:938-954/Domain: hydrophobic cluster #status predicted <HCU>
F:205-246,347,420/Active site: Asp, His, Asn, Ser #status predicted
F:259/Binding site: carboxydrate (Asn) (covalent) #status predicted

Query Match 23.9%; Score 48; DB 2; Length 962;
Best Local Similarity 37.0%; Pred. No. 3.6e+02;
Matches 10; Conservative 1; Mismatches 16; Indels 0; Gaps 0;

QY 1 CSONEYFDLSLHACIPQLRCSNTPP 27

DB 819 CERGTFDSELIRCGECHHTCGVCVP 845

RESULT 84

A39490
subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form A - huma
N:Alternate names: kexin homology
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 31-Mar-2000
C:Accession: A39490
R:Kiefer, M.C.; Tucker, J.E.; Joh, R.; Landsberg, K.E.; Salzman, D.; Barr, P.J.
DNA Cell Biol. 10, 757-769, 1991
A:Title: Identification of a second human subtilisin-like protease gene in the fes/fps re
A:Reference number: A39490; PMID:92075167; PMID:1741956
A:Accession: A39490
A:Molecule type: mRNA
A:Residues: 1-969 <KIE>
A:Cross-references: UNIPARC:UPI00001311D0; GB:M80482; NID:G189531; PIDN:AAA59998.1; PID:5
C:Genetics:
A:Gene: GDB:PACE4
A:Cross-references: GDB:131390; OMIM:167405
A:Map position: 15q26-15q26
C:Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
C:Keywords: alternative splicing; hydrolase; serine proteinase
F:150-969/Product: serine proteinase PACE4 #status predicted <SIG>
F:196-434/Domain: subtilisin homology <SBT>
F:205,246,420/Active site: Asp, His, Ser #status predicted

Query Match 23.9%; Score 48; DB 1; Length 969;
Best Local Similarity 37.0%; Pred. No. 3.6e+02;
Matches 10; Conservative 1; Mismatches 16; Indels 0; Gaps 0;

QY 1 CSONEYFDLSLHACIPQLRCSNTPP 27
DB 832 CERGTFDSELIRCGECHHTCGVCVP 858

RESULT 85

JC5570
subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form E-I - hu
C:Species: Homo sapiens (man)
C:Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 09-Jul-2004
C:Accession: JC5570
R:Morit, K.; Kii, S.; Tsuji, A.; Nagahama, M.; Imamaki, A.; Hayashi, K.; Akamatsu, T.; Na
J. Biochem. 121, 941-948, 1997
A:Title: A novel human PACE4 isoform, PACE4E is an active processing protease containing
A:Reference number: JC5570; PMID:97335942; PMID:9192737
A:Accession: JC5570
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-975 <MOR>
A:Cross-references: UNIPROT:P29122; UNIPARC:UPI000002B06E; DDBJ:D87993; NID:G2330548; PI
A:Experimental source: brain cerebellum
C:Comment: This enzyme is a processing protease and responsible for processing of various
ch it is retained intracellularly.
C:Genetics:
A:Gene: GDB:PACE4

A:Cross-references: GDB:131390; OMIM:167405
A:Map position: 15q26-15q26
C:Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
C:Keywords: alternative splicing; glycoprotein; hydrolase; serine proteinase
F:1-62/Domain: signal sequence #status predicted <SIG>
F:163-149/Domain: propeptide #status predicted <PRO>
F:196-434/Domain: subtilisin homology <SBT>
F:952-968/Domain: hydrophobic cluster #status predicted <HCU>
F:205,246,347,420/Active site: Asp, His, Asn, Ser #status predicted
F:259/Binding site: carboxydrate (Asn) (covalent) #status predicted

Query Match 23.9%; Score 48; DB 2; Length 975;
Best Local Similarity 37.0%; Pred. No. 3.6e+02;
Matches 10; Conservative 1; Mismatches 16; Indels 0; Gaps 0;

Oy 1 CSQNEYPDSLTHACIPCOLRCSSNTTP 27
 Db 832 CEPCTYFDSILRCGCHHTCTCTGCP 858

RESULT 86

JC5598
 mucin - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 03-Jul-2004
 C/Accession: J05598
 R:Rinaltom, T.; Tisale, A.S.; Zhan, Q.; Spurr-Michaud, S.; Gipson, I.K.
 Biochem. Biophys. Res. Commun. 236, 789-797, 1997
 A>Title: Cloning of rat Muc5AC mucin gene: Comparison of its structure and tissue distribution
 A/Reference number: J05598; MUID:97396181; PMID:9245735
 A/Accession: J05598
 A>Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-1034 <INA>
 A/Cross-references: UNIPROT:O35888; UNIPARC:UPI00000E7779; GB:U83139; NID:g2315984; PIDN
 A/Note: translation not complete
 C/Comment: This protein is a high molecular weight glycoprotein which is a major component
 of intestinal tract and reproductive tract.
 C/Genetics:
 A/Gene: Muc5A
 F:45-149/Domain: cysteine-rich <CYS>
 F:762-830/Domain: von Willebrand factor type C repeat homology <VWC>

Query Match 23.9%; Score 48; DB 2; Length 1034;
 Best Local Similarity 42.4%; Pred. No. 3.8e+02;
 Matches 14; Conservative 4; Mismatches 11; Indels 4; Gaps 2;

Oy 1 CSQNEYPDSLTHA---CLPCQRCSSNTTPPLTC 30
 Db 567 CSGLELYASLCAAGVCTWRSH-TNNCTPFTC 598

RESULT 87

TYFVMI
 gag-Rml1-env polypeptide - avian retrovirus IC10
 N/Contains: env polypeptide; gag polypeptide; protein kinase (EC 2.7.1.37) Rml1
 C/Species: avian retrovirus IC10
 A/Note: host Gallus gallus (chicken)
 C/Date: 31-Mar-1991 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
 C/Accession: A43095; A36753; S01645; B36753; S03832
 R:Dezelee, P.
 submitted to GenBank, December 1988
 A/Reference number: A43095
 A/Accession: A43095
 A/Molecule type: DNA
 A/Residues: 1-1079 <DEZ>
 A/Cross-references: UNIPROT:P10533; UNIPARC:UPI0000171031; GB:X13744; NID:961592; PIDN:C
 EMBO J. 7, 3369-3373, 1988
 A>Title: A novel oncogene related to c-mil is transduced in chicken neuroectina cells in
 A/Reference number: S01645; MUID:89091077; PMID:2850163
 A/Accession: A36753
 A/Molecule type: DNA
 A/Residues: 513-645 <MAR>
 A/Cross-references: UNIPARC:UPI0000172554
 A/Accession: S01645
 A/Molecule type: DNA
 A/Residues: 646-1012 <MA2>
 A/Cross-references: UNIPARC:UPI0000172554
 A/Accession: B36753
 A/Molecule type: DNA
 A/Residues: 1013-1079 <MA3>
 A/Cross-references: UNIPARC:UPI0000172554
 R:Eychene, A.; Marx, M.; Dezelee, P.; Calochy, G.
 Nucleic Acids Res. 17, 1250, 1989
 A>Title: Complete nucleotide sequence of IC10, a retrovirus containing the Rml1 oncogene
 A/Reference number: S03832; MUID:89160254; PMID:2537952
 A/Accession: S03832

A>Status: translation not shown

A/Molecule type: DNA
 A/Residues: 1-1079 <EYC>
 A/Cross-references: UNIPARC:UPI0000171031; EMBL:X13744; NID:961592; PIDN:CAA32008.1; PID
 C/Comment: This virus arose by recombination between host Rml1 and viral sequences during
 C/Genetics:
 A/Gene: gag-Rml1-env
 C/Superfamily: avian retrovirus IC10 gag-Rml1-env polypeptide; protein kinase homology
 C/Keywords: ATP, coat protein; oncogene; phosphotransferase; polypeptide; serine/threonin
 F:1-645/Region: viral gag gene-derived
 F:646-1012/Region: host Rml1 gene-derived
 F:710-976/Domain: protein kinase homology <KIN>
 F:718-726/Region: protein kinase ATP-binding motif
 F:1013-1079/Region: viral env gene-derived
 F:738/Active site: Lys #status predicted

Query Match 23.9%; Score 48; DB 1; Length 1079;
 Best Local Similarity 50.0%; Pred. No. 3.9e+02;
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Oy 10 LTHACIPCOLRCSSNT 25
 Db 1035 LHVCTLPCLQCVCSS 1050

RESULT 88

A9175
 Notch B protein - mouse (fragment)
 N/Alternate names: Notch homolog
 C/Species: Mus musculus (house mouse)
 C/Date: 21-Jan-1994 #sequence_revision 05-Jan-1996 #text_change 05-Oct-2004
 C/Accession: A49175; P1570; S32113
 R:Lardelli, M.; Lendahl, U.
 Exp. Cell Res. 204, 364-372, 1993
 A>Title: Notch A and Notch B--two mouse Notch homologues coexpressed in a wide variety of
 A/Reference number: A49175; MUID:93178563; PMID:8440332
 A/Accession: A49175
 A>Status: preliminary; nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-1203 <LAR>
 A/Cross-references: UNIPROT:O35516; UNIPARC:UPI000016CFLF; EMBL:X68279; NID:g287989; PID
 A/Experimental source: embryo
 A/Note: sequence extracted from NCBI backbone (NCBI:126158)
 C/Comment: This protein has many EGF repeats and 11-12/Notch repeats.
 C/Comment: This protein is one of the neurogenic proteins controlling the decision betwe
 C/Superfamily: notch protein; ankyrin repeat homology; EGF homology
 F:143-174/Domain: EGF homology <EGX1>
 F:482-513/Domain: EGF homology <EGF1>
 F:560-591/Domain: EGF homology <EGF>
 F:674-705/Domain: EGF homology <EGX2>
 F:712-743/Domain: EGF homology <EGF3>
 F:836-867/Domain: EGF homology <EGX3>

Query Match 23.9%; Score 48; DB 2; Length 1203;
 Best Local Similarity 50.0%; Pred. No. 4.3e+02;
 Matches 10; Conservative 4; Mismatches 4; Indels 2; Gaps 2;

Oy 17 COL-RCSSNTTPPLTC-RYC 34
 Db 1094 CELYAPSTPTATCQSQYC 1113

RESULT 89

A55677
 laminin beta-2 chain precursor (version 1) - human
 C/Species: Homo sapiens (man)
 C/Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 17-Mar-1999
 C/Accession: A55677
 R:Lewer, U.M.; Gerecke, D.R.; Durkin, M.E.; Kurtz, K.S.; Mattei, M.G.; Champiaud, M.F.;
 Genomics 24, 243-252, 1994
 A>Title: Human beta2 chain of laminin (formerly S chain): cDNA cloning, chromosomal loca
 A/Reference number: A55677; MUID:95213013; PMID:7698745
 A/Accession: A55677

A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1797 <MEM>
A:Cross-references: UNIPARC:UPI0000177436; GB:X79683
C:Genetics:
A:Gene: GDB:LAMB2
A:Cross-references: GDB:132363; OMIM:150325
A:Map position: 3p21.3-3p21.2
C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C:Keywords: basement membrane; extracellular matrix; glycoprotein; heterotrimer
F:1-32/Domain: signal sequence #status predicted <Sig>
F:33-1797/Product: laminin beta-2 chain #status predicted <MAT>
F:283-344/Domain: laminin-type EGF-like homology <LE01>
F:347-407/Domain: laminin-type EGF-like homology <LE02>
F:410-467/Domain: laminin-type EGF-like homology <LE03>
F:470-519/Domain: laminin-type EGF-like homology <LE04>
F:522-552/Domain: laminin-type EGF-like homology #status atypical <LE05>
F:783-828/Domain: laminin-type EGF-like homology <LE06>
F:831-874/Domain: laminin-type EGF-like homology <LE07>
F:877-924/Domain: laminin-type EGF-like homology <LE08>
F:927-982/Domain: laminin-type EGF-like homology <LE09>
F:985-1034/Domain: laminin-type EGF-like homology <LE10>
F:1037-1091/Domain: laminin-type EGF-like homology <LE11>
F:1094-1139/Domain: laminin-type EGF-like homology <LE12>
F:1142-1186/Domain: laminin-type EGF-like homology <LE13>

Query Match 23.9%; Score 48; DB 2; Length 1797;
Best Local Similarity 26.9%; Pred. No. 6,1e+02;
Matches 14; Conservative 4; Mismatches 10; Indels 24; Gaps 3;

OY 1 CSONEYFDSLHACIPCOLRCS--SNTPL-TC 28
DB 943 CHQDEXSQIVCHCRAGYTGRLCEACAPGQFGDPSRPAQCQLCEGSGNIDPM 994

RESULT 90
T25643
hypothetical protein C46H11.9 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T25643
R:Miller, N.; Bradshaw, H.; Wamsley, P.
submitted to the EMBL Data Library, February 1997
A:Description: The sequence of C. elegans cosmid C46H11.
A:Reference number: Z20061
A:Accession: T25643
A>Status: preliminary; translated from GB/EMBL/DBET
A:Molecule type: DNA
A:Residues: 1-249 <MIL>
A:Cross-references: UNIPROT:Q9GYJ2; UNIPARC:UPI0000081DC5; EMBL:U88314; P1DN:AB42363.1;
A:Experimental source: strain Bristol N2; clone C46H11
C:Genetics:
A:Gene: CESP.C46H11.9
A:Map position: 1
A:Introns: 28/1; 55/1; 205/1
C:Superfamily: Caenorhabditis elegans hypothetical protein F48G7.8

Query Match 23.6%; Score 47.5; DB 2; Length 249;
Best Local Similarity 39.4%; Pred. No. 1.3e+02;
Matches 13; Conservative 3; Mismatches 14; Indels 3; Gaps 2;

OY 1 CSONEYFDSLHACIPCOLRCS--SNTPL-TC 30
DB 114 CNDANFEDWWTQCCPTCGRCSCSFSSPTTGTG 146

RESULT 91
T51437
hypothetical protein F2G14.40 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C:Accession: T51437
R:Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; New

submitted to the Protein Sequence Database, August 2000
A:Reference number: Z25394
A:Accession: T51437
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-275 <SAT>
A:Cross-references: UNIPROT:Q9LFR3; UNIPARC:UPI00000A76D3; EMBL:AL391146
A:Experimental source: cultivar Columbia; BAC clone F2G14
C:Genetics:
A:Map position: 5
A:Introns: 17/3; 30/3; 215/1
A:Note: F2G14_40

Query Match 23.6%; Score 47.5; DB 2; Length 275;
Best Local Similarity 34.5%; Pred. No. 1.4e+02;
Matches 10; Conservative 4; Mismatches 14; Indels 1; Gaps 1;

OY 1 CSONEYFDSLHACIPCOLRCSNTPLT 29
DB 224 CGQHSRKNVCMRACVCCYRKC-VPPGT 251

RESULT 92
S22181
gamma-1-microglobulin precursor - plaice
C:Species: Pleuronectes platessa (plaice)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S22181
R:Leaver, M.J.
submitted to the EMBL Data Library, December 1991
A:Reference number: S22181
A:Accession: S22181
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-355 <LEA>
A:Cross-references: UNIPROT:P36992; UNIPARC:UPI000012594A; EMBL:X63762; NID:964233; P1DN:
C:Superfamily: alpha-1-microglobulin and Inter-alpha-trypsin inhibitor light chain precu
F:37-189/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F:236-286/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F:292-342/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>

Query Match 23.6%; Score 47.5; DB 1; Length 355;
Best Local Similarity 30.3%; Pred. No. 1.8e+02;
Matches 10; Conservative 4; Mismatches 14; Indels 5; Gaps 1;

OY 7 FDSLHACIP-----COLRCSNTPLTCORC 34
DB 310 FDFVGSCLMPYDGLICQANANQFYSRAECQCYC 342

RESULT 93
S67292
probable membrane protein YOR380w - Yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein O6749
C:Species: Saccharomyces cerevisiae
C>Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 05-Oct-2004
C:Accession: S67292
R:Delius, H.; Hebling, U.; Hofmann, B.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S67261
A:Accession: S67292
A:Molecule type: DNA
A:Residues: 1-546
A:Cross-references: UNIPROT:Q08904; UNIPARC:UPI000006A54E; EMBL:Z75288; NID:91420818; P1I
A:Experimental source: strain S288C
C:Genetics:
A:Gene: MTPS.YOR380w
A:Cross-references: SGD:S0005907
A:Map position: 15R
C:Keywords: transmembrane protein
F:15-51/Domain: GAL4 zinc binuclear cluster homology <GAL4>
F:204-220/Domain: transmembrane #status predicted <TM>

F;223-359/Domain: LDL receptor ligand-binding repeat homology <LDL8>
F;369-405/Domain: LDL receptor ligand-binding repeat homology <LDL9>
F;616-856/Domain: LDL receptor ligand-binding repeat homology <LD10>
F;661-903/Domain: LDL receptor ligand-binding repeat homology <LD11>
F;908-943/Domain: LDL receptor ligand-binding repeat homology <LD12>
F;948-987/Domain: LDL receptor ligand-binding repeat homology <LD13>
F;993-1027/Domain: LDL receptor ligand-binding repeat homology <LD14>
F;1031-1063/Domain: LDL receptor ligand-binding repeat homology <LD15>
F;1126-1165/Domain: LDL receptor ligand-binding repeat homology <LD16>
F;1172-1209/Domain: LDL receptor ligand-binding repeat homology <LD17>
F;1213-1246/Domain: LDL receptor ligand-binding repeat homology <LD18>

Query Match 23.6%; Score 47.5; DB 2; Length 2180;
Best Local Similarity 45.5%; Pred. No. 8.3e+02;
Matches 10; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 1 CSQNEFYDSLHACIPQCQRCS 22
DB 51 CNEHE-FRCQSGACIPSKACRN 71

RESULT 98

protein T22A3.8 [imported] - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: F87908; E87908
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998

A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A/Reference number: A75000; WUID:99069613; PMID:9651916
A/Note: see websties genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C_eleg

A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A/Accession: F87908
A/Status: preliminary

A/Molecule type: DNA
A/Residues: 1-2823 <STO>
A/Cross-references: UNIPROT:O45614; UNIPARC:UPI000017743C; GB:chr_I; PIDN:CAAL5432.1; PI

A/Accession: E87908
A/Status: preliminary
A/Molecule type: DNA

A/Residues: 1-2823 <ST2>
A/Cross-references: UNIPARC:UPI000017743C; GB:chr_I; PIDN:CAAB03385.1; PID:G3924681; GSPD

C/Genetics:
A/Map position: 1
C/Supfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h

Query Match 23.6%; Score 47.5; DB 2; Length 2823;
Best Local Similarity 20.4%; Pred. No. 1e+03;
Matches 10; Conservative 6; Mismatches 16; Indels 17; Gaps 1;

QY 1 CSQNEFYDSLHACIPQCQRCSNTPTTCQR 32
DB 925 CKEHHWGNALHTCKPCGCHTQGA VNPQCSSENGECCKENYIGAQCDR 973

RESULT 99

hypothetical protein T22A3.8 - Caenorhabditis elegans (fragment)

C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T23064; T25096

R;Barlow, K.
submitted to the EMBL Data Library, October 1997
A/Reference number: Z19669

A/Accession: T23064
A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA
A/Residues: 1-2823 <WIL>
A/Cross-references: UNIPROT:O45614; UNIPARC:UPI000017743C; EMBL:AL008585; PIDN:CAAL5432.

A/Experimental source: clone H10E24
R;McMurray, A.

submitted to the EMBL Data Library, October 1996
A/Reference number: Z19980

A/Accession: T25096
A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA
A/Residues: 1-2823 <W12>

A/Cross-references: UNIPARC:UPI000017743C; EMBL:281125; PIDN:CAAB03385.1; GSPDB:GN00019; (

C/Genetics:
A/Experimental source: clone T22A3
A/Map position: 1
A/Accession: T22A3.8

A/Residues: 45/1; 282/2; 312/3; 416/2; 1255/3; 1329/3; 1418/3; 1776/2; 1988/2; 2760/2
A/Status: preliminary; translated from GB/EMBL/DBJ

Query Match 23.6%; Score 47.5; DB 2; Length 2823;
Best Local Similarity 20.4%; Pred. No. 1e+03;
Matches 10; Conservative 6; Mismatches 16; Indels 17; Gaps 1;

QY 1 CSQNEFYDSLHACIPQCQRCSNTPTTCQR 32
DB 925 CKEHHWGNALHTCKPCGCHTQGA VNPQCSSENGECCKENYIGAQCDR 973

RESULT 100
T43291
laminin alpha chain - Caenorhabditis elegans

C/Species: Caenorhabditis elegans
C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C/Accession: T43291

R;Zhu, X.; Kao, G.; Joh, K.; Hall, D.H.; Wadsworth, V.K.; Hutter, H.; Vogel, B.E.; Huang, J.
submitted to the EMBL Data Library, June 1998

A/Description: Expression, function and evolution of laminin alpha chains.
A/Reference number: Z22397
A/Accession: T43291

A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-3102 <ZHU>

A/Cross-references: UNIPROT:O45614; UNIPARC:UPI00000763A5; EMBL:AF074902; PIDN:AAC26793.1
A/Map position: 1
A/Note: lamal/2

C/Supfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h
Query Match 23.6%; Score 47.5; DB 2; Length 3102;
Best Local Similarity 20.4%; Pred. No. 1.1e+03;

Matches 10; Conservative 6; Mismatches 16; Indels 17; Gaps 1;
QY 1 CSQNEFYDSLHACIPQCQRCSNTPTTCQR 32
DB 925 CKEHHWGNALHTCKPCGCHTQGA VNPQCSSENGECCKENYIGAQCDR 973

Search completed: July 10, 2006, 16:42:11
Job time : 16.4 secs

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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:40:38 ; Search time 48 Seconds
(without alignments)
323.862 Million cell updates/sec

Title: US-10-077-137a-1_COPY_8_41

Perfect score: 201
Sequence: 1 CS0NEXFDSLHACIPQQLRCSNNPPLTCQRYC 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

A_Geneseq_8:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

9: Geneseq2005s:*

10: Geneseq2006s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 201 | 100.0 | 34 | 5 | AAEI5486 Human B-C |
| 2 | 201 | 100.0 | 34 | 6 | ADA49366 Human BCM |
| 3 | 201 | 100.0 | 40 | 9 | ADZ67761 Human BCM |
| 4 | 201 | 100.0 | 51 | 6 | AAEI5485 Human B-C |
| 5 | 201 | 100.0 | 52 | 9 | AEC02032 Amino aci |
| 6 | 201 | 100.0 | 58 | 5 | AAEI5501 Human B-C |
| 7 | 201 | 100.0 | 181 | 5 | AAEI5484 Human B-C |
| 8 | 201 | 100.0 | 184 | 3 | AAEB0843 Amino aci |
| 9 | 201 | 100.0 | 184 | 3 | AAE94001 A human B |
| 10 | 201 | 100.0 | 184 | 4 | AAE09241 Human BCM |
| 11 | 201 | 100.0 | 184 | 4 | AAE09241 Human BCM |
| 12 | 201 | 100.0 | 184 | 4 | AAE09241 Human BCM |
| 13 | 201 | 100.0 | 184 | 4 | AAE09241 Human BCM |
| 14 | 201 | 100.0 | 184 | 4 | AAE09241 Human BCM |
| 15 | 201 | 100.0 | 184 | 4 | AAE09241 Human BCM |
| 16 | 201 | 100.0 | 184 | 4 | AAE09241 Human BCM |
| 17 | 201 | 100.0 | 184 | 4 | AAE09241 Human BCM |
| 18 | 201 | 100.0 | 184 | 4 | AAE09241 Human BCM |
| 19 | 201 | 100.0 | 184 | 4 | AAE09241 Human BCM |
| 20 | 201 | 100.0 | 184 | 4 | AAE09241 Human BCM |
| 21 | 201 | 100.0 | 184 | 4 | AAE09241 Human BCM |
| 22 | 201 | 100.0 | 184 | 4 | AAE09241 Human BCM |
| 23 | 201 | 100.0 | 184 | 4 | AAE09241 Human BCM |

| | | | | | |
|----|-----|-------|-----|---|--------------------|
| 24 | 201 | 100.0 | 184 | 8 | ADK00756 Native hu |
| 25 | 201 | 100.0 | 184 | 8 | ADQ94442 Neutrokin |
| 26 | 201 | 100.0 | 184 | 8 | ADP56014 Human PRO |
| 27 | 201 | 100.0 | 184 | 8 | ADW03432 Human BCM |
| 28 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 29 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 30 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 31 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 32 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 33 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 34 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 35 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 36 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 37 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 38 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 39 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 40 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 41 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
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| 43 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 44 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 45 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 46 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 47 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 48 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 49 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 50 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 51 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
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| 55 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 56 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 57 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 58 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 59 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 60 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 61 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 62 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 63 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 64 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 65 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
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| 75 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 76 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
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| 78 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 79 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 80 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
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| 82 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 83 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 84 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 85 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 86 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 87 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 88 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 89 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 90 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 91 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 92 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 93 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 94 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 95 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |
| 96 | 201 | 100.0 | 184 | 9 | ADZ67760 Human BCM |


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973 47 23.4 241 4 AAY72712 HTLH44 c
974 47 23.4 262 4 AAG91040 C glutami
975 47 23.4 271 2 AAM32093 Porcine r
976 47 23.4 271 8 AAG73443 Swine rec
977 47 23.4 293 9 ABM97013 M. xanthu
978 47 23.4 296 8 ADt49819 Murine PA
979 47 23.4 339 5 AAE24073 Flea peri
980 47 23.4 349 4 AAB50523 Human tum
981 47 23.4 349 8 ADj96164 Human VC2
982 47 23.4 381 5 AAE24075 Flea peri
983 47 23.4 384 4 AAG75479 Human col
984 47 23.4 397 5 AAE24074 Flea peri
985 47 23.4 428 8 ADX90736 Plant ful
986 47 23.4 428 8 ADX90723 Plant ful
987 47 23.4 459 8 ADP30331 Human sec
988 47 23.4 478 2 AAM64184 Lettuce r
989 47 23.4 478 5 AAU95499 Lettuce p
990 47 23.4 480 2 AAR85213 Blowfly 1
991 47 23.4 480 2 AAM64171 Lettuce r
992 47 23.4 480 5 AAU95484 Lettuce p
993 47 23.4 481 9 ABM93912 M. xanthu
994 47 23.4 505 8 ADX68078 Plant ful
995 47 23.4 542 4 AAB84706 Nucleotid
996 47 23.4 542 4 AAE06591 Human pro
997 47 23.4 599 7 ADM04769 Human pro
998 47 23.4 599 7 AEC87699 Human CDN
999 47 23.4 609 2 AAR88279 Ashbya go
1000 47 23.4 609 7 ADK65555 A gossypii
```

ALIGNMENTS

RESULT 1

AAE15486 ID AAE15486 standard; peptide; 34 AA.

XX AC AAE15486;

XX DT 12-MAR-2002 (first entry)

XX DE Human B-cell maturation (BCMA) protein cysteine-rich consensus region.

XX Human; transmembrane activator and intracellular CAML interactor; TACT;
XX cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
XX lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
XX prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
XX drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
XX Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
XX human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
XX rheumatoid arthritis; atherosclerosis.

XX OS Homo sapiens.

XX PN WO200187979-A2.

XX PD 22-NOV-2001.

XX PF 14-MAY-2001; 2001WO-US015567.

XX PR 12-MAY-2000; 2000US-0204039P.

XX PR 27-JUN-2000; 2000US-0214591P.

XX PR 14-MAY-2001; 2001US-00214591.

XX PA (AMGE-) AMGEN INC.

XX PI Theill LE, Yu G;

XX DR WPI; 2002-066686/09.

XX Inhibiting activity of B cell maturation protein and/or transmembrane
XX activator and intracellular cyclophilin ligand interactor, by
XX administering a binding partner for APRIL, a tumor necrosis factor family

PT ligand.

XX Claim 1; Fig 10A; 94pp; English.

XX The invention relates to a method for inhibiting TACT (transmembrane
XX activator and intracellular CAML interactor) and/or B cell maturation
XX protein (BCMA) activity in a mammal. The method comprises administering a
XX specific binding partner for APRIL (970, a tumour necrosis factor-TNF
XX family ligand), having the consensus sequence region of TACT, BCMA, or the TACT/
XX BCMA extracellular consensus sequence, but not the extracellular region
XX of TACT or BCMA. The method is useful for inhibiting activity of TACT
XX and/or BCMA in a mammal which is useful for treating B-cell or T-cell
XX lymphoproliferative disorders, one or more solid tumours such as lung,
XX gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACT
XX antagonists are useful for treating inflammation and immune function
XX diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
XX dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
XX disease), drug and insect sting allergy, inflammatory bowel disease
XX (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
XX sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
XX bacterial, protozoal and viral infections (HIV, atherosclerosis, cancer
XX with leucocyte infiltration of the skin or organs. The present sequence
XX is human BCMA protein cysteine-rich consensus region

SQ Sequence 34 AA;

Query Match 100.0%; Score 201; DB 5; Length 34;

Best local similarity 100.0%; Pred. No. 3e-18;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34

Db 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34

RESULT 2 ADA49366 ID ADA49366 standard; peptide; 34 AA.

XX AC ADA49366;

XX DT 20-NOV-2003 (first entry)

XX DE Human BCMA cysteine rich domain.

XX TALL-1; antagonsist; immunosuppressive; antirheumatic; antiinflammatory;
XX antiarthritic; dermatological; antidiabetic; neuroprotective;
XX antithyroid; antipyretic; nephrotropic; vasotropic; vaccine;
XX autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
XX insulin dependent diabetes mellitus; multiple sclerosis;
XX myasthenia gravis; Grave's disease; autoimmune hemolytic anaemia;
XX autoimmune thrombocytopenic purpura; Goodpasture's syndrome;
XX pemphigus vulgaris; acute rheumatic fever;
XX post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA; CRD;
XX cysteine rich domain.

XX OS Homo sapiens.

XX PN WO2003035846-A2.

XX PD 01-MAY-2003.

XX PF 24-OCT-2002; 2002WO-US034376.

XX PR 24-OCT-2001; 2001US-0345106P.

XX PR 14-JAN-2002; 2002US-0348962P.

XX PR 07-FEB-2002; 2002US-0354966P.

XX PR 13-AUG-2002; 2002US-0403364P.

XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.
XX Zhang G, Shu H, Liu Y, Xu L,

DR WPI; 2003-403345/38.
XX
XX Novel TALL-1 antagonist protein useful for inhibiting TALL-1 biological
PT activity in mammal, has a modification in the region connecting beta
PT strands D and E that reduces the biological activity of TALL-1
PT antagonist.
PS
XX Disclosure; Page 616; 618pp; English.
XX
XX The invention relates to a novel TALL-1 antagonist protein, comprising a
CC sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID
CC NO:2, by at least one modification in the region connecting abgq; strands
CC D and E that reduces the biological activity of the TALL-1 antagonist as
CC compared to wild-type TALL-1. A protein of the invention has
CC immunosuppressive, antinephritic, antiinflammatory, antidiabetic,
CC dermatological, antidiabetic, neuroprotective, antihypertrophic, antiproliferative,
CC nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in
CC a vaccine. A protein of the invention is useful for inhibiting TALL-1
CC biological activity in a mammal. It is useful for treating autoimmune
CC diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin
CC dependent diabetes mellitus, multiple sclerosis, myasthenia gravis,
CC Grave's disease, autoimmune hemolytic anaemia, autoimmune
CC thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris,
CC acute rheumatic fever, post-streptococcal glomerulonephritis and
CC polyarteritis nodosa. The present sequence represents a cysteine rich
CC domain (CRD) module of human BCMA.
XX
SQ Sequence 34 AA;
Query Match 100.0%; Score 201; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 3e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CSQNEYFDSLHACIPCOLRCSNTPTTCORYC 34
DB 1 CSQNEYFDSLHACIPCOLRCSNTPTTCORYC 34
RESULT 3
AD267761
ID AD267761 standard; protein; 40 AA.
AC AD267761;
XX
XX 14-JUL-2005 (first entry)
XX
DE Human tumor necrosis factor receptor BCMA Cys-rich domain.
XX
XX Tumor necrosis factor receptor; BCMA; cancer; neoplasm; diagnosis;
KW cytostatic.
XX
XX Homo sapiens.
XX
XX WO2005037865-A2.
XX
XX 28-APR-2005.
XX
XX 18-OCT-2004; 2004WO-US034375.
XX
XX 16-OCT-2003; 2003US-0511698P.
XX
XX 18-OCT-2004; 2004US-0615552P.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX
XX Fox BA, Holloway JL, Sheppard PO, Dillon SR;
XX
XX WPI; 2005-315682/32.
XX
XX New tumor necrosis factor receptor (TNFR) polypeptides, useful as
PT detecting ligands, and for modulating tumor growth, metastasis and
PT immunity, such as separating resting from stimulated immune cells.
XX
XX Disclosure; SEQ ID NO 9; 132pp; English.

XX
XX The invention provides novel tumor necrosis factor receptor zntfr14
CC polynucleotides AD267753 and polypeptides AD267754, expression vectors
CC and antibodies. Zntfr14 polynucleotides are used in claimed methods for
CC detecting a genetic abnormality in a patient and for detecting a cancer
CC in a patient. Recombinant zntfr14 polypeptide, optionally conjugated to a
CC toxin, is used in a claimed method of killing cancer cells. Zntfr14
CC polypeptides can be used to detect ligands, agonists and antagonists. The
CC polypeptides, polynucleotides and antibodies may also be used in methods
CC that modulate tumor growth, metastasis, and immunity such as separating
CC resting from stimulated immune cells. The present sequence is that of the
CC Cys-rich domain of human TNFR BCMA AD267760. This sequence was compared
CC with that of zntfr14 in the identification of zntfr14 as a member of the
CC TNFR family.
XX
SQ Sequence 40 AA;
Query Match 100.0%; Score 201; DB 9; Length 40;
Best Local Similarity 100.0%; Pred. No. 3.5e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CSQNEYFDSLHACIPCOLRCSNTPTTCORYC 34
DB 3 CSQNEYFDSLHACIPCOLRCSNTPTTCORYC 36
RESULT 4
AAE15485
ID AAE15485 standard; peptide; 51 AA.
XX
XX AAE15485;
XX
XX 12-MAR-2002 (first entry)
XX
DE Human B-cell maturation (BCMA) protein extracellular domain.
XX
XX
XX Human; transmembrane activator and intracellular CAML interactor; TAC1;
KW cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis.
XX
XX Homo sapiens.
XX
XX WO200187979-A2.
XX
XX 22-NOV-2001.
XX
XX 14-MAY-2001; 2001WO-US015567.
XX
XX 12-MAY-2000; 2000US-0204039P.
XX
XX 27-JUN-2000; 2000US-0214591P.
XX
XX 14-MAY-2001; 2001US-00214591.
XX
XX (AMGEN-) AMGEN INC.
XX
XX
XX Theill LE, Yu G;
XX
XX WPI; 2002-066686/09.
XX
XX
XX Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor family
PT ligand.
XX
XX Claim 1; Fig 10A; 94pp; English.
XX
XX The invention relates to a method for inhibiting TAC1 (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering a

CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human BCMA protein extracellular domain

XX Sequence 51 AA:

Query Match 100.0%; Score 201; DB 5; Length 51;
 Best Local Similarity 100.0%; Pred. No. 4.5e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSQNEYPDSLHACIPCOLRCSNTPPTCORXC 34
 Db 5 CSQNEYPDSLHACIPCOLRCSNTPPTCORXC 38

RESULT 5
 AEC02032
 ID AEC02032 standard; peptide; 52 AA.

XX AEC02032;
 AC
 XX
 DT 20-OCT-2005 (first entry)
 XX
 DE Amino acid sequence of an extracellular domain of BCMA.

XX APRIL; BAF; immune disorder; immunomodulator; antiinflammatory; cancer;
 KW cytostatic; neoplasm; immunosuppressive; therapeutic;
 KM B-cell maturation antigen; BCMA.

XX Synthetic.
 OS
 XX WO2005075511-A1.

XX 18-AUG-2005.
 PD
 XX 04-AUG-2004; 2004WO-US025247.
 PF
 XX 29-JAN-2004; 2004US-0540271P.
 FR
 XX (GETH) GENENTECH INC.
 PA
 XX
 PI Kelley RF, Patel D;
 PI
 XX WPI; 2005-555932/56.

XX New polypeptides that inhibit APRIL and/or BAF binding to BCMA, useful
 PT for treating immune-related disease, cancer or T-cell mediated disease
 PT such as graft rejection, graft versus host disease (GVHD) and
 PT inflammation.

XX Disclosure; SEQ ID NO 21; 140pp; English.

XX The specification describes polypeptides that bind APRIL or BAF. The
 CC polypeptides inhibit APRIL or BAF binding to B-cell maturation antigen
 CC (BCMA). APRIL and BAF are tumor necrosis factor (TNF) members. The
 CC polypeptides of the invention are useful for treating immune-related
 CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
 CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
 CC sclerosis; or T-cell mediated disease such as graft rejection, graft
 CC versus host disease (GVHD) and inflammation. The present sequence

CC represents an extracellular domain of BCMA.

XX Sequence 52 AA;
 SQ

Query Match 100.0%; Score 201; DB 9; Length 52;
 Best Local Similarity 100.0%; Pred. No. 4.5e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSQNEYPDSLHACIPCOLRCSNTPPTCORXC 34
 Db 8 CSQNEYPDSLHACIPCOLRCSNTPPTCORXC 41

RESULT 6
 AAE15501
 ID AAE15501 standard; peptide; 58 AA.

XX AAE15501;
 AC
 XX
 DT 12-MAR-2002 (first entry)
 DT
 XX
 DE Human B cell maturation protein cysteine rich extracellular region.

XX Human, transmembrane activator and intracellular CAML interactor; TACI;
 KW cytostatic; B cell maturation protein; BCMA; tumor necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis.

XX Homo sapiens.
 OS
 XX
 XX WO200187979-A2.
 PN
 XX
 PD 22-NOV-2001.

XX 14-MAY-2001; 2001WO-US015567.
 PF
 XX 12-MAY-2000; 2000US-0204039P.
 PR 27-JUN-2000; 2000US-0214591P.
 PR 14-MAY-2001; 2001US-00214591.
 PR
 XX (AMGE-) AMGEN INC.
 PA
 XX
 PI Theill LB, Yu G;
 PI
 XX WPI; 2002-066686/09.

XX Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor family
 PT ligand.

XX Disclosure; Fig 13; 94pp; English.

XX The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering a
 CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,

CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human BCMA cysteine-rich extracellular region
XX
SQ Sequence 58 AA;
Query Match 100.0%; Score 201; DB 5; Length 58;
Best Local Similarity 100.0%; Pred. No. 5,1e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCORXC 34
1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCORXC 34
Db 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCORXC 34
RESULT 7
AAE15484
ID AAE15484 standard; protein; 181 AA.
XX
AC AAE15484;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human B-cell maturation (BCMA) protein.
XX
KW Human; transmembrane activator and intracellular CAML interactor; TACI;
KW cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 5..38 /note= "Cysteine-rich consensus region; This is region is
FT specifically claimed as SEQ ID NO: 7 in claim 1 of the
FT specification"
FT 52..72
FT Domain /label= Transmembrane_domain
FT WO200187979-A2.
XX
PD 22-NOV-2001.
XX
PF 14-MAY-2001; 2001WO-US015567.
XX
XX 12-MAY-2000; 2000US-0204039P.
PR 27-JUN-2000; 2000US-0214591P.
PR 14-MAY-2001; 2001US-00214591.
XX
PA (AMGE-) AMGEN INC.
XX
PI Theell IE, Yu G;
XX
DR WPI; 2002-066666/09.
XX
PT Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor family
PT ligand.
XX
PS Disclosure; Fig 10A; 94pp; English.
XX
XX The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering a
CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region

CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human BCMA protein
XX
SQ Sequence 181 AA;
Query Match 100.0%; Score 201; DB 5; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCORXC 34
1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCORXC 34
Db 5 CSQNEYPDSLHACIPCOLRCSSNTPPLTCORXC 38
RESULT 8
AAB08843
ID AAB08843 standard; peptide; 184 AA.
XX
AC AAB08843;
XX
DT 02-JAN-2001 (first entry)
XX
DE Amino acid sequence of human.
XX
KW BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer;
KW anti-cell death gene; apoptosis; viral infection; inflammatory response;
KW rheumatoid arthritis; inflammatory bowel disease; septic shock.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 57..77 /note= "putative transmembrane domain"
FT Domain
FT WO200050633-A1.
XX
PD 31-AUG-2000.
XX
PF 24-FEB-2000; 2000WO-US004925.
XX
XX 24-FEB-1999; 99US-0121485P.
PR
XX (GEHO) GEN HOSPITAL CORP.
XX
PA Seed B, Ting A;
XX
PI WPI; 2000-558405/51.
XX
DR
XX
PT Identifying a modulator of gene expression for drug designing, by
PT contacting a compound library with a cell expressing an anti-cell death
PT gene and reporter gene, and determining alteration in reporter gene
PT expression.
XX
PS Claim 32; Fig 7A; 53pp; English.
XX
XX The present sequence represents a BCMA (not defined) polypeptide. BCMA is
CC a necrosis factor (NF)-kB activator. The method of the invention is used
CC to identify compounds which modulate BCMA activity (and thus NF-kB
CC activity). The specification describes a method of identifying a
CC polypeptide which increases gene expression from a promoter. The method
CC involves contacting a library of with a cell which expresses a
CC recombinant anti-cell death gene and a reporter gene operably linked to

CC the promoter, and then determining whether the expression of the reporter
CC gene is altered as a result of contact with library. The method is useful
CC for identifying polypeptides which increase or decrease gene expression
CC from a promoter. The BCMA polypeptide or nucleic acid are useful for
CC preparing a pharmaceutical composition for treating cancer, apoptosis,
CC viral infections, inflammatory response, such as rheumatoid arthritis,
CC inflammatory bowel disease or septic shock. BCMA is useful for
CC identifying compounds that modulate NF- κ B expression and thus for drug
CC designing

SO Sequence 184 AA;

Query Match 100.0%; Score 201; DB 3; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSONEYPDSLHACIPCOLRCSSNTPPLTCORYC 34
Db 8 CSONEYPDSLHACIPCOLRCSSNTPPLTCORYC 41
|||||

RESULT 9
ID AAY94001 standard; protein; 184 AA.
XX AAY94001;
XX 20-OCT-2000 (first entry)
XX A human BCMA protein, a B cell protein related to TACI.
XX Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
XX transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
XX ztnf4 activity; antibody production; autoimmune disease; amyloidosis;
XX systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
XX rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
XX end stage renal failure; glomerulonephritis; vasculitis; nephritis;
XX renal neoplasia; multiple myeloma; lymphoma; light chain neuropathy;
XX immune response; immunosuppression; graft rejection; joint pain;
XX graft versus host disease; inflammation; swelling; anaemia; septic shock;
XX insulin dependent diabetes mellitus; Crohn's disease; hypertension;
XX renal artery stenosis; occlusion; cholesterol; renal emboli.
XX Homo sapiens.
XX MO200040716-A2.
XX 13-JUL-2000.
XX 07-JAN-2000; 2000MO-US000396.
XX 07-JAN-1999; 99US-00226533.
XX (ZYMO) ZYMOGENETICS INC.
XX Gross JA, Xu W, Madden K, Yee DP;
XX WPI; 2000-452538/39.
XX N-PSDB; AAA58559.
XX Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,
XX renal disease, graft versus host disease, and inflammation, comprises
XX administering a BR43x2, TACI or BCMA extracellular domain polypeptide.
XX Disclosure; Page 152; 175pp; English.
XX The present sequence represents a human BCMA protein, a B cell protein
XX related to transmembrane activator and CAML-interactor (TACI) receptor.
XX TACI is a tumour necrosis factor (TNF) receptor. The extracellular
XX domains of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell
XX protein) receptor contain a cysteine rich domain, and are used for
XX inhibiting ztnf4 activity. Ztnf4 is a TNF ligand. They may also be used
XX for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated

CC with activated or resting B lymphocytes, effector T-cells, or with
CC antibody production. The antibody production is associated with an
CC autoimmune disease selected from systemic lupus erythematosus, myasthenia
CC gravis, multiple sclerosis and rheumatoid arthritis. The ztnf4 activity
CC and BR43x2, TACI or BCMA receptor-ligand engagement is associated with
CC asthma, bronchitis, emphysema, end stage renal failure,
CC glomerulonephritis, vasculitis, nephritis, pyelonephritis, renal
CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy,
CC amyloidosis, moderating immune response, immunosuppression, graft
CC rejection, graft versus host disease, inflammation, insulin dependent
CC diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or
CC septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies,
CC agonists or antagonists can be used to treat hypertension, renal artery
CC stenosis, or occlusion, and cholesterol or renal emboli

SO Sequence 184 AA;

Query Match 100.0%; Score 201; DB 3; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSONEYPDSLHACIPCOLRCSSNTPPLTCORYC 34
Db 8 CSONEYPDSLHACIPCOLRCSSNTPPLTCORYC 41
|||||

RESULT 10
ID AAE09241 standard; protein; 184 AA.
XX AAE09241;
XX 19-NOV-2001 (first entry)
XX Human BCMA protein.
XX Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;
XX TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
XX autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.
XX Homo sapiens.
XX WO200160397-A1.
XX 23-AUG-2001.
XX 28-NOV-2000; 2000MO-US032378.
XX 16-FEB-2000; 2000US-0182938P.
XX 22-AUG-2000; 2000US-0226986P.
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ, Dodge KH, Grewal I, Kim KU, Marsters SA, Picti RM;
XX Yan W;
XX WPI; 2001-541628/60.
XX N-PSDB; AAD15902.
XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
XX activity, for treating autoimmune disorders and cancer, comprises
XX exposing the cells to TALL-1 or APRIL polypeptide agonists or
XX antagonists.
XX Example 2; Fig 2; 160pp; English.
XX The invention relates to methods of using one or more agonists or
XX antagonists to modulate the activity of the members of TNF (tumour
XX necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g.
XX TACI or BCMA. The method is useful for treating pathological conditions
XX or diseases associated with increased TALL-1 and APRIL expression or
XX activity. TALL-1 and APRIL antagonists are used to block the interaction
XX between APRIL and TALL-1 with TACI or BCMA. They are useful for treating

CC a mammal suffering from cancer such as leukaemia, lymphoma, myeloma,
CC cancers of lung and colon and autoimmune diseases e.g. rheumatoid
CC arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The
CC present sequence is human BCMA protein

XX Sequence 184 AA;

Query Match 100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 34
|||
Db 8 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 11

AAV71979 standard; protein; 184 AA.

AC AAV71979;

DT 28-MAR-2001 (first entry)

XX Human B cell maturation factor (BCMA) protein.

XX Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
XX Tumour necrosis factor and Apol-related leucocyte expressed ligand 1;
XX therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
XX systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
XX thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
XX haemolytic anaemia; Grave's disease; myasthenia gravis; chromosome 16;
XX post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;
XX B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.

OS Homo sapiens.

XX Key Location/Qualifiers

XX Domain 1..62 /label= Extracellular_domain

XX WO200068378-A1.

XX 16-NOV-2000.

XX 05-MAY-2000; 2000WO-US012266.

XX 06-MAY-1999; 99US-0132892P.

XX 01-MAY-2000; 2000US-0201012P.

XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.

XX Shu HS;

XX WPI; 2001-016094/02.

XX N-PSDB; AAD02125.

XX Isolated TALL-1 protein is used to identify compounds that regulate B
XX lymphocyte proliferation, used to treat B lymphocyte associated
XX autoimmune disorders.

XX Claim 37; Page 104-105; 112pp; English.

XX The present invention relates to Tumour necrosis factor (TNF) and Apol-
XX related leucocyte expressed ligand 1 (TALL-1) nucleic acid molecules, in
XX proteins (including homologues), and their antibodies. The invention in
XX particular relates to methods for regulating the interaction between TALL
XX -1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to
XX regulate monocyte, macrophage and B lymphocyte mediated immune responses.
XX TALL-1 protein is useful for identifying compounds that regulate B
XX lymphocyte proliferation. It is also useful for treating B lymphocyte
XX associated autoimmune disorders like rheumatoid arthritis, systemic lupus
XX erythematosus (SLE), insulin dependent diabetes mellitus, multiple

CC sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome,
CC pemphigus vulgaris, acute rheumatic fever, post-streptococcal
CC glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its
CC corresponding nucleic acid sequence are also useful in diagnostic assays.
CC The present sequence is a human B cell maturation factor (BCMA) protein.
CC It is the receptor for TALL-1 protein. BCMA gene is located on chromosome
CC 16. In human tissues, BCMA is expressed by spleen and lymph nodes but not
CC by brain, muscle, heart, lung, kidney, pancreas, testis and placenta.
CC BCMA mRNA is absent in the pro-B lymphocyte stage but its expression
CC increases with B lymphocyte maturation

XX Sequence 184 AA;

Query Match 100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 34
|||
Db 8 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 12

AAAB60698 standard; protein; 184 AA.

XX AAB60698;

DT 22-MAY-2001 (first entry)

XX Human BAFF receptor (BAFF-R).

XX Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
XX immune-related disorder; B-cell growth inhibitor; BCMA;
XX B-cell maturation inhibitor; immunoglobulin production inhibitor;
XX autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
XX renal disorder; immunosuppressive disorder; HIV infection;
XX organ transplantation; antiinflammatory; systemic lupus erythematosus;
XX autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
XX B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
XX lymphoma; gene therapy; cancer; tumour.

XX Homo sapiens.

XX WO200112812-A2.

XX 22-FEB-2001.

XX 16-AUG-2000; 2000WO-US022507.

XX 17-AUG-1999; 99US-0149378P.

XX 11-FEB-2000; 2000US-0181684P.

XX 18-FEB-2000; 2000US-0183536P.

XX (BIOJ) BIOGEN INC.

XX (APOT-) APOTEC R & D SA.

XX Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;

XX Thompson J;

XX Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
XX lympho-proliferative disorder by administering BAFF-receptor polypeptide,
XX chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.

XX Claim 20; Fig 1; 59pp; English.

XX The invention relates to the use of a BAFF receptor (BAFF-R, also known
XX as BCMA) protein, or a BAFF-R fusion protein as an agent for the
XX treatment of a variety of immune-related disorders. BAFF-R is a member of

PT Novel isolated human tumor necrosis factor receptor polypeptide, termed
PT Ztnfr12, useful for treating autoimmune disorders, emphysema, end stage
PT renal failure or renal disease and lymphoma.

PS Disclosure: Page 135-136; 154pp; English.

XX
XX The present invention describes a human tumour necrosis factor receptor
CC designated Ztnfr12 (1). (1) has cytoprotective, immunosuppressive,
CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
CC antirheumatic, antiarthritic, antiaslathmic, nephrotropic and hypotensive
CC activities, and can be used in gene therapy. (1) can be used for
CC inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12
CC (e.g. ZTNF4), for treating disorders and diseases associated with B
CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
CC inhibiting the proliferation of tumour cells. (1) is useful for treating
CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
CC leukaemia, nephritis, and pyelonephritis, and for treating renal
CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
CC amyloidosis, hypertension, large vessel diseases, graft-versus host
CC disease, graft rejection and Crohn's disease. (1) is useful for
CC modulating the immune system, for regulating B cell responses and
CC development, for modulating development of other cells, antibody
CC production and cytokine production, and for modulating T and B cell
CC communication. The present sequence represents a protein which is given
CC in the exemplification of the present invention

XX Sequence 184 AA:

Query Match 100.0%; Score 201; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCORYC 34
DB 8 CSQNEYPDSLHACIPCOLRCSSNTPPLTCORYC 41

RESULT 15

ID ABP54694 standard; protein; 184 AA.

XX ABP54694;

XX 30-DEC-2002 (first entry)

DE Metastatic colorectal cancer-associated polypeptide.

KW Colorectal cancer; metastasis; differential expression; cytostatic;
KM diagnosis; gene therapy; vaccine.

XX Homo sapiens.

XX WO200268677-A2.

XX 06-SEP-2002.

XX 27-FEB-2002; 2002WO-US006001.

XX 27-FEB-2001; 2001US-0272206P.

XX 02-APR-2001; 2001US-0281149P.

XX 17-APR-2001; 2001US-0284555P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

XX (UYCA-) UNIV CASE WESTERN RESERVE.

XX Mack DH, Markowitz SD;
XX WPI: 2002-698677/75.
XX N-PSDB; AB081560.

PT New genes that are up- or down-regulated in colorectal cancer, useful for
PT diagnosing colorectal cancer in a subject, or for identifying modulators
PT of colorectal cancer-associated proteins and genes for treating
PT colorectal cancer.

PS Claim 8; Page 255; 260pp; English.

XX
XX The present sequence is the protein sequence of a human polypeptide
CC encoded by a gene that exhibits decreased expression in colon cancer-
CC derived metastases compared to normal colon tissue. It is an example of
CC claimed polypeptides that are encoded by genes which are differentially
CC expressed in metastatic colorectal cancer cells. Such polypeptides are
CC useful in diagnostic and prognostic assays, for raising antibodies useful
CC e.g. in immunotherapy, and in screening for modulator compounds of
CC therapeutic value

XX Sequence 184 AA:

Query Match 100.0%; Score 201; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCORYC 34
DB 8 CSQNEYPDSLHACIPCOLRCSSNTPPLTCORYC 41

RESULT 16

ID AAE28961 standard; protein; 184 AA.

XX AAE28961;

XX 27-JAN-2003 (first entry)

DE Human B-cell maturation antigen (BCMA).

XX Human; tumour; B-cell maturation antigen; transmembrane activator;
KW calcium-modulator; cyclophilin ligand-interactor; TACI; gene therapy;
KW neoplasm; chronic lymphocytic leukaemia; lymphoproliferative disease;
KW non-Hodgkin's lymphoma; light chain gammopathy; inflammation; asthma;
KM BCMA; multiple myeloma.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 1..54 /note= "Antigenic epitope"

FT Domain 1..48 /note= "Extracellular domain"

FT Region 8..41 /note= "Cysteine rich region"

XX WO200266516-A2.

XX 29-AUG-2002.

XX 06-FEB-2002; 2002WO-US003500.

XX 20-FEB-2001; 2001US-0270274P.

XX 12-APR-2001; 2001US-0283447P.

XX (ZYMO) ZYMOGENETICS INC.

XX Kindvogel W;

XX WPI: 2002-723183/78.

XX N-PSDB; AAD46410.

XX B-cell maturation antigen and transmembrane activator and calcium-
PT modulator and cyclophilin ligand-interactor, useful for treating
PT disorders e.g. inflammation or lymphoma.

PS Disclosure; Page 63; 67pp; English.

XX The invention relates to the manufacture of a composition for inhibiting
CC the proliferation of tumour cells. The method involves using an antibody
CC component that binds both the B-cell maturation antigen (BCMA) and the
CC transmembrane activator and calcium-modulator and cyclophilin ligand-
CC interactor (TACI). BCMA and TACI binding antibody compositions are useful
CC for inhibiting proliferation of tumour cells, particularly inhibiting
CC ZTNF4 activity in a mammal associated with increased endogenous antibody
CC production or a disorder consisting of neoplasm, chronic lymphocytic
CC leukaemia, multiple myeloma, non-Hodgkin's lymphoma, post-transplantation
CC lymphoproliferative disease or light chain gammopathy or inflammation
CC e.g. asthma. The invention is also useful in gene therapy. The present is
CC human BCMA protein

XX Sequence 184 AA;

SQ

Query Match 100.0%; Score 201; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 34
DB 8 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 41
|||||

RESULT 17
AAE35216
ID AAE35216 standard; protein; 184 AA.

XX AAE35216;
AC
XX 28-MAY-2003 (first entry)
DT
XX Human B-cell maturation receptor (BCMA) protein.

XX Transmembrane activator; calcium modulator; nephrotropic; antibacterial;
KW TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;
KW anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive;
KW glomerulonephritis; asplenia; bronchitis; graft rejection; septic shock;
KW dermatological; neuroprotective; cyclophilin ligand-interactor; human;
KW autoimmune disease; systemic lupus erythematosus; multiple sclerosis;
KW diabetes mellitus; rheumatoid arthritis; renal disease; inflammation;
KW B-cell maturation receptor; BCMA; receptor.

XX Homo sapiens.
OS
XX WO200294852-A2.
PN
XX 28-NOV-2002.
PD
XX 20-MAY-2002; 2002WO-US015910.
PF
XX 24-MAY-2001; 2001US-0293343P.
PR
XX (ZYMO) ZYMOGENETICS INC.
PA
XX Rixon MW, Gross JA;
PI
XX WPI: 2003-148455/14.
DR
XX N-PSDB; AAD53754.

XX Transmembrane activator and calcium modulator and cyclophilin ligand-
PT interactor (TACI)-immunoglobulin fusion protein, for treating cancer or
PT diabetes, comprises a TACI receptor group and an immunoglobulin group.
XX
XX Disclosure: Col 100; 71pp; English.

XX The invention relates to fusion proteins comprising transmembrane
CC activator and calcium modulator and cyclophilin ligand-interactor (TACI)
CC receptor group that binds tumour necrosis factor-like protein (ZTNF2) or
CC ZTNF4; and an immunoglobulin group comprising a constant region of an
CC immunoglobulin. The invention is used to manufacture a medicament for

CC inhibiting the proliferation of tumour cells in a mammalian subject. The
CC composition comprising the fusion protein may also be used in treating
CC autoimmune diseases (e.g. systemic lupus erythematosus, multiple
CC sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal
CC diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft
CC rejection, anaemia and septic shock. The fusion proteins are also used in
CC gene therapy. The present sequence is human B-cell maturation receptor
CC (BCMA) protein used in the invention

XX Sequence 184 AA;

SQ

Query Match 100.0%; Score 201; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 34
DB 8 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 41
|||||

RESULT 18
ADA49361
ID ADA49361 standard; protein; 184 AA.

XX ADA49361;
AC
XX 20-NOV-2003 (first entry)
DT
XX Human BCMA protein.

XX human; TALL-1; antagonist; immunosuppressive; antirheumatic;
KW antinflammatory; antiarthritic; dermatological; antidiabetic;
KW neuroprotective; antihypertoid; antipyretic; nephrotropic; vasotropic;
KW vaccine; autoimmune disease; rheumatoid arthritis;
KW systemic lupus erythematosus; insulin dependent diabetes mellitus;
KW multiple sclerosis; myasthenia gravis; Grave's disease;
KW Goodpasture's syndrome; pemphigus vulgaris; acute rheumatic fever;
KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA.

XX Homo sapiens.
OS
XX WO2003035846-A2.
PN
XX 01-MAY-2003.
PD
XX 24-OCT-2002; 2002WO-US034376.
PF
XX 24-OCT-2001; 2001US-0345106P.
PR
XX 14-JAN-2002; 2002US-0348962P.
PR
XX 07-FEB-2002; 2002US-0354966P.
PR
XX 13-AUG-2002; 2002US-0403364P.

XX (NME-) NAT JEWISH MEDICAL & RES CENT.
PA
XX Zhang G, Shu H, Liu Y, Xu L;
PI
XX WPI: 2003-403345/38.
DR
XX N-PSDB; ADA49360.

XX Novel TALL-1 antagonist protein useful for inhibiting TALL-1 biological
PT activity in mammal, has a modification in the region connecting beta
PT strands D and E that reduces the biological activity of TALL-1
PT antagonist.

XX
XX Claim 62; Page 613; 618pp; English.

XX The invention relates to a novel TALL-1 antagonist protein, comprising a
CC sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID
CC NO:2, by at least one modification in the region connecting E&G; strands
CC D and E that reduces the biological activity of the TALL-1 antagonist as
CC compared to wild-type TALL-1. A protein of the invention has
CC immunosuppressive, antirheumatic, antiinflammatory, antiarthritic,

CC dermatological, antidiabetic, neuroprotective, antihypoid, antipyretic,
CC nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in
CC a vaccine. A protein of the invention is useful for inhibiting TALL-1
CC biological activity in a mammal. TC is useful for treating autoimmune
CC diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin
CC dependent diabetes mellitus, multiple sclerosis, myasthenia gravis,
CC Grave's disease, autoimmune hemolytic anaemia, autoimmune
CC thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris,
CC acute rheumatic fever, post-streptococcal glomerulonephritis and
CC polyarthritis nodosa. The present sequence represents human BCMA.

SQ Sequence 184 AA;

Query Match 100.0%; Score 201; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCORYC 34
DB 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCORYC 41

RESULT 19

ABR40082 standard; protein; 184 AA.

AC ABR40082;

DT 27-JUN-2003 (first entry)

DE Human Genoxit.

Human; genoxit; anorectic; antilipemic; antiarteriosclerotic; cardiac;
antidiabetic; hypotensive; ophthalmological; neuroprotective;
neurotropic; obesity; Tumour Necrosis Factor Receptor Super Family;
Type III transmembrane protein; insulin resistance; atherosclerosis;
atheromatous disease; heart disease; hypertension; stroke; syndrome X;
diabetes mellitus; hyperlipidaemia; hyperuricaemia.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Domain 1..54 /label= Extracellular_domain

FT Misc-difference 3 /label= Gln, Lys

FT Domain 55..77 /label= Transmembrane_domain

FT Domain 78..184 /label= Intracellular_domain

FT Domain /label= Intracellular_domain

FT Domain /label= Intracellular_domain

FT Domain /label= Intracellular_domain

FT Domain /label= Intracellular_domain

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FT Domain /label= Intracellular_domain

FT Domain /label= Intracellular_domain

CC Genoxit activity for preventing or treating obesity. Genoxit is a member
CC of the Tumour Necrosis Factor Receptor Super Family and is a Type III
CC transmembrane protein. The agonists or antagonists of the invention are
CC useful for treating or preventing obesity-related diseases or disorders.
CC e.g. obesity, insulin resistance, atherosclerosis, atheromatous disease,
CC heart disease (e.g. cardiac insufficiency, coronary insufficiency, high
CC blood pressure), hypertension, stroke, syndrome X, diabetes mellitus
CC (type I and II), hyperlipidaemia and hyperuricaemia, also diabetic
CC complications, e.g. microangiopathic lesions, ocular lesions,
CC retinopathy, neuropathy and renal lesions

SQ Sequence 184 AA;

Query Match 100.0%; Score 201; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCORYC 34
DB 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCORYC 41

RESULT 20

ABP60552 standard; protein; 184 AA.

AC ABP60552;

DT 28-MAR-2003 (first entry)

DE Human tumour necrosis factor BCMA.

APRIL; scFv; immunospecific; tumour necrosis factor delta; TNF-delta;
dermatological; immunosuppressive; antiinflammatory; antihematic;
antiarthritic; cytoprotective; antianemic; antifibrotic; antiaesthetic;
neuroprotective; ophthalmological; tuberculostatic; antidiabetic;
antipsoriatic; anti-HIV; antiarteriosclerotic; vasotropic; thyromimetic;
haemostatic; cancer; autoimmune disease; graft versus host disease; GVHD;
inflammatory disorder; proliferative disorder; single chain antibody;
antibody; human; BCMA; tumour necrosis factor.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Domain 1..54 /label= Extracellular_domain

FT Misc-difference 3 /label= Gln, Lys

FT Domain 55..77 /label= Transmembrane_domain

FT Domain 78..184 /label= Intracellular_domain

FT Domain /label= Intracellular_domain

FT Domain /label= Intracellular_domain

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FT Domain /label= Intracellular_domain

FT Domain /label= Intracellular_domain

The invention relates to a novel antibody or its fragment, which
immunospecifically binds tumour necrosis factor delta (TNF-delta/APRIL).
The antibody of the invention has dermatological, immunosuppressive,
antiinflammatory, antitumour, antiarthritic, cystostatic, antianemic,
antiallergic, antiaesthetic, neuroprotective, ophthalmological,
tuberculostatic, antidiabetic, antipsoriatic, anti-HIV,
antiarteriosclerotic, vasotropic, thyromimetic, and haemostatic activity.
The antibody or its fragment are useful for treating, preventing or
ameliorating cancer such as Non-Hodgkin's lymphoma or multiple myeloma in

CC human, disease or disorder such as autoimmune disease, and graft versus
CC host disease (GVD). The autoimmune disease is systemic lupus
CC erythematosus, rheumatoid arthritis or Sjogren's syndrome. The antibody
CC is useful for detecting, diagnosing, prognosing, treating, preventing or
CC ameliorating a disease or disorder associated with aberrant APRIL or
CC APRIL receptor expression or aberrant function of APRIL or APRIL
CC receptor. The disease or disorders includes autoimmune and inflammatory
CC disorders such as autoimmune neutropenia, haemolytic anaemia, dermatitis,
CC asthma, allergic encephalomyelitis, myocarditis, multiple sclerosis,
CC uveitis, tuberculosis, diabetes mellitus, psoriasis, cancer of the immune
CC system, particularly B cell cancers, immune disorders such as myasthenia
CC gravis, Hashimoto's disease, immunodeficiency syndrome, Bruton's disease,
CC infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS)), and
CC proliferative disorders (e.g. leukemia). The present sequence represents
CC the tumour necrosis factor BCMA
XX

SQ Sequence 184 AA;

Query Match 100.0%; Score 201; DB 6; Length 184;

Best Local Similarity 100.0%; Pred. No. 1,6e-17; Mismatches 0; Indels 0; Gaps 0;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34
Db 8 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 41

RESULT 21

ID ABP97717 standard; protein; 184 AA.

AC ABP97717;

DT 28-MAY-2003 (first entry)

DE Amino acid sequence of human BCMA receptor.

XX Human; TACI; BR3; receptor; tumour necrosis factor ligand; TNF ligand;
KW TALL-1; APRIL; systemic lupus erythematosus; BCMA.
XX

OS Homo sapiens.

XX WO2003014294-A2.

XX PD 20-FEB-2003.

XX PF 24-JUL-2002; 2002WO-US023487.

XX PR 03-AUG-2001; 2001US-0310114P.

XX PR 30-APR-2002; 2002US-0377171P.

XX PA (GETH) GENENTECH INC.

XX PI Dixit V, Grewal I, Ridgway J, Yan M;

XX DR WPI; 2003-256560/25.

XX DR N-PSDB; ABZ68871.

XX PT New nucleic acid encoding a TACIs or BR3 polypeptide, useful for
XX preparing a composition for treating systemic lupus erythematosus.

XX PS Disclosure; Fig 2; 153pp; English.

XX CC The present sequence represents a human BCMA polypeptide. The
XX specification also describes TACI and BR3 polypeptides. TACI and BR3 are

XX receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and APRIL
XX bind to the TACI receptor, while TNF family ligands TALL-1 also binds to
XX BR3 receptor. The TACI and BR3 receptor nucleic acid is useful for
XX preparing a composition for treating systemic lupus erythematosus

SQ Sequence 184 AA;

Query Match 100.0%; Score 201; DB 6; Length 184;

Best Local Similarity 100.0%; Pred. No. 1,6e-17; Mismatches 0; Indels 0; Gaps 0;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34
Db 8 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 41

RESULT 22

ID ADD67527 standard; protein; 184 AA.

AC ADD67527;

DT 15-JAN-2004 (first entry)

DE Human LY1732P protein SEQ ID NO:4.

XX haematological malignancy; immunocjugate; cytostatic; immunostimulant;
KW vaccine; immunotherapy; cancer; multiple myeloma cell;
KW chronic lymphocytic leukaemia; B cell leukaemia; lymphoma; anti-cancer;
KW human.

XX OS Homo sapiens.

XX WO2003062401-A2.

XX PD 31-JUL-2003.

XX PF 22-JAN-2003; 2003WO-US002353.

XX PR 22-JAN-2002; 2002US-00057475.

XX PA (CORI-) CORIXA CORP.

XX PI Gaiger A, Algate PA, Mannion J, Clapper JD, Wang A, Ordonez N;

XX PI Carter L, McNeill PD;

XX DR WPI; 2003-598749/56.

XX DR N-PSDB; ADD67526.

XX New hematological malignancy-related genes and polypeptides, useful for
XX screening anti-cancer agents, and generating antibodies or
XX immunocjugates for treating e.g. multiple myeloma cell or chronic
XX lymphocytic leukemia.

XX PS Claim 9; SEQ ID NO 4; 307pp; English.

XX CC The present invention describes an isolated polynucleotide (1), which is

XX overexpressed in haematological malignancies, and which encodes a
XX polypeptide or an immunogenic fragment of the polypeptide. Also
XX described: (1) an isolated polypeptide; (2) an expression vector
XX comprising (1) operably linked to an expression control sequence; (3) a
XX host cell comprising an expression vector; (4) an isolated antibody that
XX specifically binds to the polypeptide or its immunogenic fragment; and
XX (5) immunocjugates comprising the antibody above, or an antibody that
XX specifically binds to a polypeptide, or its immunogenic fragment, encoded
XX by (1). (1) has cytostatic and immunostimulant activities, and can be
XX used in vaccines and immunotherapy. The immunocjugates are useful in
XX the manufacture of a medicament, particularly as active ingredients in a
XX composition for treating cancer, e.g. multiple myeloma cell, chronic
XX lymphocytic leukaemia, B cell leukaemias, or lymphomas in humans, sheep,
XX primates, goats, bovines, equines, porcines, lupines, canines or felines.
XX The polynucleotide (1) or polypeptide can be used for screening anti-
XX cancer agents, and generating antibodies or immunocjugates for treating
XX or preventing the above-mentioned diseases. The polynucleotide,
XX polypeptide or antibody can be used for detecting, diagnosing or
XX prognosticating the haematological malignancies described above. The
XX present sequence is used in the exemplification of the present invention.

SQ Sequence 184 AA;

Query Match 100.0%; Score 201; DB 7; Length 184;

Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
DB 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 23
ADG43715
ID ADG43715 standard; protein; 184 AA.

AC ADG43715;
DT 26-FEB-2004 (first entry)
DE Human B-cell maturation antigen SEQ ID NO.1.
KW human; neurodegenerative immunological disorder; demyelination;
KW Central Nervous System; CNS; inflammation; B-cell maturation antigen;
KW BCMA; multiple sclerosis; neuroprotective; neurotropic; antiinflammatory;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003072713-A2.
XX
PD 04-SEP-2003.
XX
PF 21-FEB-2003; 2003WO-US005147.
XX
PR 21-FEB-2002; 2002US-0358427P.
XX
PA (BIOI) BIOGEN INC.
XX
PI Kalled SL, Reid H;
XX
DR WPI; 2003-721758/68.
XX
N-PSDB; ADG43716.
XX
PT Treating a neurodegenerative immunological disorder, e.g. demyelination
PT or inflammation in a mammal comprises administering a B-cell maturation
PT antigen (BCMA), an antibody against BCMA or a BCMA ligand.
XX
PS Claim 8; Page 68-69; 72pp; English.
XX
CC The invention relates to a novel method for treating a neurodegenerative
CC immunological disorder, demyelination or Central Nervous System (CNS)
CC inflammation in a mammal. The method comprises administering B-cell
CC maturation antigen (BCMA), or an antibody against BCMA or a BCMA ligand
CC (the mammal has or is at risk of developing multiple sclerosis). The
CC method of the invention has neuroprotective, neurotropic, and
CC antiinflammatory activity, and may have a use in gene therapy. The
CC method, BCMA, and antibodies are useful for treating a neurodegenerative
CC immunological disorder such as multiple sclerosis, demyelination or CNS
CC inflammation. The present sequence represents human BCMA.
XX
SQ Sequence 184 AA;

Query Match 100.0%; Score 201; DB 7; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
DB 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 24
ADK00756
ID ADK00756 standard; protein; 184 AA.
XX
AC ADK00756;

XX 06-MAY-2004 (first entry)
DT
XX Native human BCMA.
DE
XX CAML interactor receptor; TACI; Cytostatic; Antiinflammatory;
KW Dermatological; Immunosuppressive; Anti rheumatic; Anti arthritic;
KW Antidiabetic; Neuroprotective; Antiaesthetic; Anti allergic; Anti-HIV;
KW Antibacterial; antiparasitic; systemic lupus erythematosus;
KW diabetes mellitus; AIDS; BCMA.
XX
OS Homo sapiens.
XX
PN WO2004011611-A2.
XX
PD 05-FEB-2004.
XX
PF 25-JUL-2003; 2003WO-US023421.
XX
PR 25-JUL-2002; 2002US-0398530P.
XX
PA (GENH) GENENTECH INC.
XX
PI Chuntcharapai A, Grewal I, Kim KJ, Yan M;
XX
DR WPI; 2004-143841/14.
XX
N-PSDB; ADK00755.
XX
PT New anti-TACI receptor monoclonal antibody, useful for diagnosing and
PT treating pathological conditions associated with tumor necrosis factor,
PT e.g. cancer or immune-related disease, such as rheumatoid arthritis or
PT psoriasis.
XX
PS Disclosure; SEQ ID NO 6; 110pp; English.
XX
CC The present invention relates to an isolated monoclonal antibody which
CC binds to a transmembrane activator of and CAML interactor (TACI)
CC receptor. The TACI antibodies are useful for modulating TALL-1 or TACI
CC polypeptide biological activity in mammalian cells, or for diagnosing and
CC treating pathological conditions associated with TNF and TNF receptor-
CC related molecules, e.g. cancer or immune-related disease, such as
CC systemic lupus erythematosus, rheumatoid arthritis, Sjogren's syndrome,
CC systemic vasculitis, diabetes mellitus, Crohn's disease,
CC glomerulonephritis, multiple sclerosis, psoriasis, aschma, urticaria or
CC infectious diseases including AIDS, hepatitis infection, bacterial
CC infection, fungal infection, protozoal infection and parasitic infection.
XX
SQ Sequence 184 AA;

Query Match 100.0%; Score 201; DB 8; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
DB 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 25
ADQ94442
ID ADQ94442 standard; protein; 184 AA.
XX
AC ADQ94442;
DT 07-OCT-2004 (first entry)
DE Neutrokin-alpha, BCMA.
XX
KW neutrokin-alpha; chelator; B-lymphocyte stimulator; BlyS; TALL-1; THANK;
KW BAF; neutrokin-alpha receptor; complex; metal ion; radiotherapy;
KW B-cell mediated disease; non-Hodgkin's lymphoma;
KW chronic lymphocytic leukaemia; multiple myeloma;

KW systemic lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
KW Crohn's disease; diabetes; Wegener's granulomatosis; myasthenia gravis;
KW asthma; cancer; Sjogren's syndrome; diagnostic imaging; lymphocyte;
KW B cell; cancerous cell; metastasis; lymphatic system.

XX Homo sapiens.

XX WO2004058309-A1.

XX 15-JUL-2004.

XX 22-DEC-2003; 2003WO-US040979.

XX 23-DEC-2002; 2002US-0435262P.

XX 02-MAY-2003; 2003US-0467198P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Parmelee D, Yeh R, Galperina O, Hilbert D, Rosen CA;

XX WPI; 2004-553134/53.

XX N-PSDB; ADO94441.

XX GENBANK; NM_001192.

XX Neutrokine-alpha conjugate useful for targeting complexed metal ion to
PT cells expressing receptor (predominantly lymphoid) for radiotherapy
PT treatment of, for example, non-Hodgkin's lymphoma comprises neutrokine-
PT alpha protein and chelator.

XX Disclosure; SEQ ID NO 9; 228bp; English.

XX This sequence represents neutrokine-alpha, ECMA, which may be used in the
CC protein conjugate of the invention. The neutrokine-alpha protein
CC conjugate comprises neutrokine-alpha protein and chelator, where the
CC neutrokine-alpha protein (also known as B-lymphocyte stimulator (BlyS),
CC TALL-1, THANK and BAPF) is capable of binding neutrokine-alpha receptor
CC and is selected from full length or mature neutrokine-alpha protein. The
CC protein conjugate of the invention is useful in a complex with a metal
CC ion associated with the chelator which is useful for administering
CC radiotherapy to a subject such as human who is in need of radiotherapy,
CC which involves administering the complex to the subject, where it is
CC administered as an injectable solution, and the subject has a B-cell
CC mediated disease. The subject has a condition chosen from non-Hodgkin's
CC lymphoma, chronic lymphocytic leukaemia, multiple myeloma, systemic lupus
CC erythematosus, rheumatoid arthritis, multiple sclerosis, Crohn's disease,
CC diabetes, Wegener's granulomatosis, myasthenia gravis and asthma,
CC preferably non-Hodgkin's lymphoma. The complex is useful for treating
CC cancer, which involves administering it to a subject having cancer, where
CC a cell of the cancer expresses a neutrokine-alpha receptor on its
CC surface. The cancer is a B cell cancer, which is chosen from non-
CC Hodgkin's lymphoma, multiple myeloma and chronic lymphocytic leukaemia.
CC The complex is also useful for treating an autoimmune disease or
CC disorder, chosen from systemic lupus erythematosus, rheumatoid arthritis
CC and Sjogren's syndrome. The complex may also be used for diagnostic
CC imaging. A composition comprising the protein conjugate or the complex is
CC useful for killing a cell chosen from a cell bearing a neutrokine-alpha
CC receptor, and a cell in close proximity to a cell bearing neutrokine-
CC alpha receptor, which involves contacting the cell with the composition
CC to kill the cell. The cell is lymphocyte, B cell or cancerous cell that
CC has been transfected into the lymphatic system.

XX Sequence 184 AA;

XX Query Match 100.0%; Score 201; DB 8; Length 184;

XX Best Local Similarity 100.0%; Pred. No. 1.6e-17;

XX Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 CSONEYPFSLHACTPCQLRGSSNTPPLTCQRYC 34

XX 8 CSONEYPFSLHACTPCQLRGSSNTPPLTCQRYC 41

XX .RESULT 26

ADP56014
ID ADP56014 standard; protein; 184 AA.

XX ADP56014;

XX 18-NOV-2004 (first entry)

XX Human PRO protein sequence SEQ ID NO:1990.

XX human; PRO: immune related disease; inflammatory immune response;
KW antiaesthetic; antidiabetic; antiinflammatory; antipruritic;
KW antineumatic; antithyroid; CNS; dermatological; gastrointestinal;
KW haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular;
KW nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;
KW vitricide; gene therapy.

XX Homo sapiens.

XX WO2004039956-A2.

XX 13-MAY-2004.

XX 28-OCT-2003; 2003WO-US034381.

XX 29-OCT-2002; 2002US-0422472P.

XX (GETH) GENENTECH INC.

XX Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM;

XX Wood WT, Wu TD;

XX WPI; 2004-376182/35.

XX N-PSDB; ADP56013.

XX New PRO polynucleotides and polypeptides, useful in useful in diagnosing
PT and treating an immune related disease, e.g. systemic lupus
PT erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in
PT stimulating an immune response.

XX Claim 1; SEQ ID NO 1990; 3009pp; English.

XX The present invention describes an isolated PRO nucleic acid (1). Also
CC described: (1) a vector comprising (1); (2) a host cell comprising the
CC vector of (1); (3) a process for producing a PRO polypeptides; (4) an
CC isolated PRO polypeptide; (5) a chimeric molecule comprising the
CC polypeptide of (4) fused to a heterologous amino acid sequence; (6) an
CC antibody which specifically binds to a polypeptide of (4); (7) a
CC composition of matter comprising a polypeptide of (4), an agonist or
CC antagonist of the polypeptide or an antibody that binds to the
CC polypeptide in combination with a carrier; (8) an article of manufacture
CC comprising a container, a label on the container and a composition of
CC matter of (7); (9) a method of treating an immune related disease in a
CC mammal; (10) a method for determining the presence of a PRO polypeptide
CC in a sample suspected of having the polypeptide; (11) a method of
CC diagnosing an immune related disease or an inflammatory immune response
CC in mammal; (12) a method of identifying a compound that inhibits or
CC mimics the activity of or expression of a gene encoding a PRO polypeptide
CC ; and (13) a method of stimulating the immune response in a mammal. The
CC PRO sequences have antiallergic, antianemic, antiasthmatic,
CC antiaesthetic, antidiabetic, antiinflammatory, antipruritic,
CC antineumatic, antithyroid, CNS, dermatological, gastrointestinal,
CC haemostatic, hepatotropic, immunostimulant, immunosuppressive, muscular,
CC nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and
CC vitricide activities, and can be used in gene therapy. The nucleic acid
CC (1) and the encoded polypeptides, compositions, kits and methods are
CC useful in diagnosing and treating an immune related disease and in
CC stimulating an immune response. The present sequence represents a human
CC PRO protein from the present invention.

XX Sequence 184 AA;

XX Query Match 100.0%; Score 201; DB 8; Length 184;

| | | | |
|-----------|--|---|--|
| AC | | AEA23348, | |
| XX | DT | 11-AUG-2005 (first entry) | |
| XX | DE | Tumor antigen of hematopoietic origin TAOH23. | |
| XX | KW | Cycostatic; gene therapy; therapy; cell growth; protein purification; | |
| KM | KM | DNA purification; hyperproliferation; neoplasm; | |
| XX | KM | tumor antigen of hematopoietic origin; TAOH23. | |
| OS | | Homo sapiens. | |
| XX | NN | WO2005049075-A2. | |
| PD | | 02-JUN-2005. | |
| PP | | 16-NOV-2004; 2004WO-US038262. | |
| XX | PR | 17-NOV-2003; 2003US-0520842P. | |
| XX | PR | 24-DEC-2003; 2003US-0532426P. | |
| PA | (GETH) GENENTECH INC. | | |
| PI | Crowley C, Desauvage FT, Eaton DL, Ebdens A, Polson A, Smith V, | | |
| DR | WPI; 2005-405198/41. | | |
| XX | N-PSTDB; AEA23347. | | |
| PT | Inhibiting the growth of a cell that expresses a protein by contacting | | |
| PT | the cell with anti-tumor antigens of hematopoietic origin (TAHO) | | |
| PT | polypeptide, antibody or organic molecule, useful for treating | | |
| PT | hematopoietic and malignant tumors. | | |
| PS | Disclosure; SEQ ID NO 46; 367pp; English. | | |
| XX | The invention describes a method of inhibiting the growth of a cell that | | |
| CC | expresses a protein comprising contacting the cell with an antibody, | | |
| CC | oligopeptide or organic molecule that binds to the protein, the binding | | |
| CC | of the antibody, oligopeptide or organic molecule to the protein and | | |
| CC | causing an inhibition of growth of the cell. Also described is a method | | |
| CC | for treating or preventing a cell proliferative disorder associated with | | |
| CC | increased expression or activity of a protein having at least 80 % amino | | |
| CC | acid sequence identity to: a polypeptide having any of SEQ ID NO: 2, 8, | | |
| CC | 10, 12, 16, 20, 22, 49 and 51; a polypeptide having the amino acid | | |
| CC | sequence of (a), lacking its associated signal peptide; an extracellular | | |
| CC | domain of the polypeptide having the amino acid sequence of (a), with or | | |
| CC | without its associated signal peptide; a polypeptide encoded by any of | | |
| CC | SEQ ID NO: 1, 7, 9, 11, 15, 19, 21, 48 and 50; or a polypeptide encoded | | |
| CC | by the full-length coding region of the nucleotide sequence of (d), | | |
| CC | comprising administering to a subject in need of such treatment an | | |
| CC | antagonist of the protein, and effectively treating or preventing the | | |
| CC | cell proliferative disorder. Also disclosed are anti-tumor antigens of | | |
| CC | hematopoietic origin (TAHO) polypeptides, encoding nucleic acids, | | |
| CC | oligopeptidic vectors, host cells and antibodies used in the methods of | | |
| CC | the invention. The methods and compositions of the present invention are | | |
| CC | useful for treating hematopoietic and malignant tumors in mammals. This | | |
| CC | is the amino acid sequence of tumor antigen of hematopoietic origin | | |
| CC | TAOH23. | | |
| XX | | | |
| SQ | Sequence 184 AA; | | |
| | Query Match 100.0%; Score 201; DB 9; Length 184; | | |
| | Best Local Similarity 100.0%; Pred. No. 1.6e-17; | | |
| | Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | |
| OY | 1 CSONEYFDSLHAGTFCQLRCSSNTPPLTCORYC 34 | | |
| | | | |
| Db | 8 CSONEYFDSLHAGTFCQLRCSSNPPLTCORYC 41 | | |
| RESULT 30 | | | |
| AEC02031 | | | |
| ID | AEC02031 standard; protein; 184 AA. | | |

[illegible]

XX Homo sapiens.
OS MO200187979-A2.
XX
XX 22-NOV-2001.
PD
XX 14-MAY-2001; 2001MO-US015567.
XX
XX 12-MAY-2000; 2000US-0204039P.
PR 27-JUN-2000; 2000US-0214591P.
PR 14-MAY-2001; 2001US-00214591.
XX
XX (AMGE-) AMGEN INC.
PA
XX Theell LE, Yu G;
PI
XX WPI; 2002-066686/09.
DR
XX
XX Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor family
PT ligand.
PS Disclosure; Fig 10B; 94pp; English.
XX
XX The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering a
CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human BCMA protein-immunoglobulin Fc region fusion protein
XX
XX Sequence 283 AA:
SQ
Query Match 100.0%; Score 201; DB 5; Length 283;
Best Local Similarity 100.0%; Pred. No. 2,5e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 34
DB 5 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 38
RESULT 32
ABG95060
ID ABG95060 standard; protein; 288 AA.
XX
XX ABG95060;
AC
XX
XX 04-DEC-2002 (first entry)
DT
XX
XX Human translocation (4; 16)(q26; p13) protein.
DE
XX
XX Chromosome aberration; oncogenic fusion protein; cancer;
KM Proliferative disease; cellular protein isoform; heat shock protein 90;
KM HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
KM T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
KM acute myeloid leukaemia; ALL; chronic myelomonocytic leukaemia; CMML;
KM acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;

KM papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
KM rhabdomyosarcoma; synovial sarcoma; viral infection.
XX
XX Homo sapiens.
OS MO200269900-A2.
XX
XX 12-SEP-2002.
PD
XX 01-MAR-2002; 2002MO-US006518.
XX
XX 01-MAR-2001; 2001US-0272751P.
PR
XX (CONF-) CONFORMA THERAPEUTICS CORP.
PA
XX Fritz LC, Burrows FJ;
PI
XX WPI; 2002-698710/75.
DR N-PSDB; ABS73235.
XX
XX Treating genetically-defined disease associated with chromosomal
PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
PT diseases, involves administering an inhibitor of heat shock protein 90.
PS Disclosure; Page 189-190; 389pp; English.
XX
XX The invention describes a method of treating genetically-defined disease
CC associated with chromosomal aberrations yielding oncogenic fusion
CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
CC cell population, treating proliferative diseases associated with mutant
CC protein or cellular protein isoforms (II) dependent on heat shock protein
CC (HSP)-90, or selectively treating cells expressing (II) involving
CC administering HSP90-inhibitor. The method is useful for treating
CC genetically-defined disease with chromosomal aberration yielding
CC oncogenic fusion protein, treating cancerous cells containing fusion
CC protein in heterogeneous cell population, treating proliferative disease
CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
CC p53), or selectively treating cells expressing mutant protein or cellular
CC protein isoform in a patient heterozygous for (II). The method is useful
CC for treating a disease e.g. haematopoietic disorder such as T or B cell
CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,
CC or a disease characterised by a solid tumour such as papillary thyroid
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
CC synovial sarcoma. The method is also useful for treating viral
CC infections. This represents a protein encoded by the DNA sequence of a
CC chromosome aberration
XX
XX Sequence 288 AA:
SQ
Query Match 100.0%; Score 201; DB 5; Length 288;
Best Local Similarity 100.0%; Pred. No. 2,6e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 34
DB 112 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 145
RESULT 33
AAB60699
ID AAB60699 standard; protein; 302 AA.
XX
XX AAB60699;
AC
XX
XX 11-SEP-2003 (revised)
DT 22-MAY-2001 (first entry)
XX
XX Mouse IgG signal/human BAFF-R/human IgG Fc fusion protein, BAFF-R-Fc.
DE
XX
XX Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
KM immune-related disorder; B-cell growth inhibitor;
KM B-cell maturation inhibitor; immunoglobulin production inhibitor;

KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
KW renal disorder; immunosuppressive disorder; HIV infection;
KW organ transplantation; antiinflammatory; systemic lupus erythematosus;
KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
KW lymphoma; gene therapy; cancer; tumour; IgG Fc; fusion construct.
XX
OS Homo sapiens.
OS Mus sp.
OS Chimeric.
XX
PM WO200112812-A2.
XX
PD 22-FEB-2001.
XX
PF 16-AUG-2000; 2000WO-US022507.
XX
PR 17-AUG-1999; 99US-0149378P.
PR 11-FEB-2000; 2000US-0181684P.
PR 18-FEB-2000; 2000US-0183536P.
XX
PA (BIOJ) BIOGEN INC.
PA (APOT-) APOTEC R & D SA.
XX
PI Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P,
PI Thompson J;
XX
DR WPI; 2001-202866/20.
DR N-PSDB; AAF59999.
XX
XX
PT Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
PT lympho-proliferative disorder by administering BAFf-receptor polypeptide,
PT chimeric molecule comprising receptor or anti-BAFf-R antibody homolog.
XX
PS Example 4; Fig 2; 59pp; English.
XX
XX The invention relates to the use of a BAFf receptor (BAFf-R, also known
CC as BCMa) protein, or a BAFf-R fusion protein as an agent for the
CC treatment of a variety of immune-related disorders. BAFf-R is a member of
CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory
CC agent, and also plays a role in the development of hypertension and
CC related disorders. BAFf-R, fusion proteins containing it, and BAFf-R-
CC specific antibodies can be used for inhibiting B-cell growth, dendritic
CC cell-induced B-cell growth and maturation, and immunoglobulin production,
CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative
CC disorders, hypertension and renal disorders. The BAFf-R proteins may also
CC be used in the treatment of immunosuppressive disorders and HIV
CC infection, and in patients undergoing organ transplantation. The BAFf-R
CC proteins or BAFf-R specific antibodies may be used for treating,
CC suppressing or altering an immune response involving a signalling pathway
CC between BAFf-R and BAFf, thereby inhibiting inflammation. Since BAFf-R
CC inhibits B-cell growth and maturation it is useful for treating diseases
CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
CC human BAFf-R may be used in gene therapy to treat tumours, lymphomas,
CC human autoimmune disorders and inherited B-cell-associated disorders. The
CC present sequence represents the BAFf-R fusion protein BAFf-R-Fc,
CC comprising a mouse IgG-kappa signal sequence, residues 1-153 of human
CC BAFf-R and a human IgG Fc sequence. (Updated on 11-SEP-2003 to
CC standardise OS field)
XX
SQ Sequence 302 AA;
XX
Query Match 100.0%; Score 201; DB 4; Length 302;
Best Local Similarity 100.0%; Pred. No. 2,7e-11;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 31 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 64

RESULT 34
AAE00507
ID AAE00507 standard; protein, 302 AA.
XX
AC AAE00507;
XX
DT 11-SEP-2003 (revised)
DT 31-JUL-2001 (first entry)
XX
DE Human BCMa-Immunoglobulin G Fc region fusion construct.
XX
KW Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytotoxic;
KW gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
KW carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
KW systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
KW B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;
KW organ transplantation; HIV; human immunodeficiency virus; TNF; murine;
KW tumour necrosis factor; B cell maturation protein; BCMa; fusion protein;
KW Immunoglobulin G; IgG; Fc region.
XX
OS Homo sapiens.
OS Mus sp.
OS Chimeric.
XX
XX
FH Key
FH Protein
FT Location/Qualifiers
FT 1..22
FT /label= Signal peptide
FT /note= "Derived from murine Ig kappa sequence"
FT 23..302
FT Protein
FT /label= Mature_human_BCMa_IgG_Fc_fusion_protein
FT 23..75
FT Region
FT /note= "Derived from human BCMa protein"
FT 24..302
FT Domain
FT /label= Cysteine rich domain
FT /note= "Derived from human BCMa"
FT 76..302
FT Region
FT /note= "Derived from human IgG Fc region"
XX
XX
XX WO200124811-A1.
XX
XX 12-APR-2001.
XX
XX 05-OCT-2000; 2000WO-US027579.
XX
XX 06-OCT-1999; 99US-0157933P.
XX
XX 11-FEB-2000; 2000US-0181807P.
XX
XX 30-JUN-2000; 2000US-0215688P.
XX
XX (BIOJ) BIOGEN INC.
XX (APOT-) APOTEC R & D SA.
XX
XX Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;
XX N-PSDB; AAD03847.
XX
XX WPI; 2001-266242/27.
XX
XX
XX Treating a mammal for a condition associated with undesired cell
XX proliferation such as cancer or carcinoma, comprises administering a
XX composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R)
XX antagonist.
XX
XX Example 1; Fig 3B; 85pp; English.
XX
XX
XX The invention relates to a method of treating a mammal for a condition
XX associated with undesired cell proliferation such as cancer or carcinoma.
XX The method involves administering a composition comprising A
XX Proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell
XX maturation protein (BCM or BCMa) antagonist that antagonises the
XX interaction between APRIL and its cognate receptor(s). This method is
XX useful for treating undesired cell proliferation such as cancer or
XX carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
XX prostate carcinoma, and other carcinomas whose proliferation is modulated
XX by APRIL. It is also useful for treating autoimmune diseases (Grave's

CC disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular
CC diseases, renal disorders, B-cell lympho-proliferative disorders,
CC immunosuppressive diseases, organ transplantation, inflammation and human
CC immunodeficiency virus (HIV), and for treating, suppressing or altering
CC an immune response involving a signaling pathway between APRIL-R and its
CC ligand. APRIL-R DNA is also useful in gene therapy. The present sequence
CC is a fusion construct containing human APRIL-R also referred as BCMA or
CC BCM protein, Fc region of human immunoglobulin G (IgG) and a signal
CC sequence from murine Ig kappa cDNA. (Updated on 11-SEP-2003 to
CC standardise OS field)

SQ Sequence 302 AA;

Query Match 100.0%; Score 201; DB 4; Length 302;
Best Local Similarity 100.0%; Pred. No. 2.7e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSQNEYPDSLHACIPCOLRGSSNTPPLTCORYC 34
|||
31 CSQNEYPDSLHACIPCOLRGSSNTPPLTCORYC 64

Db 31 CSQNEYPDSLHACIPCOLRGSSNTPPLTCORYC 64

RESULT 35

ID ADG43717 standard; protein; 302 AA.

XX ADG43717;

AC ADG43717;

XX 26-FEB-2004 (first entry)

DT 26-FEB-2004 (first entry)

XX Human B-cell maturation antigen-Fc SEQ ID NO:3.

XX human; neurodegenerative immunological disorder; demyelination;
XX Central Nervous System; CNS; inflammation; B-cell maturation antigen;
XX BCMA; multiple sclerosis; neuroprotective; nootropic; antiinflammatory;
XX gene therapy; mouse.

XX Chimeric.

OS Homo sapiens.

OS Mus sp.

XX

XX Key Location/Qualifiers

FT Region 1..23

FT /note= "Murine IgGkappa signal sequence"

FT Region 24..74

FT /note= "Human BCMA extracellular domain"

FT Region 75..302

FT /note= "Human Ig heavy chain Fc region"

XX

XX WO2003072713-A2.

XX

XX 04-SEP-2003.

XX

XX 21-FEB-2003; 2003WO-US005147.

XX

XX 21-FEB-2002; 2002US-0358427P.

XX

XX (BIOJ) BIOGEN INC.

XX

XX PI Kalled SL, Reid H;

XX

XX WPI, 2003-721758/68.

DR N-PSDB; ADG43718.

XX

XX Treating a neurodegenerative immunological disorder, e.g. demyelination
PT or inflammation in a mammal comprises administering a B-cell maturation
PT antigen (BCMA), an antibody against BCMA or a BCMA ligand.

XX

XX Claim 12; Page 70-71; 72pp; English.

XX

XX The invention relates to a novel method for treating a neurodegenerative
CC immunological disorder, demyelination or Central Nervous System (CNS)
CC inflammation in a mammal. The method comprises administering B-cell

CC maturation antigen (BCMA), or an antibody against BCMA or a BCMA ligand
CC (the mammal has or is at risk of developing multiple sclerosis). The
CC method of the invention has neuroprotective, nootropic, and
CC antiinflammatory activity, and may have a use in gene therapy. The
CC methods, BCMA, and antibodies are useful for treating a neurodegenerative
CC immunological disorder such as multiple sclerosis, demyelination or CNS
CC inflammation. The present sequence is used in the exemplification of the
CC invention.

SQ Sequence 302 AA;

Query Match 100.0%; Score 201; DB 7; Length 302;
Best Local Similarity 100.0%; Pred. No. 2.7e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSQNEYPDSLHACIPCOLRGSSNTPPLTCORYC 34
|||
31 CSQNEYPDSLHACIPCOLRGSSNTPPLTCORYC 64

Db 31 CSQNEYPDSLHACIPCOLRGSSNTPPLTCORYC 64

RESULT 36

ID AEC02026 standard; peptide; 34 AA.

XX AEC02026;

AC AEC02026;

XX 20-OCT-2005 (first entry)

DT 20-OCT-2005 (first entry)

XX

XX DE Formula II derived polypeptide E that binds BAPF.

XX

XX APRIL; BAPF; immune disorder; immunomodulator; antiinflammatory; cancer;
XX cytostatic; neoplasm; immunosuppressive; therapeutic.

XX OS Synthetic.

XX WO2005075511-A1.

XX

XX 18-AUG-2005.

XX

XX 04-AUG-2004; 2004WO-US025247.

XX

XX 29-JAN-2004; 2004US-0540271P.

PR (GETH) GENENTECH INC.

XX

XX PI Kelley RF, Patel D;

XX

XX WPI, 2005-555932/56.

XX

XX New polypeptides that inhibit APRIL and/or BAPF binding to BCMA, useful
PT for treating immune-related disease, cancer or T-cell mediated disease
PT such as graft rejection, graft versus host disease (GVHD) and
PT inflammation.

XX

XX Claim 13; SEQ ID NO 15; 140pp; English.

XX

XX The specification describes polypeptides that bind APRIL or BAPF. The
CC polypeptides inhibit APRIL or BAPF binding to B-cell maturation antigen
CC (BCMA). APRIL and BAPF are tumor necrosis family (TNF) members. The
CC polypeptides of the invention are useful for treating immune-related
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
CC scleroma; or T-cell mediated disease such as graft rejection, graft
CC versus host disease (GVHD) and inflammation. The present sequence
CC represents a polypeptide of the invention, derived from formula II (see
CC AEC02021), that that bind BAPF.

XX

SQ Sequence 34 AA;

Query Match 98.0%; Score 197; DB 9; Length 34;
Best Local Similarity 97.1%; Pred. No. 9.6e-18;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
XX |||||
XX 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db

RESULT 37
AEC02027
ID AEC02027 standard; peptide; 34 AA.
XX
AC AEC02027;
XX
DT 20-OCT-2005 (first entry)
XX

Formula II derived polypeptide F that binds BAPF.
XX
DE
XX
XX

APRIL; BAPF; immune disorder; immunomodulator; antiinflammatory; cancer;
KW
cytostatic; neoplasm; immunosuppressive; therapeutic.
XX
OS
XX

Synthetic.
XX

WO2005075511-A1.
XX

18-AUG-2005.
XX

04-AUG-2004; 2004WO-US025247.
XX

29-JAN-2004; 2004US-0540271P.
XX

(GETH) GENENTECH INC.
XX

Kelley RF, Patel D;
XX

WPI; 2005-555932/56.
XX

XX New polypeptides that inhibit APRIL and/or BAPF binding to BCMA, useful
PT for treating immune-related disease, cancer or T-cell mediated disease
PT such as graft rejection, graft versus host disease (GVHD) and
PT inflammation.
XX

PS Claim 13; SEQ ID NO 16; 140pp; English.
XX

XX The specification describes polypeptides that bind APRIL or BAPF. The
CC polypeptides inhibit APRIL or BAPF binding to B-cell maturation antigen
CC (BCMA). APRIL and BAPF are tumor necrosis family (TNF) members. The
CC polypeptides of the invention are useful for treating immune-related
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
CC scleroma; or T-cell mediated disease such as graft rejection, graft
CC versus host disease (GVHD) and inflammation. The present sequence
CC represents a polypeptide of the invention, derived from formula II (see
CC AEC02021), that that bind BAPF.
XX
XX

SEQ Sequence 34 AA;

Query Match 97.5%; Score 196; DB 9; Length 34;
Best Local Similarity 97.1%; Pred. No. 1.3e-17;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
XX |||||
XX 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db

RESULT 38
AEC02028
ID AEC02028 standard; peptide; 34 AA.
XX
AC AEC02028;
XX

20-OCT-2005 (first entry)
XX
DT
XX
DE Formula II derived polypeptide G that binds BAPF.
XX

KW APRIL; BAPF; immune disorder; immunomodulator; antiinflammatory; cancer;
KW
cytostatic; neoplasm; immunosuppressive; therapeutic.
XX
OS
XX

WO2005075511-A1.
XX

18-AUG-2005.
XX

04-AUG-2004; 2004WO-US025247.
XX

29-JAN-2004; 2004US-0540271P.
XX

(GETH) GENENTECH INC.
XX

Kelley RF, Patel D;
XX

WPI; 2005-555932/56.
XX

XX New polypeptides that inhibit APRIL and/or BAPF binding to BCMA, useful
PT for treating immune-related disease, cancer or T-cell mediated disease
PT such as graft rejection, graft versus host disease (GVHD) and
PT inflammation.
XX

PS Claim 13; SEQ ID NO 17; 140pp; English.
XX

XX The specification describes polypeptides that bind APRIL or BAPF. The
CC polypeptides inhibit APRIL or BAPF binding to B-cell maturation antigen
CC (BCMA). APRIL and BAPF are tumor necrosis family (TNF) members. The
CC polypeptides of the invention are useful for treating immune-related
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
CC scleroma; or T-cell mediated disease such as graft rejection, graft
CC versus host disease (GVHD) and inflammation. The present sequence
CC represents a polypeptide of the invention, derived from formula II (see
CC AEC02021), that that bind BAPF.
XX
XX

SEQ Sequence 34 AA;

Query Match 96.5%; Score 194; DB 9; Length 34;
Best Local Similarity 97.1%; Pred. No. 2.3e-17;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
XX |||||
XX 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db

RESULT 39
AEC02017
ID AEC02017 standard; peptide; 34 AA.
XX
AC AEC02017;
XX

20-OCT-2005 (first entry)
XX
DT
XX
DE Formula I derived polypeptide F that binds APRIL.
XX

APRIL; BAPF; immune disorder; immunomodulator; antiinflammatory; cancer;
KW
cytostatic; neoplasm; immunosuppressive; therapeutic.
XX
OS
XX

Synthetic.
XX

WO2005075511-A1.
XX

18-AUG-2005.
XX

04-AUG-2004; 2004WO-US025247.
XX

29-JAN-2004; 2004US-0540271P.
XX

(GETH) GENENTECH INC.
XX
PA
XX

PI Kelley RF, Patel D;
XX WPI; 2005-555932/56.
DR
XX
PT New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful
PT for treating immune-related disease, cancer or T-cell mediated disease
PT such as graft rejection, graft versus host disease (GVHD) and
PT inflammation.
XX
PS Claim 7, SEQ ID NO 6; 140pp; English.
XX
CC The specification describes polypeptides that bind APRIL or BAFF. The
CC polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen
CC (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The
CC polypeptides of the invention are useful for treating immune-related
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
CC sclerosis; or T-cell mediated disease such as graft rejection, graft
CC versus host disease (GVHD) and inflammation. The present sequence
CC represents polypeptide of the invention that binds APRIL, derived from
CC AEC02012.
XX
SQ Sequence 34 AA;
XX
Query Match 96.5%; Score 194; DB 9; Length 34;
Best Local Similarity 97.1%; Pred. No. 2.3e-17;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
DB 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
RESULT 40
AEC02042
ID AEC02042 standard; protein; 296 AA.
XX
AC AEC02042;
XX
DT 20-OCT-2005 (first entry)
XX
DE Amino acid sequence of a BCMA-Fc fusion protein.
XX
XX APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;
XX cytostatic; neoplasm; immunosuppressive; therapeutic; BCMA;
XX B-cell maturation antigen; Fc.
XX
XX Homo sapiens.
XX OS Synthetic.
XX
XX WO2005075511-A1.
XX
PD 18-AUG-2005.
XX
PF 04-AUG-2004; 2004WO-US025247.
XX
PR 29-JAN-2004; 2004US-0540271P.
XX
PA (GETH) GENENTECH INC.
XX
PI Kelley RF, Patel D;
XX
XX WPI; 2005-555932/56.
DR
XX
PT New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful
PT for treating immune-related disease, cancer or T-cell mediated disease
PT such as graft rejection, graft versus host disease (GVHD) and
PT inflammation.
XX
XX Example 6; SEQ ID NO 31; 140pp; English.
CC The specification describes polypeptides that bind APRIL or BAFF. The
CC polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen

CC (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The
CC polypeptides of the invention are useful for treating immune-related
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
CC sclerosis; or T-cell mediated disease such as graft rejection, graft
CC versus host disease (GVHD) and inflammation. The present sequence
CC represents a BCMA-Fc fusion protein, where 122 of BCMA is changed to Lys.
XX
SQ Sequence 296 AA;
XX
Query Match 96.5%; Score 194; DB 9; Length 296;
Best Local Similarity 97.1%; Pred. No. 2.1e-16;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
DB 21 CSONEYFDSLHACIPCOLRCSSNTPPLTCQRYC 54
RESULT 41
AEC02025
ID AEC02025 standard; peptide; 34 AA.
XX
AC AEC02025;
XX
DT 20-OCT-2005 (first entry)
XX
DE Formula II derived polypeptide D that binds BAFF.
XX
XX APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;
XX cytostatic; neoplasm; immunosuppressive; therapeutic.
XX
XX Synthetic.
XX
XX WO2005075511-A1.
XX
PD 18-AUG-2005.
XX
PF 04-AUG-2004; 2004WO-US025247.
XX
PR 29-JAN-2004; 2004US-0540271P.
XX
PA (GETH) GENENTECH INC.
XX
PI Kelley RF, Patel D;
XX
XX WPI; 2005-555932/56.
DR
XX
PT New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful
PT for treating immune-related disease, cancer or T-cell mediated disease
PT such as graft rejection, graft versus host disease (GVHD) and
PT inflammation.
XX
PS Claim 13; SEQ ID NO 14; 140pp; English.
XX
XX The specification describes polypeptides that bind APRIL or BAFF. The
XX polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen
XX (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The
XX polypeptides of the invention are useful for treating immune-related
XX diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
XX lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
XX sclerosis; or T-cell mediated disease such as graft rejection, graft
XX versus host disease (GVHD) and inflammation. The present sequence
XX represents a polypeptide of the invention, derived from formula II (see
XX AEC02021), that that bind BAFF.
XX
SQ Sequence 34 AA;
XX
Query Match 95.5%; Score 192; DB 9; Length 34;
Best Local Similarity 97.1%; Pred. No. 4.2e-17;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34

```
Db      |||||
        1 CSQNEFDSLHACIPCOLRGSSNTPPLTCQRYC 34

RESULT 42
AEC02024 AEC02024 standard; peptide; 34 AA.
XX
AC AEC02024;
XX
DT 20-OCT-2005 (first entry)
XX
DE Formula II derived polypeptide C that binds BAFf.
XX
KW APRIL; BAFf; immune disorder; immunomodulator; antiinflammatory; cancer;
XX cyrostatic; neoplasm; immunosuppressive; therapeutic.
XX
OS Synthetic.
XX
PN WO2005075511-A1.
XX
PD 18-AUG-2005.
XX
PF 04-AUG-2004; 2004WO-US025247.
XX
PR 29-JAN-2004; 2004US-0540271P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Kelley RF, Patel D;
XX
DR WPI; 2005-555932/56.
XX
PT New polypeptides that inhibit APRIL and/or BAFf binding to BCMA, useful
PT for treating immune-related disease, cancer or T-cell mediated disease
PT such as graft rejection, graft versus host disease (GVHD) and
PT inflammation.
XX
PS Claim 13; SEQ ID NO 13; 140bp; English.
XX
CC The specification describes polypeptides that bind APRIL or BAFf. The
CC polypeptides inhibit APRIL or BAFf binding to B-cell maturation antigen
CC (BCMA). APRIL and BAFf are tumor necrosis family (TNF) members. The
CC polypeptides of the invention are useful for treating immune-related
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
CC scleroma; or T-cell mediated disease such as graft rejection, graft
CC versus host disease (GVHD) and inflammation. The present sequence
CC represents a polypeptide of the invention, derived from formula II (see
CC AEC02021), that that bind BAFf.
XX
SQ Sequence 34 AA;

Query Match 95.5%; Score 192; DB 9; Length 34;
Best Local Similarity 97.1%; Pred. No. 4.2e-17;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSQNEFDSLHACIPCOLRGSSNTPPLTCQRYC 34
   |||||
Db 1 CSQNEFDSLHACIPCOLRGSSNTPPLTCQRYC 34

RESULT 43
AEC02033 AEC02033 standard; peptide; 38 AA.
XX
AC AEC02033;
XX
DT 20-OCT-2005 (first entry)
XX
DE Amino acid sequence of an extracellular domain of BCMA.
XX
KW APRIL; BAFf; immune disorder; immunomodulator; antiinflammatory; cancer;
```

```
KW cyrostatic; neoplasm; immunosuppressive; therapeutic;
KM B-cell maturation antigen; BCMA.
XX
OS Synthetic.
XX
PN WO2005075511-A1.
XX
PD 18-AUG-2005.
XX
PF 04-AUG-2004; 2004WO-US025247.
XX
PR 29-JAN-2004; 2004US-0540271P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Kelley RF, Patel D;
XX
DR WPI; 2005-555932/56.
XX
PT New polypeptides that inhibit APRIL and/or BAFf binding to BCMA, useful
PT for treating immune-related disease, cancer or T-cell mediated disease
PT such as graft rejection, graft versus host disease (GVHD) and
PT inflammation.
XX
PS Disclosure; SEQ ID NO 22; 140bp; English.
XX
CC The specification describes polypeptides that bind APRIL or BAFf. The
CC polypeptides inhibit APRIL or BAFf binding to B-cell maturation antigen
CC (BCMA). APRIL and BAFf are tumor necrosis family (TNF) members. The
CC polypeptides of the invention are useful for treating immune-related
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
CC scleroma; or T-cell mediated disease such as graft rejection, graft
CC versus host disease (GVHD) and inflammation. The present sequence
CC represents an extracellular domain of BCMA.
XX
SQ Sequence 38 AA;

Query Match 95.5%; Score 192; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 4.7e-17;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CSQNEFDSLHACIPCOLRGSSNTPPLTCQRYC 34
   |||||
Db 1 CSQNEFDSLHACIPCOLRGSSNTPPLTCQRYC 33

RESULT 44
AEC02020 AEC02020 standard; peptide; 34 AA.
XX
AC AEC02020;
XX
DT 20-OCT-2005 (first entry)
XX
DE Formula I derived polypeptide I that binds APRIL.
XX
KW APRIL; BAFf; immune disorder; immunomodulator; antiinflammatory; cancer;
XX cyrostatic; neoplasm; immunosuppressive; therapeutic.
XX
OS Synthetic.
XX
PN WO2005075511-A1.
XX
PD 18-AUG-2005.
XX
PF 04-AUG-2004; 2004WO-US025247.
XX
PR 29-JAN-2004; 2004US-0540271P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Kelley RF, Patel D;
```

XX WPI; 2005-555932/56.
XX New polypeptides that inhibit APRIL and/or BAFf binding to BCMA, useful
PT for treating immune-related disease, cancer or T-cell mediated disease
PT such as graft rejection, graft versus host disease (GVHD) and
PT inflammation.
XX
XX Claim 7; SEQ ID NO 9; 140pp; English.
XX
XX The specification describes polypeptides that bind APRIL or BAFf. The
CC polypeptides inhibit APRIL or BAFf binding to B-cell maturation antigen
CC (BCMA). APRIL and BAFf are tumor necrosis family (TNF) members. The
CC polypeptides of the invention are useful for treating immune-related
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
CC scleroma; or T-cell mediated disease such as graft rejection, graft
CC versus host disease (GVHD) and inflammation. The present sequence
CC represents polypeptide of the invention that binds APRIL, derived from
CC AEC02012.
XX
XX Sequence 34 AA;
SQ
Query Match 95.0%; Score 191; DB 9; Length 34;
Best Local Similarity 94.1%; Pred. No. 5, 6e-17;
Matches 32; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34
Db 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34
RESULT 45
AEC02018
ID AEC02018 standard; peptide; 34 AA.
XX
XX AEC02018;
XX
XX 20-OCT-2005 (first entry)
XX
XX Formula I derived polypeptide G that binds APRIL.
DE
XX APRIL; BAFf; immune disorder; immunomodulator; antiinflammatory; cancer;
XX cytostatic; neoplasm; immunosuppressive; therapeutic.
XX
XX Synthetic.
XX
XX WO2005075511-A1.
XX
XX 18-AUG-2005.
XX
XX 04-AUG-2004; 2004WO-US025247.
XX
XX 29-JAN-2004; 2004US-0540271P.
XX
XX (GETH) GENENTECH INC.
XX
XX Kelley RF, Patel D;
XX
XX WPI; 2005-555932/56.
XX
XX New polypeptides that inhibit APRIL and/or BAFf binding to BCMA, useful
PT for treating immune-related disease, cancer or T-cell mediated disease
PT such as graft rejection, graft versus host disease (GVHD) and
PT inflammation.
XX
XX Claim 7; SEQ ID NO 7; 140pp; English.
XX
XX The specification describes polypeptides that bind APRIL or BAFf. The
CC polypeptides inhibit APRIL or BAFf binding to B-cell maturation antigen
CC (BCMA). APRIL and BAFf are tumor necrosis family (TNF) members. The
CC polypeptides of the invention are useful for treating immune-related
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
CC scleroma; or T-cell mediated disease such as graft rejection, graft
CC versus host disease (GVHD) and inflammation. The present sequence
CC represents a polypeptide of the invention, derived from formula I (see
CC AEC02012), that binds BAFf.
XX
XX Sequence 34 AA;
SQ

CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
CC scleroma; or T-cell mediated disease such as graft rejection, graft
CC versus host disease (GVHD) and inflammation. The present sequence
CC represents polypeptide of the invention that binds APRIL, derived from
CC AEC02012.
XX
XX Sequence 34 AA;
SQ
Query Match 94.0%; Score 189; DB 9; Length 34;
Best Local Similarity 94.1%; Pred. No. 1e-16;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34
Db 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34
RESULT 46
AEC02029
ID AEC02029 standard; peptide; 34 AA.
XX
XX AEC02029;
XX
XX 20-OCT-2005 (first entry)
XX
XX Formula II derived polypeptide H that binds BAFf.
DE
XX APRIL; BAFf; immune disorder; immunomodulator; antiinflammatory; cancer;
XX cytostatic; neoplasm; immunosuppressive; therapeutic.
XX
XX Synthetic.
XX
XX WO2005075511-A1.
XX
XX 18-AUG-2005.
XX
XX 04-AUG-2004; 2004WO-US025247.
XX
XX 29-JAN-2004; 2004US-0540271P.
XX
XX (GETH) GENENTECH INC.
XX
XX Kelley RF, Patel D;
XX
XX WPI; 2005-555932/56.
XX
XX New polypeptides that inhibit APRIL and/or BAFf binding to BCMA, useful
PT for treating immune-related disease, cancer or T-cell mediated disease
PT such as graft rejection, graft versus host disease (GVHD) and
PT inflammation.
XX
XX Claim 13; SEQ ID NO 18; 140pp; English.
XX
XX The specification describes polypeptides that bind APRIL or BAFf. The
CC polypeptides inhibit APRIL or BAFf binding to B-cell maturation antigen
CC (BCMA). APRIL and BAFf are tumor necrosis family (TNF) members. The
CC polypeptides of the invention are useful for treating immune-related
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
CC scleroma; or T-cell mediated disease such as graft rejection, graft
CC versus host disease (GVHD) and inflammation. The present sequence
CC represents a polypeptide of the invention, derived from formula II (see
CC AEC02021), that binds BAFf.
XX
XX Sequence 34 AA;
SQ
Query Match 94.0%; Score 189; DB 9; Length 34;
Best Local Similarity 94.1%; Pred. No. 1e-16;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34
Db 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34

RESULT 47
AEC02019 standard; peptide; 34 AA.
AC AEC02019;
XX 20-OCT-2005 (first entry)
DT
XX
DE Formula I derived polypeptide H that binds APRIL.
XX
XX APRIL; BAFR; immune disorder; immunomodulator; antiinflammatory; cancer;
KW cyostatic; neoplasm; immunosuppressive; therapeutic.
XX
OS Synthetic.
XX WO2005075511-A1.
XX 18-AUG-2005.
XX 04-AUG-2004; 2004WO-US025247.
XX 29-JAN-2004; 2004US-0540271P.
XX (GETH) GENENTECH INC.
PA
PI Kelley RF, Patel D;
XX WPI; 2005-555932/56.
XX
XX New polypeptides that inhibit APRIL and/or BAFR binding to BCMA, useful
PT for treating immune-related disease, cancer or T-cell mediated disease
PT such as graft rejection, graft versus host disease (GVHD) and
PT inflammation.
XX
PS Claim 7; SEQ ID NO 8; 140pp; English.
XX
XX The specification describes polypeptides that bind APRIL or BAFR. The
CC polypeptides inhibit APRIL or BAFR binding to B-cell maturation antigen
CC (BCMA). APRIL and BAFR are tumor necrosis family (TNF) members. The
CC polypeptides of the invention are useful for treating immune-related
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
CC scleroma; or T-cell mediated disease such as graft rejection, graft
CC versus host disease (GVHD) and inflammation. The present sequence
CC represents polypeptide of the invention that binds APRIL, derived from
CC AEC02012.
XX
SQ Sequence 34 AA;
Query Match 90.5%; Score 182; DB 9; Length 34;
Best Local Similarity 91.2%; Pred. No. 7.9e-16;
Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CSQNEYFDSLHACIPQQLRCSSNTPTLCQRYC 34
Db 1 CSQNEYFDSLHACIPQQLRCSSNTPTLCQRYC 34

RESULT 48
AAB60700 standard; protein; 157 AA.
ID AAB60700
XX
AC AAB60700;
XX
XX 22-MAY-2001 (first entry)
DT
XX
XX Human BAFR receptor (BAFR-R) sequence encoded by A plasmid pJST535.
XX Human BAFR-R; BAFR receptor; TNF family; immunoregulatory agent;
KW immune-related disorder; B-cell growth inhibitor; BCMA;
KW B-cell maturation inhibitor; immunoglobulin production inhibitor;

KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
KW renal disorder; immunosuppressive disorder; HIV infection;
KW organ transplantation; antiinflammatory; systemic lupus erythematosus;
KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
KW B-cell carcinoma; leukemia; rapidly progressive glomerulonephritis;
KW lymphoma; gene therapy; cancer; tumour; plasmid pJST535.
XX
XX Homo sapiens.
XX
XX WO200112812-A2.
XX
XX 22-FEB-2001.
XX
XX 16-AUG-2000; 2000WO-US022507.
XX
XX 17-AUG-1999; 99US-0149378P.
XX 11-FEB-2000; 2000US-0181684P.
XX 18-FEB-2000; 2000US-0183536P.
XX
XX (BIOJ) BIOGEN INC.
PA (APOT-) APOTEC R & D SA.
PI Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;
XX Thompson J;
XX WPI; 2001-202866/20.
XX N-PSDB; AAF60000.
XX
XX Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
PT lympho-proliferative disorder by administering BAFR-receptor polypeptide,
PT chimeric molecule comprising receptor or anti-BAFR-R antibody homolog.
XX
XX Example 1; Fig 3; 59pp; English.
XX
XX The invention relates to the use of a BAFR receptor (BAFR-R, also known
CC as BCMA) protein, or a BAFR-R fusion protein as an agent for the
CC treatment of a variety of immune-related disorders. BAFR-R is a member of
CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory
CC agent, and also plays a role in the development of hypertension and
CC related disorders. BAFR-R, fusion proteins containing it, and BAFR-R-
CC specific antibodies can be used for inhibiting B-cell growth, dendritic
CC cell-induced B-cell growth and maturation, and immunoglobulin production,
CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative
CC disorders, hypertension and renal disorders. The BAFR-R proteins may also
CC be used in the treatment of immunosuppressive disorders and HIV
CC infection, and in patients undergoing organ transplantation. The BAFR-R
CC proteins or BAFR-R specific antibodies may be used for treating,
CC suppressing or altering an immune response involving a signalling pathway
CC between BAFR-R and BAFR, thereby inhibiting inflammation. Since BAFR-R
CC inhibits B-cell growth and maturation it is useful for treating diseases
CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
CC human BAFR-R may be used in gene therapy to treat tumours, lymphomas,
CC autoimmune disorders and inherited B-cell-associated disorders. The
CC present sequence represents a human BAFR-R protein sequence as encoded by
CC plasmid pJST535. However, this BAFR-R protein sequence is 27 amino acids
CC shorter than that given in AAB60698
XX
SQ Sequence 157 AA;
Query Match 79.4%; Score 159.5; DB 4; Length 157;
Best Local Similarity 90.6%; Pred. No. 2.7e-12;
Matches 29; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

OY 3 QNEYFDSLHACIPQQLRCSSNTPTLCQRYC 34
Db 7 QNEYFDSLHACIPQQLR---NTPTLCQRYC 35

RESULT 49
ADIS3060 standard; peptide; 26 AA.
ID ADIS3060

```

XX AC ADIS3060;
XX XX
XX DT 22-APR-2004 (first entry)
XX DE Human BCMA receptor binding site.
XX KW protein co-ordinate data; cytostatic; antiallergic; immunosuppressive;
XX KW antirheumatic; antiarthritic; neuroprotective; antiinflammatory;
XX KW antidiabetic; dermatological; antiasthmatic; neurokinine-alpha;
XX KW crystallography; cancer; allergic disorder; autoimmune disease;
XX KW rheumatoid arthritis; multiple sclerosis; Crohn's disease; diabetes;
XX KW systemic lupus erythematosus; asthma; receptor.
XX OS Homo sapiens.
XX PN WO2003050134-A2.
XX PD 19-JUN-2003.
XX PF 07-NOV-2002; 2002WO-US035661.
XX PR 07-NOV-2001; 2001US-0331049P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Li Y, Oren DE, Arnold E, Volovik Y;
XX PS WPI, 2003-532895/50.
XX XX
XX PT New crystalline Neurokinine-alpha protein, useful for designing compounds
XX PT that bind, inhibit or mimic a Neurokinine-alpha protein or enhance the
XX PT activity of a Neurokinine-alpha protein for treating e.g. cancer or
XX PT allergic disorders.
XX PS Disclosure, Fig 4; 362pp; English.
XX XX
XX CC The invention relates to a neurokinine-alpha protein in crystalline form.
XX CC The crystalline neurokinine-alpha protein is useful for designing
XX CC molecules that have biological activity or compounds that bind, inhibit
XX CC or mimic a neurokinine-alpha protein and/or enhance the activity of a
XX CC neurokinine-alpha protein. The three-dimensional structure of a neurokinine
XX CC -alpha protein is useful in determining the three-dimensional of other
XX CC neurokinine-alpha proteins and their homologs. The compounds that mimic,
XX CC prevent or inhibit the activity of the protein are useful for treating
XX CC cancer, allergic disorders, or autoimmune diseases such as rheumatoid
XX CC arthritis, multiple sclerosis, Crohn's disease, diabetes, systemic lupus
XX CC erythematosus or asthma. This sequence represents the residues in the
XX CC receptor for binding a cytokine ligand.
XX SQ Sequence 26 AA;

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Query Match 75.1%; Score 151; DB 7; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.4e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 5 EYFDSLHACIPQALRGSSNTPLPTC 30
DB 1 EYFDSLHACIPQALRGSSNTPLPTC 26

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RESULT 50
AAB08844
ID AAB08844 standard; peptide; 185 AA.
AC AAB08844;
XX
XX DT 02-JAN-2001 (first entry)
XX DE Amino acid sequence of murine BCMA polypeptide.
XX KW BCMA, necrosis factor-kB activator; NF-kB; gene expression; cancer;
XX anti-cell death gene; apoptosis; viral infection; inflammatory response;

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XX KW rheumatoid arthritis; inflammatory bowel disease; septic shock.
XX OS Mus musculus.
XX PH Key Location/Qualifiers
XX FT Domain 47..72 /note="putative transmembrane domain"
XX PN WO200050633-A1.
XX PD 31-AUG-2000.
XX PF 24-FEB-2000; 2000WO-US004925.
XX PR 24-FEB-1999; 99US-0121485P.
XX PA (GHEO) GEN HOSPITAL CORP.
XX PI Seed B, Ting A;
XX PD WPI; 2000-558405/51.
XX DR
XX PT Identifying a modulator of gene expression for drug designing, by
XX PT contacting a compound library with a cell expressing an anti-cell death
XX PT gene and reporter gene, and determining alteration in reporter gene
XX PT expression.
XX PS Claim 32; Fig 7B; 53pp; English.
XX XX
XX CC The present sequence represents a BCMA (not defined) polypeptide. BCMA is
XX CC a necrosis factor (NF)-kB activator. The method of the invention is used
XX CC to identify compounds which modulate BCMA activity (and thus NF-kB
XX CC activity). The specification describes a method of identifying a
XX CC polypeptide which increases gene expression from a promoter. The method
XX CC involves contacting a library of with a cell which expresses a
XX CC recombinant anti-cell death gene and a reporter gene operably linked to
XX CC the promoter, and then determining whether the expression of the reporter
XX CC gene is altered as a result of contact with library. The method is useful
XX CC for identifying polypeptides which increase or decrease gene expression
XX CC from a promoter. The BCMA polypeptide or nucleic acid are useful for
XX CC preparing a pharmaceutical composition for treating cancer, apoptosis,
XX CC viral infections, inflammatory response, such as rheumatoid arthritis,
XX CC inflammatory bowel disease or septic shock. BCMA is useful for
XX CC identifying compounds that modulate NF-kB expression and thus for drug
XX CC designing.
XX SQ Sequence 185 AA;

```

```

Query Match 67.7%; Score 136; DB 3; Length 185;
Best Local Similarity 70.6%; Pred. No. 3.2e-09;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

```

```

QY 1 GSONEYFDSLHACIPQALRGSSNTPLPTC 34
DB 5 CFHSEYFDSLHACKRCHLRCN--PPATQPCYC 36

```

```

RESULT 51
AA71980
ID AA71980 standard; protein; 185 AA.
AC AA71980;
XX
XX DT 28-MAR-2001 (first entry)
XX DE Murine B cell maturation factor (BCMA) protein.
XX KW Murine; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
XX KW Tumour necrosis factor and Apol-related leucocyte expressed ligand 1;
XX KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
XX KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
XX KW thrombocytopenia, purpura; acute rheumatic fever; Goodpasture's syndrome;
XX KW hemolytic anaemia; Grave's disease; myasthenia gravis; BCMA;

```

KM B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation;
KM post-streptococcal glomerulonephritis; polyarteritis nodosa.
XX
OS Mus musculus.
XX
PN WO20068378-A1.
XX
PD 16-NOV-2000.
XX
PF 05-MAY-2000; 2000WO-US012266.
XX
PR 06-MAY-1999; 99US-0132892P.
PR 01-MAY-2000; 2000US-0201012P.
XX
XX (NAME-) NAT JEWISH MEDICAL & RES CENT.
XX
PI Shu HS;
XX
DR WPI; 2001-016094/02.
DR N-PSDB; AAD02130.
XX
PT Isolated TALL-1 protein is used to identify compounds that regulate B
PT lymphocyte proliferation, used to treat B lymphocyte associated
PT autoimmune disorders.
XX
XX Claim 37; Page 107-108; 112pp; English.
XX
CC The present invention relates to Tumour necrosis factor (TNF) and Apol-
CC related leucocyte expressed ligand 1 (TALL-1) nucleic acid molecules,
CC proteins (including homologues), and their antibodies. The invention in
CC particular relates to methods for regulating the interaction between TALL
CC -1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to
CC regulate monocyte, macrophage and B lymphocyte mediated immune responses.
CC TALL-1 protein is useful for identifying compounds that regulate B
CC lymphocyte proliferation. It is also useful for treating B lymphocyte
CC associated autoimmune disorders like rheumatoid arthritis, systemic lupus
CC erythematosus (SLE), insulin dependent diabetes mellitus, multiple
CC sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome,
CC pemphigus vulgaris, acute rheumatic fever, post-streptococcal
CC glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its
CC corresponding nucleic acid sequence are also useful in diagnostic assays.
CC The present sequence is a murine B cell maturation factor (BCMA). BCMA is
CC the receptor for TALL-1 protein
XX
SQ Sequence 185 AA;
XX
Query Match 67.7%; Score 136; DB 4; Length 185;
Best Local Similarity 70.6%; Pred. No. 3.2e-09;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;
XX
QY 1 CSONEYPDSLHACIPCOLRCCSNTPLTCORYC 34
| : ||||| | | | | : | | | |
Db 5 CFHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36
XX
RESULT 52
AAE15490
ID AAE15490 standard; protein; 185 AA.
XX
AC AAE15490;
XX
DT 12-MAR-2002 (first entry)
XX
XX Mouse B cell maturation (BCMA) protein.
XX
XX Mouse; transmembrane activator and intracellular CAML interactor; TACI;
KM cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KM lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KM prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KM drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KM Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KM human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;

KM rheumatoid arthritis; atherosclerosis.
XX
XX Mus sp.
XX
OS
XX
PN WO200187979-A2.
XX
XX
PD 22-NOV-2001.
XX
XX
PF 14-MAY-2001; 2001WO-US015567.
XX
XX
PR 12-MAY-2000; 2000US-0204039P.
PR 27-JUN-2000; 2000US-0214591P.
PR 14-MAY-2001; 2001US-00214591.
XX
XX (AMGE-) AMGEN INC.
XX
XX
PI The111 LE, Yu G;
XX
DR WPI; 2002-066686/09.
XX
XX
PT Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor family
PT ligand.
XX
XX
XX Disclosure; Fig 11; 94pp; English.
XX
PS
XX
CC The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering a
CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is mouse BCMA protein
XX
SQ Sequence 185 AA;
XX
Query Match 67.7%; Score 136; DB 5; Length 185;
Best Local Similarity 70.6%; Pred. No. 3.2e-09;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;
XX
QY 1 CSONEYPDSLHACIPCOLRCCSNTPLTCORYC 34
| : ||||| | | | | : | | | |
Db 5 CFHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36
XX
RESULT 53
ADZ67762
ID ADZ67762 standard; protein; 185 AA.
XX
AC ADZ67762;
XX
DT 14-JUL-2005 (first entry)
XX
XX Mouse tumor necrosis factor receptor BCMA.
XX
XX Tumor necrosis factor receptor; BCMA; cancer; neoplasm; diagnosis;
KM cytosolic.
XX
OS Mus musculus.

PN WO2005037865-A2.
 XX
 XX 28-APR-2005.
 PD
 PF 18-OCT-2004; 2004WO-US034375.
 XX
 XX 16-OCT-2003; 2003US-0511698P.
 PR 18-OCT-2004; 2004US-0619552P.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 PI Fox BA, Holloway JL, Sheppard PO, Dillon SR;
 XX WPI; 2005-315682/32.
 DR
 XX
 XX New tumor necrosis factor receptor (TNFR) polypeptides, useful as
 PT detecting ligands, and for modulating tumor growth, metastasis and
 PT immunity, such as separating resting from stimulated immune cells.
 XX
 XX Disclosure; SEQ ID NO 10; 132pp; English.
 PS
 XX
 CC The invention provides novel tumor necrosis factor receptor ztnfr14
 CC polynucleotides AD267753 and polypeptides AD267754, expression vectors
 CC and antibodies. Human ztnfr14 polynucleotides are used in claimed methods
 CC for detecting a genetic abnormality in a patient and for detecting a
 CC cancer in a patient. Recombinant ztnfr14 polypeptide, optionally
 CC conjugated to a toxin, is used in a claimed method of killing cancer
 CC cells. Ztnfr14 polypeptides can be used to detect ligands, agonists and
 CC antagonists. The polypeptides, polynucleotides and antibodies may also be
 CC used in methods that modulate tumor growth, metastasis, and immunity such
 CC as separating resting from stimulated immune cells. The present sequence
 CC is that of murine TNFR BCMA. This sequence was compared with that of
 CC murine ztnfr14 AD267756 in the identification of ztnfr14 as a member of
 CC the TNFR family.
 XX
 XX Sequence 185 AA;
 SQ
 Query Match 67.7%; Score 136; DB 9; Length 185;
 Best Local Similarity 70.6%; Pred. No. 3.2e-09;
 Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;
 QY 1 CSQNEYFDSLHACTPQCRGSSNTPLTCQRYC 34
 Db | : ||||| ||||| : ||||| |||||
 5 CFHSEYFDSLHACKRCHLRCSN--PPATCQPYC 36
 RESULT 54
 AAE15489
 ID AAE15489 standard; protein; 281 AA.
 XX
 XX AAE15489;
 AC
 XX
 XX 29-AUG-2003 (revised)
 DT 12-MAR-2002 (first entry)
 XX
 XX Mouse BCMA-human immunoglobulin Fc region fusion protein.
 DE
 XX Human; transmembrane activator and intracellular CAML interactor; TACI;
 KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis; fusion protein; mouse.
 XX
 XX Homo sapiens.
 OS Mus sp.
 OS Chimeric.
 XX
 XX WO200187979-A2.
 PN
 XX 22-NOV-2001.

XX
 PF 14-MAY-2001; 2001WO-US015567.
 XX
 XX 12-MAY-2000; 2000US-0204039P.
 PR 27-JUN-2000; 2000US-0214591P.
 PR 14-MAY-2001; 2001US-00214591.
 XX
 XX (AMGE-) AMGEN INC.
 PA
 PI Theell LE, Yu G;
 XX WPI; 2002-066686/09.
 DR
 XX
 XX Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor family
 PT ligand.
 XX
 XX Disclosure; Fig 10B; 94pp; English.
 PS
 XX
 CC The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering a
 CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is mouse BCMA protein-human immunoglobulin Fc region fusion protein.
 CC (Updated on 29-AUG-2003 to standardise OS field)
 XX
 XX Sequence 281 AA;
 SQ
 Query Match 67.7%; Score 136; DB 5; Length 281;
 Best Local Similarity 70.6%; Pred. No. 4.9e-09;
 Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;
 QY 1 CSQNEYFDSLHACTPQCRGSSNTPLTCQRYC 34
 Db | : ||||| ||||| : ||||| |||||
 5 CFHSEYFDSLHACKRCHLRCSN--PPATCQPYC 36
 RESULT 55
 ABJ38417
 ID ABJ38417 standard; protein; 42 AA.
 XX
 XX ABJ38417;
 AC
 XX
 XX 12-JUN-2003 (first entry)
 DT TALL-1 related protein SEQ ID NO 197.
 XX
 XX TALL-1 binding protein; TALL-1; B-cell-mediated autoimmune disease;
 DE systemic lupus erythematosus; B-cell-mediated cancer; lymphoma;
 KW inflammation; rheumatoid arthritis; acute pancreatitis; atherosclerosis;
 KW Alzheimer's disease; asthma; cachexia; cirrhosis; diabetes; osteoporosis;
 KW glomerulonephritis; Hashimoto's thyroiditis; ischaemic injury; psoriasis;
 KW multiple myeloma; multiple sclerosis; Parkinson's disease; vasculitis;
 KW gene therapy.
 XX
 XX Homo sapiens.
 OS
 OS WO200292620-A2.
 PN

XX 21-NOV-2002.
XX
XX 13-MAY-2002; 2002MO-US015273.
PF
XX 11-MAY-2001; 2001US-0290196P.
PR
XX (AMGE-) AMGEN INC.
PA
XX Min H, Hsu H;
PI
XX WPI; 2003-156719/15.
DR
XX New TALL-1-binding polypeptide, useful for modulating the activity of
PT TALL-1 and in treating, preventing or diagnosing a B-cell-mediated
PT autoimmune diseases, cancers or lymphomas.
XX
XX Disclosure; Page 26; 236pp; English.
PS
XX The invention relates to a novel TALL-1-binding polypeptide comprising a
CC defined sequence in the specification. The composition is useful in
CC modulating the activity of TALL-1, and in treating, preventing,
CC ameliorating, diagnosing or prognosing a B-cell-mediated autoimmune
CC disease (e.g. systemic lupus erythematosus) or B-cell-mediated cancer or
CC lymphoma. The composition may also be used in treating inflammations
CC (e.g. rheumatoid arthritis), acute pancreatitis, Alzheimer's disease,
CC asthma, atherosclerosis, cachexia, cirrhosis, diabetes,
CC glomerulonephritis, Hashimoto's thyroiditis, ischaemic injury, multiple
CC myeloma, multiple sclerosis, osteoporosis, Parkinson's disease, psoriasis
CC and vasculitis. Disorders may be treated with the novel composition using
CC gene therapy. This sequence represents a TALL-1 related protein of the
CC invention
XX
SQ Sequence 42 AA;
Query Match 61.7%; Score 124; DB 6; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CSQNEYPDSLHACIPCOLRC 21
Do 22 CSQNEYPDSLHACIPCOLRC 42
AAE15491
ID AAE15491 standard; protein; 117 AA.
XX
XX AAE15491;
AC
XX 29-AUG-2003 (revised)
DT 12-MAR-2002 (first entry)
XX
XX Human-murine B cell maturation protein (BCMA) consensus sequence.
DE
XX Human; transmembrane activator and intracellular CAML interactor; TACT;
KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis; mouse.
XX
XX Homo sapiens.
OS Mus sp.
OS Chimeric.
XX
XX WO200187979-A2.
XX
XX 22-NOV-2001.
PD
XX 14-MAY-2001; 2001WO-US015567.
PF

XX 12-MAY-2000; 2000US-0204039P.
PR 27-JUN-2000; 2000US-0214591P.
PR 14-MAY-2001; 2001US-00214591.
XX
XX (AMGE-) AMGEN INC.
PA
XX The111 LE, Yu G;
PI
XX WPI; 2002-066686/09.
DR
XX Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor family
PT ligand.
XX
XX Disclosure; Fig 11; 94pp; English.
PS
XX The invention relates to a method for inhibiting TACT (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering a
CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
CC family ligand), having the consensus region of TACT, BCMA, or the TACT/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TACT or BCMA. The method is useful for inhibiting activity of TACT
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACT
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC bacterial, protozoal arthritis, systemic lupus erythematosus), fungal,
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human-murine B cell maturation protein (BCMA) consensus sequence.
CC (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 117 AA;
Query Match 46.5%; Score 93.5; DB 5; Length 117;
Best Local Similarity 69.7%; Pred. No. 0.00053;
Matches 23; Conservative 1; Mismatches 2; Indels 7; Gaps 4;
QY 2 SQNEYPDSLHACIPCOLRCSTNPTTCORYC 34
Do 2 AQCEYFDSLHAC-PC-LRCS---PPTCQ-YC 27
AAE15492
ID AAE15492 standard; peptide; 24 AA.
XX
XX AAE15492;
AC
XX 29-AUG-2003 (revised)
DT 12-MAR-2002 (first entry)
XX
XX Human-murine BCMA consensus sequence cysteine rich region.
DE
XX Human; transmembrane activator and intracellular CAML interactor; TACT;
KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis; mouse.
XX
XX Homo sapiens.
OS Mus sp.
OS Chimeric.
OS

XX WO200187979-A2.
 XX 22-NOV-2001.
 XX 14-MAY-2001; 2001WO-US015567.
 XX 12-MAY-2000; 2000US-0204039P.
 XX 27-JUN-2000; 2000US-0214591P.
 XX 14-MAY-2001; 2001US-00214591.
 XX (AMGE-) AMGEN INC.
 XX The111 LE, Yu G;
 XX WPI; 2002-066686/09.
 XX
 XX Inhibiting activity of B cell maturation protein and/or transmembrane
 XX activator and intracellular cyclophilin ligand interactor, by
 XX administering a binding partner for APRIL, a tumor necrosis factor family
 XX ligand.
 XX
 XX Disclosure; Fig 11; 94pp; English.
 XX
 XX The invention relates to a method for inhibiting TNF α (transmembrane
 XX activator and intracellular CAML interactor) and/or B cell maturation
 XX protein (BCMA) activity in a mammal. The method comprises administering a
 XX specific binding partner for APRIL (G70, a tumor necrosis factor-TNF
 XX family ligand), having the consensus region of TNF α , BCMA, or the TNF α /BCMA
 XX extracellular consensus sequence, but not the extracellular region
 XX of TNF α or BCMA. The method is useful for inhibiting activity of TNF α
 XX and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 XX lymphoproliferative disorders, one or more solid tumours such as lung,
 XX gastrointestinal, pancreatic or prostate tumour, APRIL, BCMA and TNF α
 XX antagonists are useful for treating inflammation and immune function
 XX diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 XX dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 XX disease), drug and insect sting allergy, inflammatory bowel disease
 XX (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 XX sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 XX bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 XX with leucocyte infiltration of the skin or organs. The present sequence
 XX is human-murine B cell maturation protein (BCMA) consensus sequence
 XX cysteine rich region. (Updated on 29-AUG-2003 to standardise OS field)
 XX
 XX Sequence 24 AA;
 XX
 XX Query Match 45.0%; Score 90.5; DB 5; Length 24;
 XX Best Local Similarity 73.3%; Pred. No. 0.00026;
 XX Matches 22; Conservative 0; Mismatches 1; Indels 7; Gaps 4;
 XX
 XX Db 5 EYFDSLHACIPQRCSSNTPPLTCORYC 34
 XX 2 EYFDSLHAC-PC-LRCS-PTCQ-YC 24
 XX
 XX RESULT 58
 XX AAY94006
 XX ID AAY94006 standard; protein; 249 AA.
 XX AC AAY94006;
 XX DT 20-OCT-2000 (first entry)
 XX DE A murine znf4, a tumour necrosis factor ligand.
 XX
 XX Human; BR43x2; TNF α receptor; extracellular domain; BCMA; B cell protein;
 XX transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
 XX znf4 activity; antibody production; autoimmune disease; amyloidosis;
 XX systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
 XX rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
 XX end stage renal failure; glomerulonephritis; vasculitis; nephritis;
 XX renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy;

KW immune response; immunosuppression; graft rejection; joint pain;
 KW graft versus host disease; inflammation; swelling; anaemia; septic shock;
 KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;
 KW renal artery stenosis; occlusion; cholesterol; renal emboli.
 XX
 XX Mus musculus.
 XX
 XX WO200040716-A2.
 XX 13-JUL-2000.
 XX 07-JAN-2000; 2000WO-US000396.
 XX 07-JAN-1999; 99US-00226533.
 XX (ZYMO) ZYMOGENETICS INC.
 XX Gross JA, Xu W, Madden K, Yee DP;
 XX WPI; 2000-452538/39.
 XX N-PSDB; AAA58566.
 XX
 XX Inhibiting znf4 activity in a mammal, to treat autoimmune diseases,
 XX renal disease, graft versus host disease, and inflammation, comprises
 XX administering a BR43x2, TNF α or BCMA extracellular domain polypeptide.
 XX
 XX Disclosure; Page 163; 175pp; English.
 XX
 XX The present sequence represents murine znf4, a tumour necrosis factor
 XX ligand. The extracellular domains of BR43x2 (an isoform of the
 XX transmembrane activator and CAML-interactor (TNF α), TNF α or
 XX BCMA (a related B cell protein) contain a cysteine rich domain, and are
 XX used for inhibiting znf4 activity. They may also be used for inhibiting
 XX BR43x2, TNF α or BCMA receptor-ligand engagement associated with activated
 XX or resting B lymphocytes, effector T-cells, or with antibody production.
 XX The antibody production is associated with an autoimmune disease selected
 XX from systemic lupus erythematosus, myasthenia gravis, multiple sclerosis
 XX and rheumatoid arthritis. The znf4 activity and BR43x2, TNF α or BCMA
 XX receptor-ligand engagement is associated with asthma, bronchitis,
 XX emphysema, end stage renal failure, glomerulonephritis, vasculitis,
 XX nephritis, pyelonephritis, renal neoplasms, multiple myelomas, lymphomas,
 XX light chain neuropathy, amyloidosis, moderating immune response,
 XX immunosuppression, graft rejection, graft versus host disease,
 XX inflammation, insulin dependent diabetes mellitus, Crohn's disease, joint
 XX pain, swelling, anaemia, or septic shock. BR43x2, TNF α , and BCMA
 XX polypeptides, fusions, antibodies, agonists or antagonists can be used to
 XX treat hypertension, renal artery stenosis, or occlusion, and cholesterol
 XX or renal emboli
 XX
 XX Sequence 249 AA;
 XX
 XX Query Match 35.6%; Score 71.5; DB 3; Length 249;
 XX Best Local Similarity 35.3%; Pred. No. 0.73;
 XX Matches 12; Conservative 8; Mismatches 13; Indels 1; Gaps 1;
 XX
 XX Db 1 CSONEYFDSLHACIPQRCSSNTPPLTCORYC 34
 XX 6 CPKQDYWDSRKSVCVSCALTCSSQRS-QRTCTDFC 38
 XX
 XX RESULT 59
 XX ABM85744
 XX ID ABM85744 standard; protein; 249 AA.
 XX AC ABM85744;
 XX DT 18-NOV-2004 (first entry)
 XX DE Mouse protein sequence MCP1369.
 XX
 XX Cytostatic; carcinoma; lymphoma; cancer; murine.
 XX Mus musculus.


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ADRI8913
ID   ADRI8913 standard; protein; 2258 AA.
XX
AC   ADRI8913;
XX
DT   04-NOV-2004 (first entry)
XX
DE   Human mucin-like protein, SCS0004, variant SEQ ID 3.
XX
KW   Antibacterial; Virucide; Antiallergic; Antiasthmatic; Antiinflammatory;
KW   Ophthalmological; Auditory; Vulnereary; Gastrointestinal; Cytostatic;
KW   Gene Therapy; Mucin-like protein; human; mucin; bacterial infection;
KW   allergic asthma; inflammation; viral infection; allergic conjunctivitis;
KW   otitis; tissue injury; epithelial wounding; inflammatory bowel disease;
KW   Crohn's disease; small adenocarcinoma of the lung; lung cancer;
KW   gastric intestinal metaplasia; chronic cholecystitis; skin cancer.
XX
OS   Homo sapiens.
XX
FH   Key
FH   Peptide
FT   /label= Signal_peptide
FT   Protein
FT   /label= Mature_protein
XX
PE   WO2004069136-A2.
XX
PD   19-AUG-2004.
XX
PE   04-FEB-2004; 2004WO-EP050082.
XX
PR   05-FEB-2003; 2003US-0445217P.
XX
PA   (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
XX
PI   Bienkowska J, Mcallister G;
XX
DR   WPI; 2004-604324/58.
XX
PT   New isolated mucin-like polypeptides, useful for diagnosing or treating,
PT   e.g. bacterial infections, allergic asthma, inflammation, allergic
PT   conjunctivitis, otitis, inflammatory bowel disease, Crohn's disease, lung
PT   cancer, or skin cancer.
XX
PS   Claim 2; SEQ ID NO 3; 170pp; English.
XX
CC   The present invention relates to novel mucin-like proteins (I) and their
CC   coding sequences. The present sequence is one such human mucin-like
CC   protein. The mucin-like proteins and coding sequences are useful in the
CC   therapy or in the prevention of a disease when the increase in the mucin-
CC   like activity of a polypeptide is needed e.g. bacterial infections,
CC   allergic asthma, inflammation, respiratory syncytial virus (RSV)-induced
CC   disease, allergic conjunctivitis, otitis, tissue injury, epithelial
CC   wounding, inflammatory bowel disease, Crohn's disease, small
CC   adenocarcinoma of the lung, lung cancer, gastric intestinal metaplasia,
CC   chronic cholecystitis, or skin cancer.
XX
SQ   Sequence 2258 AA;
XX
Query Match          34.1%; Score 68.5; DB 8; Length 2258;
Best Local Similarity 45.2%; Pred. No. 16;
Matches 14; Conservative 2; Mismatches 8; Indels 7; Gaps 1;
XX
QY   1 CSQNEYFDSLHACIPQLRCSSNTPPLTQ 31
    |||:|||||:|:|
Db    1179 CSQDEYFDHEGVCVPCM-----PPTTPQ 1202
XX
RESULT 65
ADRI8915
ID   ADRI8915 standard; protein; 2264 AA.
XX
AC   ADRI8915;
XX

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```

XX
DT   04-NOV-2004 (first entry)
XX
DE   His-tagged Human mucin-like protein, SCS0004, variant SEQ ID 5.
XX
KW   Antibacterial; Virucide; Antiallergic; Antiasthmatic; Antiinflammatory;
KW   Ophthalmological; Auditory; Vulnereary; Gastrointestinal; Cytostatic;
KW   Gene Therapy; Mucin-like protein; human; mucin; bacterial infection;
KW   allergic asthma; inflammation; viral infection; allergic conjunctivitis;
KW   otitis; tissue injury; epithelial wounding; inflammatory bowel disease;
KW   Crohn's disease; small adenocarcinoma of the lung; lung cancer;
KW   gastric intestinal metaplasia; chronic cholecystitis; skin cancer.
XX
OS   Homo sapiens.
XX
PN   WO2004069136-A2.
XX
PD   19-AUG-2004.
XX
PE   04-FEB-2004; 2004WO-EP050082.
XX
PR   05-FEB-2003; 2003US-0445217P.
XX
PA   (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
XX
PI   Bienkowska J, Mcallister G;
XX
DR   WPI; 2004-604324/58.
XX
PT   New isolated mucin-like polypeptides, useful for diagnosing or treating,
PT   e.g. bacterial infections, allergic asthma, inflammation, allergic
PT   conjunctivitis, otitis, inflammatory bowel disease, Crohn's disease, lung
PT   cancer, or skin cancer.
XX
PS   Claim 2; SEQ ID NO 5; 170pp; English.
XX
CC   The present invention relates to novel mucin-like proteins (I) and their
CC   coding sequences. The present sequence is one such human mucin-like
CC   protein. The mucin-like proteins and coding sequences are useful in the
CC   therapy or in the prevention of a disease when the increase in the mucin-
CC   like activity of a polypeptide is needed e.g. bacterial infections,
CC   allergic asthma, inflammation, respiratory syncytial virus (RSV)-induced
CC   disease, allergic conjunctivitis, otitis, tissue injury, epithelial
CC   wounding, inflammatory bowel disease, Crohn's disease, small
CC   adenocarcinoma of the lung, lung cancer, gastric intestinal metaplasia,
CC   chronic cholecystitis, or skin cancer.
XX
SQ   Sequence 2264 AA;
XX
Query Match          34.1%; Score 68.5; DB 8; Length 2264;
Best Local Similarity 45.2%; Pred. No. 16;
Matches 14; Conservative 2; Mismatches 8; Indels 7; Gaps 1;
XX
QY   1 CSQNEYFDSLHACIPQLRCSSNTPPLTQ 31
    |||:|||||:|:|
Db    1179 CSQDEYFDHEGVCVPCM-----PPTTPQ 1202
XX
RESULT 66
ADCI71568
ID   ADCI71568 standard; protein; 1548 AA.
XX
AC   ADCI71568;
XX
DT   18-DEC-2003 (first entry)
XX
DE   Mouse subtilisin-like protein convertase 6 (SPC6).
XX
KW   neuroleptic; subtilisin-like protein convertase 6 agonist;
KW   subtilisin-like protein convertase 6 antagonist; transgenic;
KW   subtilisin-like protein convertase 6; SPC6; schizophrenia.
XX
OS   Mus sp.
XX

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XX PF US2003093824-A1.
XX
XX PD 15-MAY-2003.
XX
XX PF 25-JUN-2002; 2002US-00180903.
XX
XX PR 26-JUN-2001; 2001US-0300978P.
XX PR 24-SEP-2001; 2001US-0324820P.
XX
XX PA (ALLEN) ALLEN K D.
XX
XX PI Allen KD;
XX
XX DR WPI: 2003-777261/73.
XX DR N-PSDB; ADC71567.
XX
XX PS New transgenic mouse useful in methods for identifying potential
PT therapeutic agents for treating a variety of diseases, including
PT schizophrenia, comprises a disruption in a subtilisin-like protein
PT convertase 6 (SPC6) gene.
XX
XX PS Disclosure; SEQ ID NO 2; 34pp; English.
XX
XX CC The invention describes a transgenic mouse (1) comprising a disruption in
XX an subtilisin-like protein convertase (SPC6) gene, where there is no
XX native expression of an endogenous SPC6 gene. The therapeutic agent is
XX administered by inhalation or insufflation or oral, buccal, parenteral,
XX topical, subcutaneous, intraperitoneal, intravenous, intrapleural,
XX intraocular, intraarterial, or rectal route. The transgenic mouse and
XX associated methods are useful for identifying potential therapeutic
XX agents (e.g. SPC6 agonists and antagonists) for treating conditions
XX associated with SPC6. The identified agents are potentially useful for
XX treating diseases such as schizophrenia. The mouse is useful for
XX investigating the biological roles of SPC6. This is the amino acid
XX sequence of mouse SPC6.
XX
XX SQ Sequence 1548 AA;
XX
XX Query Match 33.6%; Score 67.5; DB 7; Length 1548;
XX Best Local Similarity 37.8%; Pred. No. 15;
XX Matches 14; Conservative 4; Mismatches 14; Indels 5; Gaps 1;
XX
XX QY 1 CSQNEFYFDSLHACIPQQLRCSSTNPP-----LTCOR 32
XX DB 1152 CAAVEYWDGSHRCQPCCHKKCSRCSGSPSDQCYTCPR 1188
XX
XX RESULT 67
XX ABB80243
XX ID ABB80243 standard; protein; 1877 AA.
XX
XX AC ABB80243;
XX
XX DT 04-DEC-2003 (first entry)
XX
XX DE Murine subtilase.
XX
XX KW Subtilase; chromosome 9q21.13; EST: expressed sequence tag; kidney;
XX renal cell; head; neck; heart; multiple sclerosis; lesion; cervix;
XX pooled germ cell; tumour; uterus; adenocarcinoma; retina II; stomach;
XX proprotein convertase subtilisin; furin-like repeat; Alzheimer's disease;
XX Parkinson's disease; pain; colon; pelvic pain; pre-oesophageal dysphagia;
XX gastritis; ulcers; urinary incontinence; lupus nephritis;
XX renal transplant rejection; myocardial infarction; erectile dysfunction;
XX ovary; lung; thyroid; carcinoma; lymphoma; Kaposi's sarcoma;
XX congestive heart failure; ischaemia; hypertensive vascular disease.
XX
XX OS Mus musculus.
XX
XX PN WO2003060109-A2.
XX
XX PD 24-JUL-2003.

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XX PF 14-JAN-2003; 2003WO-EP000253.
XX
XX PR 15-JAN-2002; 2002US-0347876P.
XX PR 29-JUL-2002; 2002US-0398734P.
XX
XX PA (FARB ) BAYER AG.
XX
XX PI Koehler RH;
XX
XX DR WPI: 2003-608065/57.
XX
XX PS New subtilase-encoding polynucleotide and its encoded protein, useful for
PT identifying modulators of subtilase activity, and in gene therapy for
PT treating e.g. Alzheimer's disease, cancers, congestive heart failure or
PT ischemia.
XX
XX PS Disclosure; Page 122-26; 135pp; English.
XX
XX CC This sequence shows a murine subtilase. The homologous human subtilase
XX coding sequence is located on chromosome 9q21.13. Related EST's are
XX expressed in kidney (renal cell adenocarcinoma), head and neck tissue,
XX heart, multiple sclerosis lesions, cervix, pooled germ cell tumours,
XX uterus tumour, adenocarcinoma, retina II and stomach. The subtilisin
XX protein is a long membrane bound protein which shows 96% identity to
XX human proprotein convertase subtilisin. There are two blocks of 11 furin-
XX like repeats in the C-terminal portion of the protein. It has one
XX transmembrane domain, also in the C-terminal portion, suggesting that the
XX protein is localised on the outside of the membrane. The subtilase
XX polynucleotide and polypeptide are useful for identifying test compounds,
XX which may act as agonists or antagonists at the receptor site and which
XX can be regulated to provide therapeutic effects. Vectors comprising the
XX polynucleotide are useful for modulating the activity of subtilase in a
XX disease, e.g. a central nervous system disorder, a gastrointestinal
XX disorder, cancer, a cardiovascular disorder, a genitourinary disorder, or
XX diabetes. In particular, these diseases are Alzheimer's disease,
XX Parkinson's disease, pain, colon tumour, pre-oesophageal dysphagia,
XX gastritis, ulcers, urinary incontinence, lupus nephritis, renal
XX transplant rejection, pelvic pain, erectile dysfunction, ovary tumour,
XX lung tumour, thyroid tumour, carcinoma, lymphoma, Kaposi's sarcoma,
XX congestive heart failure, myocardial infarction, ischemia, hypertensive
XX vascular diseases, etc. These are also useful for preventing or
XX ameliorating the diseases cited above
XX
XX SQ Sequence 1877 AA;
XX
XX Query Match 33.6%; Score 67.5; DB 7; Length 1877;
XX Best Local Similarity 37.8%; Pred. No. 18;
XX Matches 14; Conservative 4; Mismatches 14; Indels 5; Gaps 1;
XX
XX QY 1 CSQNEFYFDSLHACIPQQLRCSSTNPP-----LTCOR 32
XX DB 1481 CAAVEYWDGSHRCQPCCHKKCSRCSGSPSDQCYTCPR 1517
XX
XX RESULT 68
XX AAE15495
XX ID AAE15495 standard; peptide; 33 AA.
XX
XX AC AAE15495;
XX
XX DT 12-MAR-2002 (first entry)
XX
XX DE Human TACI cysteine-rich consensus region #1.
XX
XX KW Human; transmembrane activator and intracellular CAML interactor; TACI;
XX cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
XX lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
XX prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
XX drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
XX Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
XX human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
XX rheumatoid arthritis; atherosclerosis.

```


| | | |
|-----------|--|---|
| XX | OS | Homo sapiens. |
| XX | PN | WO200187979-A2. |
| XX | PD | 22-NOV-2001. |
| XX | PF | 14-MAY-2001; 2001WO-US015567. |
| XX | PR | 12-MAY-2000; 2000US-0204039P. |
| XX | PR | 27-JUN-2000; 2000US-0214591P. |
| XX | PR | 14-MAY-2001; 2001US-00214591. |
| XX | PA | (AMGE-) AMGEN INC. |
| XX | PI | Theill LE, Yu G; |
| XX | DR | WPI; 2002-066686/09. |
| XX | PT | Inhibiting activity of B cell maturation protein and/or transmembrane |
| XX | PT | activator and intracellular cyclophilin ligand interactor, by |
| XX | PT | administering a binding partner for APRIL, a tumor necrosis factor family |
| XX | PT | ligand. |
| XX | PS | Claim 1; Fig 12B; 94pp; English. |
| XX | CC | The invention relates to a method for inhibiting TACI (transmembrane |
| XX | CC | activator and intracellular CAML interactor) and/or B cell maturation |
| XX | CC | protein (BCMA) activity in a mammal. The method comprises administering a |
| XX | CC | specific binding partner for APRIL (G70, a tumour necrosis factor-TNF |
| XX | CC | family ligand), having the consensus region of TACI, BCMA, or the TACI/ |
| XX | CC | BCMA extracellular consensus sequence, but not the extracellular region |
| XX | CC | of TACI or BCMA. The method is useful for inhibiting activity of TACI |
| XX | CC | and/or BCMA in a mammal which is useful for treating B-cell or T-cell |
| XX | CC | lymphoproliferative disorders, one or more solid tumours such as lung, |
| XX | CC | gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI |
| XX | CC | antagonists are useful for treating inflammation and immune function |
| XX | CC | diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic |
| XX | CC | dermatitis, respiratory allergic disease (asthma, hypersensitivity lung |
| XX | CC | disease), drug and insect sting allergy, inflammatory bowel disease |
| XX | CC | (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple |
| XX | CC | sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, |
| XX | CC | bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer |
| XX | CC | with leucocyte infiltration of the skin or organs. The present sequence |
| XX | CC | is human TACI cysteine-rich consensus region |
| XX | SQ | Sequence 33 AA; |
| XX | Query Match | 33.1%; Score 66.5; DB 5; Length 33; |
| XX | Best Local Similarity | 32.4%; Pred. No. 0.41; Mismatches 14; Indels 1; Gaps 1 |
| XX | Matches 11; Conservative | 8; |
| OY | 1 CSONEYPDSLTHACIPCOLRCSNTPPLTLCQRVC 34 :: :: :: :: :: | |
| Ddb | 1 CPEDGYMDPILCTCMSCRTKCHQS-QRTCAFC 33 | |
| RESULT 69 | | |
| ADAA49368 | | |
| AC | ADA49368 standard; peptide; 33 AA. | |
| XX | ADA49368; | |
| DT | 20-NOV-2003 (first entry) | |
| DE | Human TACII cysteine rich domain. | |
| KW | TACTL-I; antagonist; immunosuppressive; antirheumatic; antiinflammatory; | |
| KW | antiarthritic; dermatological; antididiabetic; neuroprotective; | |
| KW | anticholel; antipyloric; nephrotoxic; vasotropic; vaccine; | |
| KW | autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus; | |
| KW | insulin dependent diabetes mellitus; multiple sclerosis; | |
| KW | myaethenia gravis; Grave's disease; autoimmune hemolytic anaemia; | |

| | | |
|-----------|---|--|
| KM | | autoimmune thrombocytopenic purpura; Goodpasture's syndrome; |
| KM | | pemphigus vulgaris; acute rheumatic fever; |
| KW | | post-streptococcal glomerulonephritis; polyarteritis nodosa; TAC1L; CRD; |
| KX | | cysteine rich domain. |
| OS | Homo sapiens. | |
| PN | MO2003035846-A2. | |
| PD | 01-MAY-2003. | |
| PF | 24-OCT-2002; 2002WO-US034376. | |
| PR | 24-OCT-2001; 2001US-0345106P. | |
| PR | 14-JAN-2002; 2002US-0348962P. | |
| PR | 07-FEB-2002; 2002US-0354966P. | |
| PR | 13-AUG-2002; 2002US-0403364P. | |
| XX | (NAJE-) NAT JEWISH MEDICAL & RES CENT. | |
| XX | | |
| PI | Zhang G, Shu H, Liu Y, Xu L; | |
| DR | WPI: 2003-403345/38. | |
| XX | | |
| PT | Novel TAL1-1 antagonist protein useful for inhibiting TAL1-1 biological | |
| PT | activity in mammal, has a modification in the region connecting beta | |
| PT | strands D and E that reduces the biological activity of TAL1-1 | |
| PT | antagonist. | |
| XX | | |
| P8 | Disclosure; Page 617; 618pp; English. | |
| XX | | |
| CC | The invention relates to a novel TAL1-1 antagonist protein, comprising a | |
| CC | sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID | |
| CC | NO:2, by at least one modification in the region connecting fbrg; strands | |
| CC | D and E that reduces the biological activity of the TAL1-1 antagonist as | |
| CC | compared to wild-type TAL1-1. A protein of the invention has | |
| CC | immunosuppressive, antirheumatic, antiinflammatory, antiarthritic, | |
| CC | dermatological, antidiabetic, neuroprotective, antihypertic, | |
| CC | nephrotropic, and vasotropic activity. A TAL1-1 antagonist may be used in | |
| CC | a vaccine. A protein of the invention is useful for inhibiting TAL1-1 | |
| CC | biological activity in a mammal. TC is useful for treating autoimmune | |
| CC | diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin | |
| CC | dependent diabetes mellitus, multiple sclerosis, myasthenia gravis, | |
| CC | Grove's disease, autoimmune hemolytic anaemia, autoimmune | |
| CC | thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris, | |
| CC | acute rheumatic fever, post-streptococcal glomerulonephritis and | |
| CC | polyarteritis nodosa. The present sequence represents a cysteine rich | |
| CC | domain (CRD) modle of human TAC1L. | |
| XX | | |
| SQ | Sequence 33 AA; | |
| | | |
| | Query Match 33.1%; Score 66.5; DB 6; Length 33; | |
| | Best Local Similarity 32.4%; Pred. No. 0.41; | |
| | Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1. | |
| OY | 1 CSONEFPESLHACIPCOLRCSSTMPPLTCORYC 34 | |
| | : : : : : : : : | |
| Db | 1 CPBEOYMDPLIGTMCSCRTICNHQS-ORTCAFC 33 | |
| | : : : : : : : : | |
| RESULT 70 | | |
| AAU10951 | | |
| ID | AAU10951 standard; protein, 37 AA. | |
| XX | | |
| XX | AAU10951; | |
| XX | | |
| DT | 12-MAR-2002 (first entry) | |
| DE | Human AGP-3 receptor cysteine rich repeat region #1. | |
| KM | Human; AGP-3; antiinflammatory; antiarthritic; immunosuppressive; | |
| KM | dermatologic; neuroprotective; nootropic; immunomodulator; metabolic; | |
| KM | antidiabetic; analgesic; nephrotropic; osteopathic; cytostatic; fever; | |

OS antiparkinsonian; antisociatic; vasotropic; antibacterial; asthma;
KM AGP-3 receptor; tumor necrosis factor ligand family; AGP-3 receptor;
KM mesenteric lymph node; AGP-3R; inflammatory disease; immune disorder;
KM rheumatoid arthritis; graft-versus-host disease; Crohn's disease;
KM pancreatitis; amyotrophic lateral sclerosis; ALS; Alzheimer's disease;
KM diabetes; glomerulonephritis; inflammatory bowel disease; ischemia;
XX multiple sclerosis; Parkinson's disease; transgenic animal.
XX Homo sapiens.
PN WO200185782-A2.
XX
PD 15-NOV-2001.
XX
PF 12-FEB-2001; 2001WO-US004568.
XX
PR 11-FEB-2000; 2000US-0181800P.
PA (AMGE-) AMGEN INC.
PI Boyle WJ, Hsu H;
DR WPI; 2002-049441/06.
XX
PS Claim 1; Fig 18; 124pp; English.

The invention relates to a composition (I) comprising AGP-3 receptor
(tumor necrosis factor ligand family member) related protein (II)
attached to a vehicle protein. (I) is useful for modulating AGP-3-related
activity in mesenteric lymph nodes (MLN) of a mammal. (II) is useful in
assays to identify cells and tissues that express AGP-3R or proteins
related to AGP-3R-related protein and for identifying compounds (agonists
or antagonists) that interact with AGP-3R proteins. (II) is also useful
for identifying intracellular proteins that interact with the respective
cytoplasmic domains by yeast two-hybrid screening process. (II) is
involved in B cell growth, survival and activation particularly in lymph
node, spleen, and Peyer's patches. AGP-3R agonists and antagonists
identified using (II) are used for modulating B cell response and are
used to treat diseases characterised by inflammatory processes or
deregulated immune response such as rheumatoid arthritis, graft-versus-
host disease, Crohn's disease, lupus, etc. (II) is also useful in the
production of hybridoma cells which are derived from B cells, which
involve treating the hybridoma cells with (II). (II) is useful in the
treatment of inflammatory conditions of joints, e.g., rheumatoid
arthritis, osteoarthritis, etc. (II), its agonists or antagonists are
useful for treating acute pancreatitis, amyotrophic lateral sclerosis
(ALS), Alzheimer's disease, asthma, atherosclerosis, cachexia/anorexia,
diabetes, fever, glomerulonephritis, inflammatory bowel disease,
ischemic injury including cerebral ischemia, multiple myeloma, multiple
sclerosis, osteoporosis, Parkinson's disease, pain, reperfusion injury,
septic shock, etc. The nucleic acids are also useful for developing the
transgenic animals expressing (II), which are useful for producing the
polypeptides and for the study of in vivo biological activity. The
present sequence represents the amino acid sequence of human AGP-3
cysteine-rich repeat region #1

Sequence 37 AA;

| Query Match | 33.1% | Score 66.5 | DB 5 | Length 37 |
|-----------------------|------------------|----------------|------------|-----------|
| Best Local Similarity | 32.4% | Pred. No. 0.46 | | |
| Matches | 11; Conservative | 8; Mismatches | 14; Indels | 1; Gaps |

```

QY      1 CSONEYFDSLHACIPCOLRCSSNPPLTCORYC 34
       |||::|||::|||::|||::|||::|||::|||
Db      2 CPBEGYWDPLLGTGCMSCKTIQHGS-QRTCAAF C 34

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| | | |
|--------------------------|--|---------------------------------|
| ID | ADZ67772 | standard; protein; 48 AA. |
| AC | ADZ67772; | |
| DT | 14-JUL-2005 | (first entry) |
| XX | | |
| XX | Human tumor necrosis factor receptor TNFRI Cys-rich domain. | |
| XX | Tumor necrosis factor receptor; TNFRI; cancer; neoplasm; diagnosis; | |
| KW | cytostatic. | |
| XX | | |
| OS | Homo sapiens. | |
| XX | | |
| XX | WO2005037865-A2. | |
| PN | | |
| PD | 28-APR-2005. | |
| XX | | |
| XX | 18-OCT-2004; 2004MO-US034375. | |
| XX | | |
| PR | 16-OCT-2003; 2003US-0511698P. | |
| PR | 18-OCT-2004; 2004US-0619552P. | |
| XX | | |
| PA | (ZYMO) ZYMOGENETICS INC. | |
| XX | | |
| FI | Fox BA, Holloway JL, Sheppard PO, Dillon SR; | |
| XX | | |
| DR | WPI; 2005-315682/32. | |
| XX | | |
| PT | New tumor necrosis factor receptor (TNFR) polypeptides, useful as | |
| PT | detecting ligands, and for modulating tumor growth, metastasis and | |
| PT | immunity, such as separating resting from stimulated immune cells. | |
| XX | | |
| PS | Disclosure; SEQ ID NO 20; 132pp; English. | |
| XX | | |
| XX | The invention provides novel tumor necrosis factor receptor (TNFR) | |
| CC | zntfr14 polynucleotides ADZ67753 and polypeptides ADZ67754, expression | |
| CC | vectors and antibodies. Zntfr14 polynucleotides are used in claimed | |
| CC | methods for detecting a genetic abnormality in a patient and for | |
| CC | optionally a cancer in a patient. Recombinant zntfr14 polypeptide, | |
| CC | optionally conjugated to a toxin, is used in a claimed method of killing | |
| CC | cancer cells. Zntfr14 polypeptides can be used to detect ligands, | |
| CC | agonists and antagonists. The polypeptides, polynucleotides and | |
| CC | antibodies may also be used in methods that modulate tumor growth, | |
| CC | metastasis, and immunity such as separating resting from stimulated | |
| CC | immune cells. The present sequence is that of the Cys-rich domain of | |
| CC | human TNFR TNFRI ADZ67771. This sequence was compared with that of zntfr14 | |
| CC | in the identification of zntfr14 as a member of the TNFR family. | |
| XX | | |
| SO | Sequence 48 AA: | |
| Query Match | 33.1%; | Score 66.5; DB 9; Length 48; |
| Best Local Similarity | 32.4%; | Pred. No. 0.6; |
| Matches 11; Conservative | 8; | Mismatches 14; Indels 1; Gaps 1 |
| YY | 1 CSQNEFYDSLHACIPQCLRGSSNPPPLTCQRYC 34 | |
| DB | 13 CPBEQYWDPLGLGTCMSCKTICNHQS-QRTCAFC 45 | |
| RESULT 72 | | |
| AAE15500 | | |
| ID | AAE15500 | standard; peptide; 59 AA. |
| XX | | |
| XX | AAE15500; | |
| DT | 12-MAR-2002 | (first entry) |
| XX | | |
| DE | Human TNFRI cysteine rich extracellular region. | |
| XX | | |
| XX | Human, transmembrane activator and intracellular CAML interactor; TNFRI; | |
| KW | cytostatic; B cell maturation protein; BCMA; tumor necrosis factor; TNF; | |
| KW | lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; | |
| KW | prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; | |

KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis.
XX
OS Homo sapiens.
XX
PN MO200187979-A2.
XX
PD 22-NOV-2001.
XX
PF 14-MAY-2001; 2001WO-US015567.
XX
PR 12-MAY-2000; 2000US-0204039P.
PR 27-JUN-2000; 2000US-0214591P.
PR 14-MAY-2001; 2001US-00214591.
XX
PA (AMGE-) AMGEN INC.
XX
PI The111 LE, YU G;
XX
PI WPI; 2002-066686/09.
DR
XX
PT Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor family
PT ligand.
XX
PS Disclosure; Fig 13; 94pp; English.
XX
CC The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering a
CC specific binding partner for APRIL (G70, a tumor necrosis factor-TNF
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human TACI cysteine-rich extracellular region
XX
SQ Sequence 59 AA;
XX
Query Match 33.1%; Score 66.5; DB 5; Length 59;
Best Local Similarity 32.4%; Pred. No. 0.74; Mismatches 1;
Matches 11; Conservative 8; Indels 1; Gaps 1;
XX
QY 1 CSONEYPDSLHACIPQQLRCSSTPPLTQRCYC 34
Db 1 CPBEQYWDPLGTGTCWCKTICNHQS-QRTCAFC 33
XX
RESULT 73
AAW75785
ID AAW75785 standard; protein; 166 AA.
XX
AC AAW75785;
XX
DT 18-JAN-1999 (first entry)
XX
DE Human lymphocyte surface receptor extracellular domain.
XX
KW TACI; transmembrane activator and CAML-interactor;
KW calcium signal-modulating cyclophilin ligand; human;
KW

KW lymphocyte surface receptor; human; B-cell; B lymphocyte; infection;
KW cancer; rheumatoid arthritis; autoimmune disease; glomerulonephritis;
KW immunosuppressive; graft versus host disease; transplant rejection;
KW therapy; signal transduction.
XX
OS Homo sapiens.
XX
PN MO9839361-A1.
XX
PD 11-SEP-1998.
XX
PF 03-MAR-1998; 98WO-US004270.
XX
PR 03-MAR-1997; 97US-00810572.
XX
PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX
PI Bram RJ, Von Bulow G;
XX
PI WPI; 1998-506346/43.
DR
DR N-PSDB; AAV57330.
XX
PT New isolated transmembrane activator protein - used to develop products
PT for treating e.g. infections, cancers, autoimmune and inflammatory
PT conditions, transplant rejection or graft-versus-host disease.
XX
PS Claim 8; Page 73; 89pp; English.
XX
CC This is the amino acid sequence of the N-terminal, i.e. the
CC extracellular, domain of novel human transmembrane activator and CAML-
CC interactor (TACI) protein (see AAW75783). TACI is a lymphocyte receptor
CC protein that is involved in the calcium activation pathway. It is
CC normally present in B-lymphocytes, and to a much lesser extent in
CC immature T-lymphocytes, and can therefore be targeted to specifically
CC regulate B cell responses without affecting T cell activity. The
CC extracellular domain of TACI functions as a binding site for a ligand
CC that stimulates the activation of the cell by inducing the binding of the
CC C-terminal portion (see AAW75784) of TACI to the N-terminal domain of
CC CAML. A recombinant form of the extracellular portion of TACI acts as a
CC dominant-negative or blocking agent and acts to suppress the immune
CC system. It can be used to treat or prevent autoimmune disease, graft
CC rejection or graft versus host disease. The extracellular region is also
CC used in a claimed method for identifying a ligand for TACI, in which
CC binding of a candidate molecule is determined by detecting cellular
CC activation of the AP-1, CAMP or NF-KB pathway, of NF-AT transcription
CC factor, or of NF-AT dependent transcription
XX
SQ Sequence 166 AA;
XX
Query Match 33.1%; Score 66.5; DB 2; Length 166;
Best Local Similarity 32.4%; Pred. No. 2.1;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;
XX
QY 1 CSONEYPDSLHACIPQQLRCSSTPPLTQRCYC 34
Db 34 CPBEQYWDPLGTGTCWCKTICNHQS-QRTCAFC 66
XX
RESULT 74
AAE15494
ID AAE15494 standard; protein; 166 AA.
XX
AC AAE15494;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human TACI extracellular domain.
XX
KW Human; transmembrane activator and intracellular CAML interactor; TACI;
KW cyclostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW

KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis.

OS Homo sapiens.

PN WO200187979-A2.

XX 22-NOV-2001.

XX 14-MAY-2001; 2001WO-US015567.

XX 12-MAY-2000; 2000US-0204039P.

XX 27-JUN-2000; 2000US-0214591P.

XX 14-MAY-2001; 2001US-00214591.

PA (AMGE-) AMGEN INC.

XX Theell LE, Yu G;

PI WPI; 2002-066686/09.

DR Inhibiting activity of B cell maturation protein and/or transmembrane

XX activator and intracellular cyclophilin ligand interactor, by

PT administering a binding partner for APRIL, a tumor necrosis factor family

PT ligand.

PS Claim 1; Fig 12A; 94pp; English.

XX The invention relates to a method for inhibiting TACI (transmembrane

XX activator and intracellular CAML interactor) and/or B cell maturation

CC protein (BCMA) activity in a mammal. The method comprises administering a

CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF

CC family ligand), having the consensus region of TACT, BCMA, or the TACT/

CC BCMA extracellular consensus sequence, but not the extracellular region

CC of TACT or BCMA. The method is useful for inhibiting activity of TACT

CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell

CC lymphoproliferative disorders, one or more solid tumours such as lung,

CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACT

CC antagonists are useful for treating inflammation and immune function

CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic

CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung

CC disease), drug and insect sting allergy, inflammatory bowel disease

CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple

CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,

CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer

CC with leucocyte infiltration of the skin or organs. The present sequence

CC is human TACT protein extracellular domain

XX

SQ Sequence 166 AA;

Query Match 33.1%; Score 66.5; DB 5; Length 166;

Best Local Similarity 32.4%; Pred. No. 2.1;

Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

OY 1 CSONEYFDSLHACIPCOLRCSGNTPLTCQRYC 34

DB 34 CPBEQYWDPLLTGTCMSCKTICNHQS-QRTCAAF 66

RESULT 75

ADN03188

ID ADN03188 standard; protein; 171 AA.

XX

XX ADN03188;

XX 15-JUL-2004 (first entry)

XX Human TACI-HSBP fragment SEQ ID NO:18.

DE transmembrane activator and CAML interactor; TACI; extracellular domain;

XX trimerizing polypeptide; homotrimeric protein complex; antiinflammatory;

KW antiarthritic; antirheumatic; immunosuppressive; antiarteriosclerotic;

KW cytostatic; gene therapy; inflammatory disease; rheumatoid arthritis; inflammatory bowel disease; autoimmune disease; atherosclerosis;

KW osteoporosis; allograft rejection; cancer; human;

KW heat shock binding protein; HSBP; fusion protein.

XX

OS Homo sapiens.

PN WO2004033486-A2.

XX 22-APR-2004.

XX 10-OCT-2003; 2003WO-US032878.

XX 11-OCT-2002; 2002US-0417801P.

XX (ZYMO) ZYMOGENETICS INC.

XX West JW, Brandt CS, Uaspers SR;

PI WPI; 2004-364855/34.

XX N-PSDB; ADN03187.

DR New polypeptide comprising an extracellular domain of the transmembrane

XX activator and calcium-signal modulating cyclophilin ligand (CAML)

PT interactor (TRAC1), and a trimerizing polypeptide, useful for treating

PT inflammatory diseases.

XX

PS Example 4; SEQ ID NO 18; 36pp; English.

XX The present invention describes an isolated polypeptide comprising an

XX extracellular domain of the transmembrane activator and calcium-signal

CC modulating cyclophilin ligand (CAML) interactor (TRAC1), and a trimerizing

CC polypeptide. Also described: (1) a homotrimeric protein complex

CC comprising the polypeptide; (2) an expression vector comprising the

CC following operably linked elements, a transcription promoter, the nucleic

CC acid sequence encoding the polypeptide, and a transcription terminator;

CC (3) a cultured cell into which has been introduced the expression vector,

CC where the cell expresses the polypeptide; (4) producing a homotrimeric

CC protein complex by culturing the cell, and recovering the homotrimeric

CC protein complex; and (5) inhibiting tumour necrosis factor (TNF)-induced

CC B cell proliferation by exposing the B cells to the homotrimeric protein

CC complex. The polypeptide has antiinflammatory, antiarthritic,

CC antirheumatic, immunosuppressive, antiarteriosclerotic and cyostatic

CC activities, and can be used in gene therapy. The polypeptides are useful

CC for treating and controlling inflammatory diseases, e.g. rheumatoid

CC arthritis or inflammatory bowel disease, autoimmune disease,

CC atherosclerosis, osteoporosis, allograft rejection and cancer. The

CC present sequence represents a human TACI and heat shock binding protein

CC (HSBP) fusion protein fragment, which is used in the exemplification of

CC the present invention.

XX

SQ Sequence 171 AA;

Query Match 33.1%; Score 66.5; DB 8; Length 171;

Best Local Similarity 32.4%; Pred. No. 2.2;

Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

OY 1 CSONEYFDSLHACIPCOLRCSGNTPLTCQRYC 34

DB 6 CPBEQYWDPLLTGTCMSCKTICNHQS-QRTCAAF 38

RESULT 76

AAE09244

ID AAE09244 standard; protein; 265 AA.

XX

XX AAE09244;

XX 19-NOV-2001 (first entry)

XX Human TACI splice variant protein.

```

KW Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;
KM TAC1; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
KN autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.
XX Homo sapiens.
OS
XX WO200160397-A1.
XX
XX 23-AUG-2001.
XX
XX 28-NOV-2000; 2000WO-US032378.
XX
XX 16-FEB-2000; 2000US-0182938P.
XX
XX 22-AUG-2000; 2000US-0226986P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pittl RM,
PI Yan M;
XX
XX WPI; 2001-541628/60.
XX
XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
PT activity, for treating autoimmune disorders and cancer, comprises
PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
PT antagonists.
XX
XX Example 1; Fig 6; 160pp; English.
XX
XX The invention relates to methods of using one or more agonists or
CC antagonists to modulate the activity of the members of TNF (tumour
CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g.
CC TAC1 or BCMA. The method is useful for treating pathological conditions
CC or diseases associated with increased TALL-1 and APRIL expression or
CC activity. TALL-1 and APRIL antagonists are used to block the interaction
CC between APRIL and TALL-1 with TAC1 or BCMA. They are useful for treating
CC a mammal suffering from cancer such as leukaemia, lymphoma, myeloma,
CC cancers of lung and colon and autoimmune diseases e.g. rheumatoid
CC arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The
CC present sequence is human TAC1 splice variant protein
XX
XX Sequence 265 AA:
XX
XX Query Match 33.1%; Score 66.5; DB 4; Length 265;
XX Best Local Similarity 32.4%; Pred. No. 3.4;
XX Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps
OY 1 CSONEYFDSLHACIPCOLRGSSWTPPLTCORVC 34
DB 34 CPBQYMDPLIGTCKSKTICNHOS-ORTCAFC 66
XX
XX RESULT 77
XX ABP97723
XX ID ABP97723 standard; protein; 266 AA.
XX
XX ABP97723;
XX
XX 28-MAY-2003 (first entry)
XX
XX Amino acid sequence of an alternatively spliced human TAC1 receptor.
DE
XX Human; TAC1; BR3; receptor; tumour necrosis factor ligand; TNF ligand;
KM TALL-1; April; systemic lupus erythematosus.
XX
XX Homo sapiens.
XX
XX WO2003014294-A2.
XX
XX 20-FEB-2003.
XX
XX 24-JUL-2002; 2002WO-US023487.
XX

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| | |
|-----------------------|---|
| PR | 03-AUG-2001; 2001US-0310114P. |
| PR | 30-APR-2002; 2002US-03771171P. |
| XX | |
| PA | (GETH) GENENTECH INC. |
| XX | |
| PI | Dixit V, Grewal I, Ridgway J, Yan M, |
| DR | WPI; 2003-256560/25. |
| XX | |
| PT | New nucleic acid encoding a TACIs or BR3 polypeptide, useful for |
| PT | preparing a composition for treating systemic lupus erythematosus. |
| XX | |
| PS | Disclosure; Fig 8; 153pp; English. |
| XX | |
| CC | The present sequence represents an alternatively spliced human TACI |
| CC | polypeptide. The specification also describes BR3 polypeptides. TACI and |
| CC | BR3 are receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and |
| CC | CC April bind to the TACI receptor, while TNF family ligands TALL-1 also |
| CC | binds to BR3 receptor. The TACI and BR3 receptor nucleic acid is useful |
| CC | for preparing a composition for treating systemic lupus erythematosus |
| XX | |
| SO | Sequence 266 AA; |
| | |
| Query Match | 33.1%; Score 66.5; DB 6; Length 266; |
| Best Local Similarity | 32.4%; Pred. No. 3.4; |
| Matches | 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1. |
| QY | 1 CSQNEHYPSILHACIPQGLRCSSNTPTTCGRYC 34 |
| | : : : : : : : : : |
| DB | 34 CPEQYWDPLGTGTCMSCKTICNHS-QRTCAFC 66 |
| | |
| RESULT 78 | |
| ID | ADM03442 |
| ID | ADM03442 standard; protein; 266 AA. |
| AC | ADM03442; |
| XX | |
| DT | 24-MAR-2005 (first entry) |
| XX | |
| DE | Human TACI protein amino acid sequence #3. |
| XX | |
| KM | B-lymphocyte; b-cell lymphoma; autoimmune disease; immunosuppressive; |
| KM | non-hodgkin lymphoma; hodgkins disease; cytostatic; |
| KM | chronic lymphocytic leukemia; hairy cell leukemia; rheumatoid arthritis; |
| KM | antiarthritic; antiinflammatory; systemic lupus erythematosus; |
| KM | Wegener granulomatosis; antiallergic; antiinflammatory; vasotropic; |
| KM | inflammatory bowel disease; gastrointestinal-gen; |
| KM | idiopathic thrombocytopenic purpura; hemostatic; multiple sclerosis; |
| KM | asthma; antisthmatic; psoriasis; antipsoriatic; myasthenia gravis; |
| KM | muscular-gen; neuroprotective; vasculitis; diabetes; antidiabetic; |
| KM | glomerulonephritis; nephrotropic; TACI. |
| OS | |
| OS | Homo sapiens. |
| XX | |
| PN | WO2005000351-A2. |
| XX | |
| PD | 06-JAN-2005. |
| XX | |
| PF | 04-JUN-2004; 2004WO-US017693. |
| XX | |
| PR | 05-JUN-2003; 2003US-0476414P. |
| PR | 05-JUN-2003; 2003US-0476481P. |
| PR | 06-JUN-2003; 2003US-0476531P. |
| XX | |
| PA | (GETH) GENENTECH INC. |
| XX | |
| PI | Chan A, Gong Q, Martin F; |
| XX | |
| WPI | WPI; 2005-058069/06. |
| XX | |
| PT | Depleting B cells from a mixed population of cells by contacting the |
| PT | cells with a Blyv antagonist and a CD20 binding antibody, useful for |

| | |
|-----------|---|
| PT | treating B cell malignancies and autoimmune disorders. |
| XX | |
| PS | Disclosure; Fig 8; 114pp; English. |
| CC | |
| XX | |
| CC | The invention comprises a method of depleting B cells from a mixed |
| CC | population of cells, the method involves contacting the mixed population |
| CC | of cells with Bly's antagonist (e.g. an immunoadhesin) and a CD20 binding |
| CC | antibody (e.g. hu2H7.v16). The method of the invention is useful for |
| CC | treating B cell malignancies and autoimmune disorders, such as: non- |
| CC | Hodgkin's lymphoma, Hodgkin's disease, follicular center cell lymphomas, |
| CC | lymphocytic leukemia, hairy cell leukemia, rheumatoid arthritis, systemic |
| CC | lupus erythematosus, Wegener's disease, inflammatory bowel disease, |
| CC | idiopathic thrombocytopenic purpura, multiple sclerosis, asthma, |
| CC | psoriasis, IgA nephropathy, wastrenia gravis, vasculitis, diabetes and |
| CC | glomerulonephritis. The present amino acid sequence represents a human |
| CC | TAC1 protein. |
| XX | |
| XX | Sequence 266 AA: |
| XX | |
| QY | Query Match 33.1%; Score 66.5; DB 9; Length 266; |
| Db | Best Local Similarity 32.4%; Pred. No.3.4; |
| | Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1; |
| RESULT 79 | |
| ID | AAU10949 standard; protein; 291 AA. |
| XX | |
| AC | AAU10949; |
| XX | |
| DT | 12-MAR-2002 (first entry) |
| XX | |
| DE | Human ACP-3 receptor extracellular domain. |
| XX | |
| KW | Human; ACP-3; antiinflammatory; antiarthritic; immunosuppressive; |
| KW | dermatological; neuroprotective; nootropic; immunomodulator; metabolic; |
| KW | antidiabetic; analgesic; nephrotropic; osteopathic; cytostatic; fever; |
| KW | antiparkinsonian; antispasmodic; vasotropic; antibacterial; asthma; |
| KW | ACP-3 receptor; tumour necrosis factor ligand family; ACP-3 receptor; |
| KW | neuroenteric lymph node; ACP-3R; inflammatory disease; immune disorder; |
| KW | rheumatoid arthritis; graft-versus-host disease; Crohn's disease; |
| KW | pancreatitis; amyotrophic lateral sclerosis; ALS; Alzheimer's disease; |
| KW | diabetes; glomerulonephritis; inflammatory bowel disease; ischaemia; |
| KW | multiple sclerosis; Parkinson's disease; transgenic animal. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| XX | WO200185782-A2. |
| PN | |
| XX | |
| PD | 15-NOV-2001. |
| XX | |
| PF | 12-FEB-2001; 2001WO-US004568. |
| XX | |
| PR | 11-FEB-2000; 2000US-0181800P. |
| XX | |
| PA | (AMGE-) AMGEN INC. |
| XX | |
| PI | Boyle WJ, Hsu H; |
| XX | |
| DR | WPI; 2002-049441/06. |
| XX | |
| PT | Composition, useful for identifying modulator of receptor for treating |
| PT | asthma and glomerulonephritis, comprises ACP-3 (tumour necrosis factor |
| PT | ligand family member) receptor and encoding nucleic acids. |
| PS | Claim 1; Fig 18; 124pp; English. |
| XX | |
| CC | The invention relates to a composition (I) comprising ACP-3 receptor |
| CC | (tumour necrosis factor ligand family member) related protein (II) |

| | |
|-----------|---|
| CC | attached to a vehicle protein. (I) is useful for modulating AGP-3-related |
| CC | activity in mesenteric lymph nodes (MLN) of a mammal. (II) is useful in |
| CC | assays to identify cells and tissues that express AGP-3R or proteins |
| CC | related to AGP-3R-related protein and for identifying compounds (agonists |
| CC | or antagonists) that interact with AGP-3R protein. (II) is also useful |
| CC | for identifying intracellular proteins that interact with the respective |
| CC | cytoplasmic domains by yeast two-hybrid screening process. (II) is |
| CC | involved in B cell growth, survival and activation particularly in lymph |
| CC | node, spleen, and Peyer's patches. AGP-3R agonists and antagonists |
| CC | identified using (II) are used for modulating B cell response and are |
| CC | used to treat diseases characterized by inflammatory processes or |
| CC | deregulated immune response such as rheumatoid arthritis, graft-versus- |
| CC | host disease, Crohn's disease, lupus, etc. (II) is also useful in the |
| CC | production of hybridoma cells which are derived from B cells, which |
| CC | involve treating the hybridoma cells with (II). (II) is useful in the |
| CC | treatment of inflammatory conditions of joints, e.g., rheumatoid |
| CC | arthritis, osteoarthritis, etc. (II), its agonists or antagonists are |
| CC | useful for treating acute pancreatitis, amyotrophic lateral sclerosis |
| CC | (ALS), Alzheimer's disease, asthma, atherosclerosis, cachexia/anorexia, |
| CC | diabetes, fever, glomerulonephritis, inflammatory bowel disease, |
| CC | ischemic injury including cerebral ischemia, multiple myeloma, multiple |
| CC | sclerosis, osteoporosis, Parkinson's disease, pain, reperfusion injury, |
| CC | septic shock, etc. The nucleic acids are also useful for developing the |
| CC | transgenic animals expressing (II), which are useful for producing the |
| CC | polypeptides and for the study of in vivo biological activity. The |
| CC | present sequence represents the amino acid sequence of human AGP-3 |
| CC | extracellular domain |
| CC | |
| SO | Sequence 291 AA; |
| QY | Query Match 33.1%; Score 66.5; DB 5; Length 291; |
| Db | Best Local Similarity 32.4%; Pred. No. 3.7; |
| | Matches 11; Conservative %; Mismatches 14; Indels 1; Gaps 1; |
| | 1 CSQNEVFDLSLHACIPCOLRGSSNTPPLTCORVC 34 |
| | : : : : : : : : : |
| | 34 CPBQYMDPLGTGTCMCKTTCNHOS-ORTCAFC 66 |
| RESULT 80 | |
| ADZ67771 | |
| ID | ADZ67771 standard; protein: 292 AA. |
| AC | |
| XX | ADZ67771; |
| XX | |
| DT | 14-JUL-2005 (first entry) |
| XX | |
| DE | Human tumor necrosis factor receptor TAC1. |
| XX | |
| KW | Tumor necrosis factor receptor; TAC1; cancer; neoplasm; diagnosis; |
| KW | cytostatic. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| TH | Key |
| FT | Domain |
| XX | |
| XX | Location/Qualifiers |
| XX | 22..43 |
| XX | /note= "Cys-rich domain" |
| PN | |
| XX | MO2005037865-A2. |
| XX | |
| PD | 28-APR-2005. |
| XX | |
| PF | 18-OCT-2004; 2004MO-US034375. |
| XX | |
| XX | 16-OCT-2003; 2003US-0511698P. |
| XX | 18-OCT-2004; 2004US-0619552P. |
| XX | |
| PA | (ZYMO) ZYMOGENETICS INC. |
| XX | |
| FI | Fox BA, Holloway JL, Shepard PO, Dillon SR; |
| XX | |
| XX | WPI; 2005-315682/32. |

| | |
|-----------------------|---|
| PT | New tumor necrosis factor receptor (TNFR) polypeptides, useful as |
| PT | detecting ligands, and for modulating tumor growth, metastasis and |
| PT | immunity, such as separating resting from stimulated immune cells. |
| XX | |
| PS | Disclosure; SEQ ID NO 19; 132pp; English. |
| XX | |
| CC | The invention provides novel tumor necrosis factor receptor (TNFR) |
| CC | ztnfr14 polynucleotides AD67753 and polypeptides AD67754, expression |
| CC | vectors and antibodies. ztnfr14 polynucleotides are used in claimed |
| CC | methods for detecting a genetic abnormality in a patient and for |
| CC | detecting a cancer in a patient. Recombinant ztnfr14 polypeptide, |
| CC | optionally conjugated to a toxin, is used in a claimed method of killing |
| CC | cancer cells. Ztnfr14 polypeptides can be used to detect ligands, and |
| CC | agonists and antagonists. The polypeptides, polynucleotides and |
| CC | antibodies may also be used in methods that modulate tumor growth, |
| CC | metastasis, and immunity such as separating resting from stimulated |
| CC | immune cells. The present sequence is that of human TNFR TACI. This |
| CC | sequence was compared with that of ztnfr14 in the identification of |
| CC | ztnfr14 as a member of the TNFR family. |
| XX | |
| SQ | Sequence 292 AA; |
| | |
| Query Match | 33.1%; Score 66.5; DB 9; Length 292; |
| Best Local Similarity | 32.4%; Pred. No. 3.7; |
| Matches | 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1; |
| OY | 1 CSONEYFDSLHACIPCOLRCSSNPPTYCQRG 34 : : : : : : : : |
| Dd | 34 CPBEGYWDPLGTCTMCKTICNHQS-QRTCAAF 66 |
| | |
| RESULT 81 | |
| AAM75783 | |
| ID | AAM75783 standard; protein; 293 AA. |
| XX | |
| AAW75783; | |
| XX | |
| DT | 18-JAN-1999 (first entry) |
| DE | Human lymphocyte surface receptor TACI. |
| XX | |
| KW | TACI: transmembrane activator and CAML-interactor; |
| KW | calcium signal-modulating cyclophilin ligand; human; |
| KW | lymphocyte surface receptor; human; B-cell; B lymphocyte; infection; |
| KW | cancer; rheumatoid arthritis; autoimmune disease; glomerulonephritis; |
| KW | immunosuppressive; graft versus host disease; transplant rejection; |
| KW | therapy. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| FH | Key |
| FT | Domain |
| FT | Location/Qualifiers |
| FT | 1..166 |
| FT | /label= Extracellular_domain |
| FT | /note= "Claim 8" |
| FT | 34..71 |
| FT | /note= "TNFR_NGFR motif" |
| FT | 167..186 |
| FT | /label= Transmembrane_domain |
| FT | 187..294 |
| FT | /label= Cytoplasmic_domain |
| FT | /note= "Claim 6" |
| XX | |
| PN | WO9839361-A1. |
| XX | |
| PD | 11-SEP-1998. |
| XX | |
| PP | 03-MAR-1998; |
| PF | 98WO-US004270. |
| PR | 03-MAR-1997; |
| PX | 97US--00810572. |
| PA | (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL. |
| PI | Bram RJ, Von Bulow G; |

| | |
|--|--|
| XX | WP1; 1998-506346/43. |
| DR | N-PSDB; AAW57328. |
| XX | |
| PT | New isolated transmembrane activator protein - used to develop products |
| PR | for treating e.g. infections, cancers, autoimmune and inflammatory |
| PT | conditions, transplant rejection or graft-versus-host disease. |
| XX | |
| PS | Claim 20; Fig 2a; 89pp; English. |
| XX | |
| CC | This is the amino acid sequence of novel human transmembrane activator |
| CC | and CML-interactor (TRCII) protein, a lymphocyte receptor protein that is |
| CC | involved in the calcium activation pathway. TRCII is normally present in B |
| CC | -lymphocytes, and to a much lesser extent in immature T-lymphocytes, and |
| CC | can therefore be targeted to specifically regulate B cell responses |
| CC | without affecting T cell activity. TRCII cDNA (see57328) was isolated |
| CC | from a B-lymphocyte cDNA library using a yeast two-hybrid assay. Also |
| CC | claimed are the C-terminal (see AAW5784) and N-terminal (see AAW5785) |
| CC | fragments of TRCII, recombinant DNA constructs, unicellular hosts, and |
| CC | antibodies to TRCII protein. Methods are claimed for identifying a ligand |
| CC | for TRCII and for identifying immunosuppressive drugs that selectively |
| CC | block the action of B lymphocytes without affecting mature T lymphocytes. |
| CC | TRCII can be activated to increase immune system activity, e.g. for |
| CC | treating infections or cancers. It can be blocked to provide |
| CC | immunosuppression, e.g. for treating autoimmune and inflammatory |
| CC | conditions such as immune complex- induced vasculitis, |
| CC | glomerulonephritis, haemolytic anaemia, myasthenia gravis, type II |
| CC | collagen-induced arthritis, experimental allergic and hyperacute |
| CC | xenograft rejection, rheumatoid arthritis, systemic lupus erythematosus, |
| CC | transplant rejection, cancer or graft versus host disease |
| XX | |
| SO | Sequence 293 AA; |
| | |
| Query Match | 33.1%; Score 66.5; DB 2; Length 293; |
| Best Local Similarity | 32.4%; Pred. No. 3.7; |
| Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1; | |
| Qy | 1 CSQNEYFDLSLHACIPQQLRCSSNTPLTCQRYC 34 |
| | : : : : : : : : : : |
| Db | 34 CPSEQYWDPLLGTGTCMSCKTICNHQS-ORTCAAFc 66 |
| | |
| RESULT 82 | |
| AAB36312 | |
| ID | AAB36312 standard; protein: 293 AA. |
| XX | |
| AC | AAB36312; |
| XX | |
| DT | 26-FEB-2001 (first entry) |
| XX | |
| DE | Human neutrokinine-alpha binding protein TR17 SEQ ID NO:2. |
| XX | |
| KW | Human; neutrokinine-alpha binding protein; NAR protein; TR17; cytostatic; |
| KW | immunosuppressive; nocrotropic; neuroprotective; antiviral; antiallergic; |
| KW | hepatotropic; antidiabetic; antiinflammatory; antitumor; cardiatic; |
| KW | ophthalmological; gene therapy; immunodeficiency disorder; diagnosis; |
| KW | autoimmune disorder. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| PN | WO200058362-A1. |
| XX | |
| PD | 05-OCT-2000. |
| XX | |
| XX | 24-MAR-2000; 2000WO-US007966. |
| PF | |
| XX | 26-MAR-1999; 99US-0126599P. |
| PR | 10-MAR-2000; 2000US-0188208P. |
| XX | |
| PA | (HUMA-) HUMAN GENOME SCI INC. |
| XX | |
| PI | Ruben SM, Ullrich S, Baker K; |
| XX | |

| | | |
|-----------|---|--------------------------------------|
| DR | | WPI: 2000-602359/57. |
| DR | N-PSDB; AAC64602. | |
| PT | | |
| XX | | |
| PT | | |
| PT | | |
| XX | | |
| PS | Claim 1; Fig 1; 398pp; English. | |
| CC | The present sequence represents the human neutrokin-alpha binding (NAR) | |
| CC | protein designated TR17. TR17 has cytostatic, immunosuppressive, | |
| CC | nootropic, neuroprotective, antiviral, antiallergic, hepatotropic, | |
| CC | antidiabetic, antiinflammatory, anticancer, cardiant and ophthalmological | |
| CC | activities and can be used in gene therapy. The TR17 protein and | |
| CC | antibodies are useful for treating and diagnosing immunodeficiency | |
| CC | disorders and autoimmune disorders. The TR17 polypeptides, | |
| CC | polynucleotides, antibodies, agonists and/or antagonists are used for | |
| CC | treating various other diseases defined in the specification and as | |
| CC | research tools for studying the phenotypic effects that result from | |
| CC | inhibiting TR17/TR17 ligand interactions on various cell types | |
| SQ | Sequence 293 AA; | |
| OY | Query Match | 33.1%; Score 66.5; DB 3; Length 293; |
| | Best Local Similarity | 32.4%; Pred. No. 3.7; |
| Db | Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 14 | |
| | 1 CSONEYPDSLHACIPCOLRCSNTPPELTQRVC 34 | |
| | : : : : : : : | |
| | 34 CPEGYMDPLGLGTCTMCKTTCNHGS-QRTCAFC 66 | |
| RESULT 83 | | |
| ID | AAV94000 | |
| AC | AAV94000 standard; protein; 293 AA. | |
| XX | AAV94000; | |
| DT | 20-OCT-2000 (first entry) | |
| DE | A transmembrane activator and CAML-interactor (TACI). | |
| KW | Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein; | |
| KW | transmembrane activator and CAML-interactor; tumour necrosis factor; TNF; | |
| KW | zeta4 activity; antibody production; autoimmune disease; amyloidosis; | |
| KW | systemic lupus erythematosus; myasthenia gravis; multiple sclerosis; | |
| KW | rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis; | |
| KW | end stage renal failure; glomerulonephritis; vasculitis; nephritis; | |
| KW | renal neoplasia; multiple myeloma; lymphoma; light chain neuropathy; | |
| KW | immune response; immunosuppression; graft rejection; joint pain; | |
| KW | graft versus host disease; inflammation; swelling; anaemia; septic shock; | |
| KW | insulin dependent diabetes mellitus; Crohn's disease; hypertension; | |
| KW | renal artery stenosis; occlusion; cholesterol; renal emboli. | |
| OS | Homo sapiens. | |
| PN | WO200040716-A2. | |
| XX | 13-JUL-2000. | |
| PD | | |
| XX | | |
| Pf | 07-JAN-2000; 2000WO-US000396. | |
| XX | | |
| PR | 07-JAN-1999; 99US-00226533. | |
| XX | | |
| PA | (ZYMO) ZYMOGENETICS INC. | |
| XX | | |
| PI | Gross JA, Xu W, Madden K, Yee DP; | |
| XX | | |
| XX | WPI: 2000-452538/39. | |
| DR | N-PSDB; AAA58558. | |
| XX | | |
| PT | Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases, | |
| PT | renal disease, graft versus host disease, and inflammation, comprises | |

| | | |
|-----------|--|---|
| PT | | administering a BR43x2, TACI or BCMA extracellular domain polypeptide. |
| PS | Disclosure; Page 149-150; 175pp; English. | |
| CC | | The present sequence represents a human transmembrane activator and CAML- |
| XX | | interactor (TACI) receptor. TACI is a tumor necrosis factor (TNF) |
| CC | | receptor. The extracellular domains of BR43x2 (an isoform of TACI), TACI |
| CC | | or BCMA (a related B cell protein) receptor contain a cysteine rich |
| CC | | domain, and are used for inhibiting tnfr4 activity. Tnfr4 is a TNF |
| CC | | ligand. They may also be used for inhibiting BR43x2, TACI or BCMA |
| CC | | receptor-ligand engagement associated with activated or resting B |
| CC | | lymphocytes, effector T-cells, or with antibody production. The antibody |
| CC | | production is associated with an autoimmune disease selected from |
| CC | | systemic lupus erythematosus, myasthenia gravis, multiple sclerosis and |
| CC | | rheumatoid arthritis. The tnfr4 activity and BR43x2, TACI or BCMA |
| CC | | receptor-ligand engagement is associated with asthma, bronchitis, |
| CC | | emphysema, end stage renal failure, glomerulonephritis, vasculitis, |
| CC | | neuropitis, ptyelonephritis, renal neoplasms, multiple myelomas, lymphomas, |
| CC | | light chain neuropathy, amyloidosis, moderating immune response, |
| CC | | immunosuppression, graft rejection, graft versus host disease, |
| CC | | inflammation, insulin dependent diabetes mellitus, Crohn's disease, joint |
| CC | | pain, swelling, anaemia, or septic shock. BR43x2, TACI, and BCMA |
| CC | | polypeptides, fusions, antibodies, agonists or antagonists can be used to |
| CC | | treat hypertension, renal artery stenosis, or occlusion, and cholesterol |
| CC | | or renal emboli |
| SQ | Sequence 293 AA; | |
| | | |
| | Query Match | 33.1%; Score 66.5; DB 3; Length 293; |
| | Best Local Similarity | 32.4%; Pred. No.3.7; Mismatches 8; Indels 14; Gaps 1. |
| Oy | 1 CSQNEYPDSLHACIPQLRCSNTPLTCORC 34 | |
| | : : : : : : | |
| Db | 34 CPREGYMDPLLGTGCMSCKTCINHQDS-QRTCAFC 66 | |
| | | |
| RESULT 84 | | |
| ID | AAB09240 standard; protein; 293 AA. | |
| AAE09240 | | |
| AC | AAE09240; | |
| XX | | |
| DT | 19-NOV-2001 (first entry) | |
| XX | | |
| DE | Human TACI protein. | |
| XX | | |
| KW | Human; TNF; tumor necrosis factor; TALL-1; APRIL; TNF receptor; TNFR; | |
| KM | TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma; | |
| KW | autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis. | |
| OS | Homo sapiens. | |
| XX | | |
| PN | WO200160397-A1. | |
| PD | 23-AUG-2001. | |
| XX | | |
| PF | 28-NOV-2000; 2000WO-USO32378. | |
| PR | 16-FEB-2000; 2000US-0182938P. | |
| PR | 22-AUG-2000; 2000US-0226986P. | |
| PA | (GETH) GENENTECH INC. | |
| XX | | |
| P1 | Ashkenazi AJ, Dodge KJ, Grewal I, Kim KJ, Masters SA, Picci RM; | |
| PI | Yan M; | |
| DR | WPI; 2001-541628/60. | |
| DR | N-PSDB; AAD15901. | |
| XX | | |
| PT | Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological | |
| XX | activity, for treating autoimmune disorders and cancer, comprises | |
| PT | exposing the cells to TALL-1 or APRIL polypeptide agonists or | |

PT mammal comprises administering transmembrane activator CAML interactor
PT protein reagent.
PS Claim 8; Fig 1; 42pp; English.
XX
XX This sequence represents the human transmembrane activator CAML
CC interactor protein (TACI). The invention relates to treating a mammal for
CC a condition associated with undesired cell proliferation (e.g. a solid
CC tumour, or reducing the size of a solid tumour located on or in a mammal)
CC comprising administering a transmembrane activator CAML interactor
CC protein (TACI) reagent. The TACI reagent has cytostatic and vulnerary
CC activity. Treating a mammal (e.g. human, cow, horse, dog, mouse, rat or
CC cat) for a condition associated with undesired cell proliferation (e.g.
CC cancer such as renal cell cancer, Kaposi's sarcoma, breast cancer,
CC sarcoma, ovarian carcinoma, rectal cancer, throat cancer, melanoma, colon
CC cancer, bladder cancer, mastocytoma, lung cancer, mammary adenocarcinoma,
CC pharyngeal squamous cell carcinoma, gastrointestinal cancer or stomach
CC cancer). The method is also useful for treating cellular
CC hyperproliferation (hyperplasia) such as scleroderma, pannus formation in
CC rheumatoid arthritis, post-surgical scarring and lung, liver and uterine
CC fibrosis. The TACI reagent of the invention can extend mean survival time
CC of a mammal by 25% as compared to the mean survival time of a mammal in
CC the absence of administering the TACI reagent. The TACI reagent also
CC reduces the size of the tumour by 25% or more
SQ Sequence 293 AA;
SQ
Query Match 33.1%; Score 66.5; DB 5; Length 293;
Best Local Similarity 32.4%; Pred. No. 3.7; Mismatches 14; Indels 1; Gaps 1;
Matches 11; Conservative 8;
OY 1 CSONEYFDSLHACIPCOLRCSSNPPTLCQRYC 34
ID 34 CPBEQYWDPLGTGCMSCRTICNHQS-QRTCAFC 66
DB
RESULT 87
ABB81488
ID ABB81488 standard; protein; 293 AA.
XX
XX ABB81488;
AC
XX
XX 02-SEP-2002 (first entry)
DT
XX
XX Human TACI receptor related protein SEQ ID NO:8.
DE
XX
XX Human; Ztnfr12; tumour necrosis factor receptor; cytostatic;
KW immunosuppressive; dermatological; antiinflammatory; antidiabetic;
KW neuroprotective; antirheumatic; antiarthritic; antialasthmatic;
KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;
KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
KW pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;
KW light chain neuropathy; hypertension; large vessel disease;
KW graft-versus host disease; graft rejection; Crohn's disease.
XX
XX Homo sapiens.
OS
XX
XX WO200238766-A2.
PN
XX
XX 16-MAY-2002.
PD
XX
XX 05-NOV-2001; 2001WO-US047018.
PF
XX
XX 07-NOV-2000; 2000US-0246449P.
PR 20-DEC-2000; 2000US-0257131P.
PR 28-JUN-2001; 2001US-0301715P.
PR 29-AUG-2001; 2001US-0315565P.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX

PI Gross JA, Xu W, Henne RM, Grant FJ;
XX
XX WPI; 2002-508212/54.
DR
XX
XX Novel isolated human tumor necrosis factor receptor polypeptide, termed
PT Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage
PT renal failure or renal disease and lymphoma.
PS Disclosure; Page 136-137; 154pp; English.
XX
XX The present invention describes a human tumour necrosis factor receptor
CC designated Ztnfr12 (1). (1) has cytostatic, immunosuppressive,
CC dermatologic, antiinflammatory, neuroprotective, antidiabetic,
CC antirheumatic, antiarthritic, antialasthmatic, nephrotropic and hypotensive
CC activities, and can be used in gene therapy. (1) can be used for
CC inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12
CC (e.g. ZTNF4), for treating disorders and diseases associated with B
CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
CC inhibiting the proliferation of tumour cells. (1) is useful for treating
CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
CC leukaemia, nephritis, and pyelonephritis, and for treating renal
CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
CC amyloidosis, hypertension, large vessel diseases, graft-versus host
CC disease, graft rejection and Crohn's disease. (1) is useful for
CC modulating the immune system, for regulating B cell responses and
CC development, for modulating development of other cells, antibody
CC production and cytokine production, and for modulating T and B cell
CC communication. The present sequence represents a protein which is given
CC in the exemplification of the present invention
SQ Sequence 293 AA;
SQ
Query Match 33.1%; Score 66.5; DB 5; Length 293;
Best Local Similarity 32.4%; Pred. No. 3.7; Mismatches 14; Indels 1; Gaps 1;
Matches 11; Conservative 8;
OY 1 CSONEYFDSLHACIPCOLRCSSNPPTLCQRYC 34
ID 34 CPBEQYWDPLGTGCMSCRTICNHQS-QRTCAFC 66
DB
RESULT 88
AAU99512
ID AAU99512 standard; protein; 293 AA.
XX
XX AAU99512;
AC
XX
XX 07-OCT-2002 (first entry)
DT
XX
XX Human TACI-IgG Fc fusion protein.
DE
XX
XX Human; tumour necrosis factor; TNF delta; pulmonary system disorder;
KW immunoglobulin production; B-cell proliferation; immune system disorder;
KW autoimmune disease; cancer; lymphoproliferative disorder; pain;
KW microbial infection; parasitic infection; bone disease; atherosclerosis;
KW cardiovascular disorder; neurodegenerative disease; wound healing;
KW graft versus host disease; haematopoietic cell disorder; nephritis;
KW transmembrane activator and CAML-interactor; TACI; TNF epsilon; IgG;
KW immunoglobulin G; Fc portion.
XX
XX Homo sapiens.
OS
XX
XX US2002064829-A1.
PN
XX
XX 30-MAY-2002.
PD
XX
XX 14-JUN-2001; 2001US-00879919.
PF
XX
XX 14-MAR-1996; 96US-0016812P.
PR 12-MAR-1997; 97US-00815783.
XX

| | | | |
|--------------------------|---|---------------------|-------------------|
| PR | 15-JUN-2000; | 2000US-0211537P. | |
| PR | 23-OCT-2000; | 2000US-0241952P. | |
| PR | 13-DEC-2000; | 2000US-0254875P. | |
| PR | 16-MAR-2001; | 2001US-0276248P. | |
| PR | 23-MAR-2001; | 2001US-0277978P. | |
| PR | 25-MAY-2001; | 2001US-0293499P. | |
| PA | (HUMA-) HUMAN GENOME SCI INC. | | |
| XX | | | |
| PI | Yu G, Ni J, Gentz RL, Dillon PJ; | | |
| DR | WPI; 2002-556722/59. | | |
| XX | | | |
| PT | Novel human multimeric tumor necrosis factor delta or epsilon protein | | |
| PT | useful for treating disease or disorder of immune system such as | | |
| PT | autoimmune disease, immunodeficiency, or cancer of immune system. | | |
| XX | | | |
| PS | Example 29; Page 125; 143pp; English. | | |
| XX | | | |
| CC | The present invention relates to the isolation of human tumour necrosis | | |
| CC | factor (TNF) delta and TNF epsilon proteins, and the polynucleotide | | |
| CC | sequences encoding them. The proteins are useful for modulating | | |
| CC | immunoglobulin production or for modulating proliferation of B-cells. The | | |
| CC | sequences of the invention are useful for treating diseases or disorders | | |
| CC | of the immune system. Such disorders include autoimmune diseases (e.g. | | |
| CC | systemic lupus erythematosus (SLE), acquired immunodeficiency syndrome | | |
| CC | (AIDS)), cancers of the immune system (e.g. chronic lymphocytic leukaemia | | |
| CC | (CLL), multiple myeloma, non-Hodgkin's lymphoma or Hodgkin's disease), | | |
| CC | lymphoproliferative disorders, microbial infections (e.g. viral, | | |
| CC | bacterial), parasitic infections, nephritis, bone disease (e.g. | | |
| CC | osteoporosis), atherosclerosis, pain, cardiovascular disorders (e.g. | | |
| CC | myocardial infarction, stroke), neurodegenerative diseases (e.g. | | |
| CC | Alzheimer's disease, Parkinson's disease), graft versus host disease, | | |
| CC | wound healing, hematopoietic cell disorders (e.g. anaemia), inflammatory | | |
| CC | disorders (e.g. asthma) diseases or disorders associated with various | | |
| CC | mucous membranes of the body (e.g. mucositis), and disorders of the | | |
| CC | pulmonary system. The proteins are also useful as a vaccine adjuvant that | | |
| CC | enhances immune responsiveness to specific antigens. The present sequence | | |
| CC | for human transmembrane activator and CAML-interactor (TACI) - | | |
| CC | immunoglobulin G (IgG) Fc fusion protein is used in the examples of the | | |
| CC | present invention | | |
| SQ | Sequence 293 AA; | | |
| Query Match | 33.1%; | Score 66.5; | DB 5; Length 293; |
| Best Local Similarity | 32.4%; | Pred. No. 3.7; | |
| Matches 11; Conservative | 8; | Mismatches 14; | Indels 1; Gaps 1 |
| Oy | 1 CSQNEYPDSLHACIPQOLRGSSNTPPLTCCNYC 34 | | |
| | : : : : : : : : : | | |
| Db | 34 CPEEQYMDPLGLGTCSCKTICNHQS-QRTCAFC 66 | | |
| RESULT 89 | | | |
| ID | AAE28962 | | |
| | AAE28962 standard; protein; 293 AA. | | |
| XX | AAE28962; | | |
| XX | | | |
| DT | 27-JAN-2003 (first entry) | | |
| XX | | | |
| DE | Human TACI protein. | | |
| XX | | | |
| KW | Human; tumour; B-cell maturation antigen; transmembrane activator; | | |
| KW | calcium-modulator; cyclophilin ligand-interactor; TACI; gene therapy; | | |
| KW | neoplasm; chronic lymphocytic leukaemia; lymphoproliferative disease; | | |
| KW | non-Hodgkin's lymphoma; light chain gammopathy; inflammation; asthma; | | |
| XX | BCNA; multiple myeloma. | | |
| OS | Homo sapiens. | | |
| XX | | | |
| FT | Key | Location/Qualifiers | |
| FT | Domain | 30..154 | |

| | | |
|-----------------------|---|--|
| FT | | /note= "Extracellular domain; antigenic epitope" |
| FT | Region | 34..66 |
| FT | | /note= "Cysteine rich region" |
| FT | Region | 71..104 |
| FT | | /note= "Cysteine rich region" |
| PX | | |
| PN | WO20026516-A2. | |
| PD | | |
| XX | 29-AUG-2002. | |
| PF | 06-FEB-2002; 2002WO-US003500. | |
| PR | 20-FEB-2001; 2001US-0270274P. | |
| PR | 12-APR-2001; 2001US-0283447P. | |
| XX | (ZYMO) ZYMOGENETICS INC. | |
| PA | | |
| PI | Kindsvogel W; | |
| XX | | |
| DR | WPI; 2002-723183/78. | |
| DR | N-PSDB; AAD46411. | |
| XX | | |
| PT | B-cell maturation antigen and transmembrane activator and calcium-modulator and cyclophilin ligand-interactor, useful for treating disorders e.g. inflammation or lymphoma. | |
| XX | | |
| PS | Claim 9; Page 66; 67pp; English. | |
| XX | | |
| CC | The invention relates to the manufacture of a composition for inhibiting the proliferation of tumour cells. The method involves using an antibody component that binds both the B-cell maturation antigen (BCMA) and the transmembrane activator and calcium-modulator and cyclophilin ligand-interactor (TACI). BCMA and TACI binding antibody compositions are useful for inhibiting proliferation of tumour cells, particularly inhibiting ZTNF4 activity in a mammal associated with increased endogenous antibody production or a disorder consisting of neoplasia, chronic lymphocytic leukaemia, multiple myeloma, non-Hodgkin's lymphoma, post-transplantation lymphoproliferative disease or light chain gammopathy or inflammation e.g. asthma. The invention is also useful in gene therapy. The present is human TACI protein | |
| SO | Sequence 293 AA; | |
| Query Match | 33.1%; Score 66.5; DB 5; Length 293; | |
| Best Local Similarity | 32.4%; Pred. No. 3.7; | |
| Matches | 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1, | |
| Oy | 1 CSQNEYPDSLHACIPCOLRGSSNMPPLTCGRYC 34 | |
| Db | 34 CPBEOYMDPLGLGTGMSCKTTGNHS-QRTCAFC 66 | |
| RESULT 90 | | |
| AU075408 | | |
| ID | AU075408 standard; protein: 293 AA. | |
| XX | | |
| DT | 09-APR-2002 (first entry) | |
| DE | Tumour necrosis factor (TNF) receptor TACI-Fc fusion. | |
| XX | | |
| KM | Tumour necrosis factor; TNF; cytostatic; arteriosclerosis; analgesic; cerebioprotective; neurotropic; neuroprotective; hepatotropic; immunoglobulin production; B cell proliferation; immunosuppressive; HIV; human immunodeficiency virus; autoimmune disease; immunodeficiency; Sjogren's syndrome; systemic lupus erythematosus; Hodgkin's disease; common variable immunodeficiency; CVID; non-Hodgkin's lymphoma; AIDS; acquired immunodeficiency virus; cancer; multiple myeloma; CLL; chronic lymphocytic leukaemia; lymphoproliferative disorder; bacterial infection; viral infection; osteoporosis; atherosclerosis; pain; cardiovascular disorder; stroke; allergy; Alzheimer's disease; neurodegenerative disease; inflammation; liver disease; cirrhosis; | |
| KW | | |

KW cardiomyopathy; diabetes; asthma; psoriasis; glomerulonephritis;
 KW ulcerative colitis; angiodenesis; septic shock; wound healing;
 KW tumour necrosis factor receptor; TACI; immunoglobulin; IgG.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO200196528-A2.
 XX
 PD 20-DEC-2001.
 XX
 PF 14-JUN-2001; 2001WO-US019026.
 XX
 PR 15-JUN-2000; 2000US-0211537P.
 PR 23-OCT-2000; 2000US-0241952P.
 PR 13-DEC-2000; 2000US-0254875P.
 PR 16-MAR-2001; 2001US-0276248P.
 PR 23-MAR-2001; 2001US-0277978P.
 PR 25-MAY-2001; 2001US-0293499P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Yu G, Ni J, Gentz RL, Dillon RJ, Hilbert D;
 XX
 DR WPI; 2002-130727/17.
 DR N-PSDB; ABR13415.
 XX
 PT Novel multimeric human tumor necrosis factor delta or epsilon protein
 PT useful for treating cancer, immune system disorders, infection,
 PT cardiovascular disorders, liver disease, cardiomyopathy, diabetes and
 PT psoriasis.
 PT
 PS Example 29; Page 341-342; 344pp; English.
 XX
 XX The invention describes a multimeric human tumour necrosis factor (TNF)
 CC delta or epsilon protein (I) or a composition containing them (II)
 CC are useful for modulating immunoglobulin production or proliferation of B
 CC cells. (I) or (II) is useful: for treating a disease or disorder of the
 CC immune system, preferably an autoimmune disease (e.g. Sjogren's syndrome,
 CC systemic lupus erythematosus or common variable immunodeficiency (CVID));
 CC an immunodeficiency e.g. acquired immunodeficiency syndrome (AIDS);
 CC cancer of the immune system (e.g. Hodgkin's disease, non-Hodgkin's
 CC lymphoma, multiple myeloma and chronic lymphocytic leukaemia (CLL)); in
 CC the diagnosis and treatment or prevention of cancer, lymphoproliferative
 CC disorder, bacterial and viral infections, osteoporosis, atherosclerosis,
 CC pain, cardiovascular disorders (e.g. stroke), allergy, inflammation,
 CC neurodegenerative disease (e.g. Alzheimer's disease), liver disease, (e.g.
 CC cirrhosis), cardiomyopathy, diabetes, asthma, psoriasis, septic shock,
 CC glomerulonephritis, ulcerative colitis, arteriosclerosis; for promoting
 CC angiogenesis and wound healing; as a diagnostic research reagent; as an
 CC agent to target and kill cells expressing a TNFdelta and/or TNFepsilon
 CC receptor; in apoptosis of transformed cell lines; mediation of cell
 CC activation and proliferation; and as an immunogen to produce (II). (II)
 CC is useful to purify, detect and target (I), for measuring levels of (I)
 CC in biological samples, for immunophenotyping samples, and to treat,
 CC inhibit or prevent diseases and disorders associated with aberrant
 CC expression and/or activity of (I). This is the amino acid sequence of a
 CC fusion protein of tumour necrosis factor receptor TNCI and immunoglobulin
 CC G (IgG) crystallisation fragment, described in the method of the
 CC invention
 CC
 XX
 SQ Sequence 293 AA;
 Query Match 33.1%; Score 66.5; DB 5; Length 293;
 Best Local Similarity 32.4%; Pred. No. 3.7;
 Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

AAU09900
 ID AAU09900 standard; protein; 293 AA.
 XX
 AC AAU09900;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human AGP-3 related protein receptor.
 XX
 KW Human AGP-3; antiinflammatory; antiarthritic; immunosuppressive;
 KW dermatological; neuroprotective; nocotropic; immunomodulator; metabolic;
 KW antidiabetic; analgesic; nephrotoxic; osteopathic; cyostatic; fever;
 KW antiparkinsonian; antipsoriatic; vasotropic; antibacterial; asthma;
 KW AGP-3 receptor; tumour necrosis factor ligand family; AGP-3 receptor;
 KW mesenteric lymph node; AGP-3R; inflammatory disease; immune disorder;
 KW rheumatoid arthritis; graft-versus-host disease; Crohn's disease;
 KW pancreatitis; amyotrophic lateral sclerosis; ALS; Alzheimer's disease;
 KW diabetes; glomerulonephritis; inflammatory bowel disease; ischaemia;
 KW multiple sclerosis; Parkinson's disease; transgenic animal.
 XX
 OS Homo sapiens.
 OS
 PN WO200185782-A2.
 XX
 PD 15-NOV-2001.
 PD
 PF 12-FEB-2001; 2001WO-US004568.
 XX
 PR 11-FEB-2000; 2000US-0181800P.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Boyle WJ, Hsu H;
 XX
 DR WPI: 2002-049441/06.
 DR N-PSDB; AAS18558.
 XX
 PT Composition, useful for identifying modulator of receptor for treating
 PT asthma and glomerulonephritis, comprises AGP-3 (tumour necrosis factor
 PT ligand family member) receptor and encoding nucleic acids.
 PT
 PS Disclosure; Page 117-119; 124pp; English.
 XX
 XX The invention relates to a composition (I) comprising AGP-3 receptor
 CC (tumour necrosis factor ligand family member) related protein (II)
 CC attached to a vehicle protein. (I) is useful for modulating AGP-3-related
 CC activity in mesenteric lymph nodes (MLN) of a mammal. (II) is useful in
 CC assays to identify cells and tissues that express AGP-3R or proteins
 CC related to AGP-3R-related protein and for identifying compounds (agonists
 CC or antagonists) that interact with AGP-3R proteins. (II) is also useful
 CC for identifying intracellular proteins that interact with the respective
 CC cytoplasmic domains by yeast two-hybrid screening process. (II) is
 CC involved in B cell growth, survival and activation particularly in lymph
 CC node, spleen, and Peyer's patches. AGP-3R agonists and antagonists
 CC identified using (II) are used for modulating B cell response and are
 CC used to treat diseases characterised by inflammatory processes or
 CC deregulated immune response such as rheumatoid arthritis, graft-versus-
 CC host disease, Crohn's disease, lupus, etc. (II) is also useful in the
 CC production of hybridoma cells which are derived from B cells, which
 CC involves treating the hybridoma cells with (II). (II) is useful in the
 CC treatment of inflammatory conditions of joints, e.g., rheumatoid
 CC arthritis, osteoarthritis, etc. (II), its agonists or antagonists are
 CC useful for treating acute pancreatitis, amyotrophic lateral sclerosis
 CC (ALS), Alzheimer's disease, asthma, atherosclerosis, cachexia/anorexia,
 CC diabetes, fever, glomerulonephritis, inflammatory bowel disease,
 CC ischaemic injury including cerebral ischaemia, multiple myeloma, multiple
 CC sclerosis, osteoporosis, Parkinson's disease, pain, reperfusion injury,
 CC septic shock, etc. The nucleic acids are also useful for developing the
 CC transgenic animals expressing (II), which are useful for producing the
 CC polypeptides and for the study of in vivo biological activity. The
 CC present sequence represents the amino acid sequence of human AGP-3
 CC related protein receptor
 XX

CC rheumatic heart disease, polyendocrinopathies, autoimmune pulmonary
CC inflammation, multiple sclerosis, diabetes mellitus, asthma, vitiligo,
CC hepatitis, cirrhosis, Sjogren's syndrome, rheumatoid arthritis,
CC autoimmune thyroiditis, reticular dysgenesis, ataxia-telangiectasia,
CC systemic lupus erythematosus, B cell lymphoproliferative disorder, kappa
CC chain deficiency, neuritis, resenosis and short limbed dwarfism, cancer,
CC Crohn's disease, bronchitis, otitis media, sepsis, meningitis, ulcerative
CC colitis and AIDS. The polypeptide is also useful for increasing or
CC inhibiting B-cell proliferation and immunoglobulin production and for
CC killing a cell that expresses the TR17 polypeptide on its cell surface.
CC This sequence represents the human TR17 polypeptide
XX
SQ Sequence 293 AA;

Query Match 33.1%; Score 66.5; DB 5; Length 293;
Best Local Similarity 32.4%; Pred. No. 3.7;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

OY 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
DB 34 CPEQYWDPLGLGTGCMCKTICNHQS-QRTCAFC 66

RESULT 94
AAE35211
ID AAE35211 standard; protein; 293 AA.

AC AAE35211;

DT 28-MAY-2003 (first entry)

DE Human TACI protein.

KW Transmembrane activator; calcium modulator; nephrotoxic; antibacterial;
KW TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;
KW anaemia; gene therapy; cytosolic; antiinflammatory; immunosuppressive;
KW glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;
KW dermatological; neuroprotective; cyclophilin ligand-interactor; human;
KW autoimmune disease; systemic lupus erythematosus; multiple sclerosis;
KW diabetes mellitus; rheumatoid arthritis; renal disease; inflammation.
XX

OS Homo sapiens.

Key Location/Qualifiers

Region 34..104 /note="Cysteine rich pseudo repeat"

Region 105..166 /note="stalk region"

Domain 167..186 /note="Transmembrane domain"

WO200294852-A2.

28-NOV-2002.

20-MAY-2002; 2002WO-US015910.

24-MAY-2001; 2001US-0293343P.

(ZYMO) ZYMOGENETICS INC.

Rixon MW, Gross JA;

WPI; 2003-148455/14.

N-PSDB; AAD53734.

Transmembrane activator and calcium modulator and cyclophilin ligand-
interactor (TACI)-immunoglobulin fusion protein, for treating cancer or
diabetes, comprises a TACI receptor group and an immunoglobulin group.
Claim 17; Col 87-88; 71pp; English.

The invention relates to fusion proteins comprising transmembrane

CC activator and calcium modulator and cyclophilin ligand-interactor (TACI)
CC receptor group that binds tumour necrosis factor-like protein (ZTNF2 or
CC ZTNF4; and an immunoglobulin group comprising a constant region of an
CC immunoglobulin. The invention is used to manufacture a medicament for
CC inhibiting the proliferation of tumour cells in a mammalian subject. The
CC composition comprising the fusion protein may also be used in treating
CC autoimmune diseases (e.g. systemic lupus erythematosus, multiple
CC sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal
CC diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft
CC rejection, anaemia and septic shock. The fusion proteins are also used in
CC gene therapy. The present sequence is human TACI protein
XX
SQ Sequence 293 AA;

Query Match 33.1%; Score 66.5; DB 6; Length 293;
Best Local Similarity 32.4%; Pred. No. 3.7;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

OY 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
DB 34 CPEQYWDPLGLGTGCMCKTICNHQS-QRTCAFC 66

RESULT 95
ABP60551
ID ABP60551 standard; protein; 293 AA.

AC ABP60551;

DT 28-MAR-2003 (first entry)

DE Human tumour necrosis factor TACI.

KW APRIL; scFv; immunospecific; tumour necrosis factor delta; TNF-delta;
KW dermatological; immunosuppressive; antiinflammatory; antihemetic;
KW antirheumatic; cytosolic; antianemic; antiallergic; antiaesthetic;
KW neuroprotective; ophthalmological; tuberculostatic; antidiabetic;
KW antipsoriatic; anti-HIV; antiarteriosclerotic; vasotropic; thymimetic;
KW haemostatic; cancer; autoimmune disease; graft versus host disease; GVHD;
KW inflammatory disorder; proliferative disorder; single chain antibody;
KW antibody; human; TACI; tumour necrosis factor.
XX

OS Homo sapiens.

WO200294192-A2.

28-NOV-2002.

22-MAY-2002; 2002WO-US016106.

24-MAY-2001; 2001US-0293100P.

(HUMA-) HUMAN GENOME SCI INC.

Ruben SM;

WPI; 2003-156740/15.

Novel isolated antibody that immunospecifically binds tumor necrosis
factor delta, useful for treating, preventing or ameliorating Non-
Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's
syndrome.

Disclosure; Page 220-221; 225pp; English.

The invention relates to a novel antibody or its fragment, which
immunospecifically binds tumour necrosis factor Delta (TNF-delta/APRIL).
The antibody of the invention has dermatological, immunosuppressive,
CC antiinflammatory, antineuritic, antiallergic, cytosolic, antianemic,
CC antiallergic, antiaesthetic, neuroprotective, ophthalmological,
CC tuberculostatic, antidiabetic, antipsoriatic, anti-HIV,
CC antiarteriosclerotic, vasotropic, thymimetic, and haemostatic activity.
The antibody or its fragment are useful for treating, preventing or

CC ameliorating cancer such as Non-Hodgkin's lymphoma or multiple myeloma in
 CC human, disease or disorder such as autoimmune disease, and graft versus
 CC host disease (GVHD). The autoimmune disease is systemic lupus
 CC erythematosus, rheumatoid arthritis or Sjogren's syndrome. The antibody
 CC is useful for detecting, diagnosing, prognosing, treating, preventing or
 CC ameliorating a disease or disorder associated with aberrant APRIL or
 CC APRIL receptor expression or aberrant function of APRIL or APRIL
 CC receptor. The disease or disorders includes autoimmune and inflammatory
 CC disorders such as autoimmune neutropenia, haemolytic anaemia, dermatitis,
 CC asthma, allergic encephalomyelitis, myocarditis, multiple sclerosis,
 CC uveitis, tuberculosis, diabetes mellitus, psoriasis, cancer of the immune
 CC system, particularly B cell cancers, immune disorders such as myasthenia
 CC gravis, Hashimoto's disease, immunodeficiency syndrome, Bruton's disease,
 CC infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS)), and
 CC proliferative disorders (e.g. leukemia). The present sequence represents
 CC the tumour necrosis factor TACI

XX Sequence 293 AA;

Query Match 33.1%; Score 66.5; DB 6; Length 293;

Best Local Similarity 32.4%; Pred. No. 3.7; Mismatches 14; Indels 1; Gaps 1;

Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

1 CSQNEYPDSLHACIPCOLRSSNTPTTCQRYC 34

34 CPBEQYWPDLGTGCMSCRTICNHOS-ORTCAFC 66

RESULT 96

ABP97716 standard; protein; 293 AA.

ABP97716;

28-MAY-2003 (first entry)

Amino acid sequence of human TACI receptor.

Human; TACI; BR3; receptor; tumour necrosis factor ligand; TNF ligand;

TALL-1; April; systemic lupus erythematosus.

Homo sapiens.

WO2003014294-A2.

20-FEB-2003.

24-JUL-2002; 2002WO-US023487.

03-AUG-2001; 2001US-0310114P.

30-APR-2002; 2002US-0377171P.

(GENE) GENENTECH INC.

Dixit V, Grewal I, Ridgway J, Yan M;

WPI; 2003-256560/25.

N-PSDB; AB268870.

New nucleic acid encoding a TACI or BR3 polypeptide, useful for

preparing a composition for treating systemic lupus erythematosus.

Disclosure; Fig 1A-B; 153pp; English.

The present sequence represents a human TACI polypeptide. The

specification also describes BR3 polypeptides. TACI and BR3 are

receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and April

bind to the TACI receptor, while TNF family ligands TALL-1 also binds to

BR3 receptor. The TACI and BR3 receptor nucleic acid is useful for

preparing a composition for treating systemic lupus erythematosus

Query Match 33.1%; Score 66.5; DB 6; Length 293;

Best Local Similarity 32.4%; Pred. No. 3.7; Mismatches 14; Indels 1; Gaps 1;

Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

1 CSQNEYPDSLHACIPCOLRSSNTPTTCQRYC 34

34 CPBEQYWPDLGTGCMSCRTICNHOS-ORTCAFC 66

RESULT 97

AA029592 standard; protein; 293 AA.

AA029592;

27-AUG-2003 (first entry)

Human DTRACIN protein.

Metabolic disorder; DTRACIN; obesity-related disease; hyperlipidaemia;

antidepressant; chronic inflammatory disease; cachexia; immunomodulator;

glucose uptake; insulin sensitivity; anorexia; cerebroprotective; AIDS;

atherosclerosis; insulin resistance; diabetes; stroke; hypertension;

Cancer; weight loss; human.

Homo sapiens.

WO2003041730-A1.

22-MAY-2003.

03-OCT-2002; 2002WO-IB004582.

16-NOV-2001; 2001US-0332361P.

(BEST) GENSET SA.

Lucas J, Briggs K, Dialynas D, Scalia A;

WPI; 2003-468587/44.

N-PSDB; AAL60089.

New agonist and antagonist of DTRACIN activity, useful for preventing or

treating obesity-related diseases (e.g. hyperlipidaemia or stroke), or

increasing body mass (e.g. by treating excessive weight loss, cachexia),

respectively.

Disclosure; Page 33-34; 37pp; English.

The invention relates to agonist or antagonist of DTRACIN useful in the

treatment of metabolic disorders. The antagonist or agonist of DTRACIN or

the composition comprising the agonist or antagonist, is useful for

treating or preventing obesity-related disease, e.g. hyperlipidaemia,

atherosclerosis, insulin resistance, diabetes, stroke or hypertension.

The agonist is useful for reducing body mass and maintaining weight loss

by: lowering circulating levels or concentrations of free fatty acids,

glucose and/or triglycerides; stimulating muscle lipid or free fatty acid

oxidation; increasing leptin uptake in a liver cell; reducing the

postprandial increase in plasma free fatty acids or triglycerides,

particularly following a high fat meal; reducing or eliminating ketone

body production, particularly following a high fat meal; increasing

glucose uptake in skeletal muscle cells, adipose cells, neuronal cells,

red blood cells or brain; reducing or preventing the postprandial

increase in plasma glucose following a high carbohydrate meal; or

improving insulin sensitivity. The antagonist of DTRACIN activity is

CC upregulated cell proliferation, or inhibition of apoptosis, e.g. 'cancer'
CC autoimmune diseases, viral infections, inflammation, graft-versus-host
CC disease, acute graft rejection, chronic graft rejection, AIDS,
CC neurodegenerative disorders, myelodysplastic syndromes, ischaemic injury
CC toxin-induced liver disease, septic shock, cachexia, and anorexia. The
CC present sequence represents human tumour necrosis factor receptor 'TACT',
CC included for comparison with TR20.
XX
SQ Sequence 293 AA,

Sequence 293 AA;

| | | | | | | | |
|-----------------------|-------|--------------|------|------------|----|--------|-----|
| Query Match | 33.1% | Score | 66.5 | DB | 7 | Length | 293 |
| Best Local Similarity | 32.4% | Pred. No. | 3.7 | | | | |
| Matches | 11 | Conservative | 8 | Mismatches | 14 | Indels | 1 |
| | | | | | | Gaps | 1 |

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QY      1 CSQNEYFBDLLHACIPQQLRCSNTPELTCQRYC 34
          | : : | | | : : : : : |
Db      34 CPEEQYWDPLLGTCSCKTICHHQS-QRTCAFC 66

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RESULT 100
ABM85745
ID ABM85745 standard; protein; 293 AA.

AC ABM85745;

DT 18-NOV-2004 (first entry)

Human protein sequence hCP45156.

Cytostatic; carcinoma; lymphoma; cancer; human.

OS Homo sapiens.

PN WO2003073826-A2.

PD 12-SEP-2003

PF 28-FEB-2003; 2003WO-US006235.

PR 01-MAR-2002; 2002US-00087192.

PA (SAGR-) SAGRES DISCOVERY.

PI Morris DW;

DR WPI; 2003-328604/31.

PT Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprising a nucleotide sequence.

PS Claim 5; SEQ ID NO 1650; opp; English.

CC The present invention relates to novel DNA and protein sequences which
CC are associated with carcinomas. The sequences are useful for: (i) for
CC screening drug candidates; (ii) for screening of bioactive agent capable
CC of binding to Carcino Associated Protein (CAP); (iii) for screening of
CC a bioactive agent capable of modulating the activity of CAP; (iv) for
CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biotrip;
CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
CC determining Carcino Associated (CA) gene copy number. In addition, the
CC CA genes are useful as DNA vaccines and the CAP are useful as markers of
CC carcinoma including Lymphoma. The present sequence is one such CAP. Note:
CC This patent is an equivalent to basic patent US2002182586A1, for which no
CC sequence data was published

SQ Sequence 293 AA;

| | | | | | | | |
|-----------------------|-------|--------------|------|------------|----|--------|-----|
| Query Match | 33.1% | Score | 66.5 | DB | 7 | Length | 293 |
| Best Local Similarity | 32.4% | Pred. NO. | 3.7 | | | | |
| Matches | 11 | Conservative | 8 | Mismatches | 14 | Indels | 1 |
| | | | | | | Gaps | 1 |

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QY      1 CSQNEYPDSLHACIFCQLRCSSTNPPLTCQRYC 34
      2  | : : | | | : : | : : | | : : |
Db      34 CPBEQYMDPLLGTCMCKTICNHQS-QRTCAAF 66

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Search completed: July 10, 2006, 16:43:22
Job time : 58 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 10, 2006, 16:42:25 ; Search time 7.8 Seconds
(without alignments)
175.440 Million cell updates/sec

Title: US-10-077-137a-1_COPY_1_51

Perfect score: 283
Sequence: 1 MLQVAGGCSQNEYPDSLHA.....TPPLTCORYCNASVTNSVKG 51

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112942 segs, 26832045 residues

Total number of hits satisfying chosen parameters: 112942

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 158 | 55.8 | 42 | 7 | US-11-272-521-197 |
| 2 | 67.5 | 23.9 | 166 | 7 | US-11-318-156-6 |
| 3 | 67.5 | 23.9 | 293 | 7 | US-11-318-156-2 |
| 4 | 64 | 22.6 | 175 | 7 | US-11-291-698A-55 |
| 5 | 63 | 22.3 | 175 | 7 | US-11-291-698A-38 |
| 6 | 62.5 | 22.1 | 308 | 6 | US-10-553-349-20717 |
| 7 | 62.5 | 22.1 | 985 | 7 | US-11-293-697-2874 |
| 8 | 61 | 21.6 | 247 | 6 | US-10-496-758-2 |
| 9 | 58.5 | 20.7 | 1182 | 6 | US-10-449-902-41231 |
| 10 | 57.5 | 20.3 | 282 | 6 | US-10-953-349-22125 |
| 11 | 57.5 | 20.3 | 341 | 6 | US-10-953-349-22124 |
| 12 | 57.5 | 20.3 | 360 | 6 | US-10-953-349-22123 |
| 13 | 57.5 | 20.3 | 576 | 6 | US-10-449-902-35358 |
| 14 | 57.5 | 20.3 | 645 | 6 | US-10-449-902-52038 |
| 15 | 57.5 | 20.3 | 807 | 6 | US-10-449-902-43388 |
| 16 | 54.5 | 19.3 | 419 | 6 | US-10-505-928-436 |
| 17 | 54.5 | 19.3 | 419 | 6 | US-10-505-928-864 |
| 18 | 54.5 | 19.3 | 419 | 7 | US-11-346-806-3 |
| 19 | 54 | 19.1 | 298 | 7 | US-11-293-697-2712 |
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| 21 | 53.5 | 18.9 | 272 | 6 | US-10-449-902-28786 |
| 22 | 53.5 | 18.9 | 272 | 6 | US-10-449-902-49738 |
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| 24 | 53 | 18.7 | 103 | 6 | US-10-953-349-29073 |
| 25 | 53 | 18.7 | 122 | 6 | US-10-953-349-29072 |

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| 26 | 53 | 18.7 | 159 | 7 | US-11-293-697-3150 | Sequence 3150, Ap |
| 27 | 53 | 18.7 | 247 | 6 | US-10-504-973-6 | Sequence 6, Appl |
| 28 | 53 | 18.7 | 398 | 6 | US-10-449-902-40143 | Sequence 40143, A |
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| 30 | 52.5 | 18.6 | 577 | 6 | US-10-449-902-44810 | Sequence 44810, A |
| 31 | 52 | 18.4 | 95 | 6 | US-10-953-349-18161 | Sequence 18161, A |
| 32 | 52 | 18.4 | 102 | 6 | US-10-953-349-18160 | Sequence 18160, A |
| 33 | 52 | 18.4 | 115 | 6 | US-10-953-349-18159 | Sequence 18159, A |
| 34 | 52 | 18.4 | 286 | 6 | US-10-449-902-31482 | Sequence 31482, A |
| 35 | 52 | 18.4 | 513 | 6 | US-11-174-307B-1284 | Sequence 12782, A |
| 36 | 51 | 18.0 | 111 | 6 | US-10-953-349-13782 | Sequence 12782, A |
| 37 | 51 | 18.0 | 197 | 6 | US-10-953-349-24349 | Sequence 2499, Ap |
| 38 | 51 | 18.0 | 348 | 6 | US-10-953-349-38340 | Sequence 38340, A |
| 39 | 51 | 18.0 | 357 | 6 | US-10-953-349-38339 | Sequence 38339, A |
| 40 | 51 | 18.0 | 442 | 6 | US-10-953-349-38338 | Sequence 38338, A |
| 41 | 51 | 18.0 | 645 | 6 | US-10-953-349-10968 | Sequence 10968, A |
| 42 | 51 | 18.0 | 660 | 6 | US-10-953-349-10967 | Sequence 10967, A |
| 43 | 51 | 18.0 | 868 | 6 | US-10-449-902-44069 | Sequence 44069, A |
| 44 | 50.5 | 17.8 | 364 | 6 | US-10-449-902-36200 | Sequence 36200, A |
| 45 | 50.5 | 17.8 | 463 | 6 | US-10-953-349-2382 | Sequence 2983, Ap |
| 46 | 50.5 | 17.8 | 464 | 6 | US-10-953-349-2381 | Sequence 2982, Ap |
| 47 | 50.5 | 17.8 | 483 | 6 | US-10-953-349-2381 | Sequence 2981, Ap |
| 48 | 50 | 17.7 | 351 | 6 | US-10-449-902-54639 | Sequence 54639, A |
| 49 | 50 | 17.7 | 420 | 7 | US-11-293-697-3438 | Sequence 3438, Ap |
| 50 | 50 | 17.7 | 458 | 7 | US-11-024-544A-22 | Sequence 12, Appl |
| 51 | 50 | 17.7 | 458 | 7 | US-11-190-750-136 | Sequence 36, Appl |
| 52 | 50 | 17.7 | 458 | 7 | US-11-264-737-129 | Sequence 88, Appl |
| 53 | 50 | 17.7 | 458 | 7 | US-11-264-737-129 | Sequence 129, Appl |
| 54 | 50 | 17.7 | 458 | 7 | US-11-265-761-101 | Sequence 101, Appl |
| 55 | 50 | 17.7 | 592 | 6 | US-10-505-928-146 | Sequence 146, Appl |
| 56 | 50 | 17.7 | 801 | 6 | US-10-449-902-43722 | Sequence 43722, A |
| 57 | 50 | 17.7 | 1617 | 7 | US-11-174-307B-2182 | Sequence 2182, Ap |
| 58 | 50 | 17.7 | 1682 | 7 | US-11-174-307B-2458 | Sequence 2458, Ap |
| 59 | 49.5 | 17.5 | 152 | 7 | US-11-174-307B-5090 | Sequence 5090, Ap |
| 60 | 49.5 | 17.5 | 324 | 7 | US-11-289-102-3378 | Sequence 328, Ap |
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| 65 | 49 | 17.3 | 17 | 7 | US-11-291-698A-1132 | Sequence 132, Appl |
| 66 | 49 | 17.3 | 343 | 6 | US-10-953-349-10623 | Sequence 10623, A |
| 67 | 49 | 17.3 | 369 | 6 | US-10-953-349-10622 | Sequence 10622, A |
| 68 | 49 | 17.3 | 497 | 7 | US-11-217-557-4 | Sequence 4, Appl1 |
| 69 | 49 | 17.3 | 820 | 7 | US-11-174-307B-1540 | Sequence 1540, Ap |
| 70 | 49 | 17.3 | 1116 | 7 | US-11-174-307B-2106 | Sequence 2106, Ap |
| 71 | 49 | 17.3 | 1238 | 7 | US-11-178-724-22 | Sequence 22, Appl1 |
| 72 | 49 | 17.3 | 1238 | 7 | US-11-071-796A-21 | Sequence 21, Appl1 |
| 73 | 49 | 17.3 | 1882 | 7 | US-11-174-307B-1388 | Sequence 1388, Ap |
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| 75 | 48 | 17.0 | 58 | 7 | US-11-287-121A-19 | Sequence 19, Appl1 |
| 76 | 48 | 17.0 | 58 | 7 | US-11-253-176-56 | Sequence 56, Appl1 |
| 77 | 48 | 17.0 | 115 | 6 | US-10-953-349-3386 | Sequence 3386, Ap |
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| 86 | 48 | 17.0 | 392 | 7 | US-11-293-697-2797 | Sequence 2797, Ap |
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| 88 | 48 | 17.0 | 405 | 6 | US-10-449-902-36362 | Sequence 36362, A |
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| 90 | 48 | 17.0 | 450 | 6 | US-10-449-902-38759 | Sequence 38759, A |
| 91 | 48 | 17.0 | 450 | 6 | US-10-449-902-55688 | Sequence 55688, A |
| 92 | 48 | 17.0 | 686 | 6 | US-10-515-422-43 | Sequence 43, Appl1 |
| 93 | 48 | 17.0 | 775 | 6 | US-10-449-902-47388 | Sequence 47388, A |
| 94 | 48 | 17.0 | 952 | 7 | US-11-221-333-86 | Sequence 86, Appl1 |
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| 97 | 48 | 17.0 | 1305 | 7 | US-11-174-307B-1760 | Sequence 1760, Ap |
| 98 | 48 | 17.0 | 1324 | 7 | US-11-174-307B-2708 | Sequence 2708, Ap |


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975 39.5 14.0 17 7 US-11-291-698A-80 Sequence 80, Appl
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977 39.5 14.0 67 7 US-11-350-749-136 Sequence 126, App
978 39.5 14.0 72 6 US-10-449-902-41872 Sequence 41872, A
979 39.5 14.0 111 7 US-11-293-697-2584 Sequence 2584, Ap
980 39.5 14.0 112 6 US-10-449-902-34513 Sequence 34513, A
981 39.5 14.0 131 6 US-10-953-349-2850 Sequence 2850, Ap
982 39.5 14.0 135 6 US-10-953-349-12882 Sequence 12882, A
983 39.5 14.0 138 6 US-10-449-902-56498 Sequence 56498, A
984 39.5 14.0 140 7 US-11-284-236-2228 Sequence 228, App
985 39.5 14.0 161 6 US-10-449-902-41918 Sequence 41918, A
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988 39.5 14.0 181 6 US-10-953-349-34919 Sequence 34919, A
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990 39.5 14.0 198 6 US-10-449-902-43880 Sequence 43880, A
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995 39.5 14.0 244 6 US-10-953-349-20730 Sequence 20730, A
996 39.5 14.0 244 6 US-10-449-902-54105 Sequence 54105, A
997 39.5 14.0 248 6 US-10-953-349-34477 Sequence 34477, A
998 39.5 14.0 258 6 US-10-643-588-4 Sequence 4, Appl
999 39.5 14.0 267 6 US-10-953-349-25038 Sequence 25038, A
1000 39.5 14.0 267 6 US-10-449-902-39299 Sequence 39299, A
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ALIGNMENTS

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RESULT 1
US-11-272-521-197
; Sequence 197, Application US/11272521
; Publication No. US20060135431A1
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```
; GENERAL INFORMATION:
; APPLICANT: HSU, HAILING
; APPLICANT: XIONG, FEI
; TITLE OF INVENTION: PEPTIDES AND RELATED MOLECULES THAT BIND TO TALL-1
; FILE REFERENCE: A-743
; CURRENT APPLICATION NUMBER: US/11/272,521
; CURRENT FILING DATE: 2005-11-10
; PRIOR APPLICATION NUMBER: US/10/145,206
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,196
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatencIn version 3.1
; SEQ ID NO 197
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Human
US-11-272-521-197
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Best Local Similarity 100.0%; Pred. No. 3e-13;
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RESULT 2
US-11-318-156-6
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; Sequence 6, Application US/11318156
; Publication No. US20060101529A1
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: Von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML AND METHODS OF USE THEREOF
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; FILE REFERENCE: 44158/254623
; CURRENT APPLICATION NUMBER: US/11/318,156
; CURRENT FILING DATE: 2005-12-23
; PRIOR APPLICATION NUMBER: US/10/293,816
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 09/782,857
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/290,333
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US 08/810,572
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-318-156-6
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Best Local Similarity 30.6%; Pred. No. 0.17;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
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DB 34 CPEEQYWDPLGTGTCWCKTICNHOS-QRTCAAFCRS 68
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RESULT 3
US-11-318-156-2
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; Sequence 2, Application US/11318156
; Publication No. US20060101529A1
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: Von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; FILE REFERENCE: 44158/254623
; CURRENT APPLICATION NUMBER: US/11/318,156
; CURRENT FILING DATE: 2005-12-23
; PRIOR APPLICATION NUMBER: US/10/293,816
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 09/782,857
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/290,333
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US 08/810,572
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-318-156-2
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Best Local Similarity 30.6%; Pred. No. 0.29;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
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QY 8 CSQNEYFDSLHACTPCQLRCSSNTPPLTCQRYCNA 43
DB 34 CPEEQYWDPLGTGTCWCKTICNHOS-QRTCAAFCRS 68
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RESULT 4
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US-11-291-698A-55
; Sequence 55, Application US/11291698A
; Publication No. US20060135430A1
; GENERAL INFORMATION:
; APPLICANT: Chan, Andrew Chee-Yuen
; APPLICANT: Gordon, Nathaniel C.
; APPLICANT: Kelley, Robert F.
```



```
; APPLICANT: Koehler, Michael F.T.
; APPLICANT: Starovasinik, Melissa A.
; TITLE OF INVENTION: BLVS ANTAGONISTS AND USES THEREOF
; FILE REFERENCE: 11669.174USC1
; CURRENT APPLICATION NUMBER: US/11/291,698A
; CURRENT FILING DATE: 2005-11-30
; PRIOR APPLICATION NUMBER: PCT/US04/17682
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 55
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Rat
US-11-291-698A-55
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Best Local Similarity 38.9%; Pred. No. 0.47;
Matches 14; Conservative 6; Mismatches 10; Indels 6; Gaps 1;
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; Sequence 38, Application US/11291698A
; Publication No. US20060135430A1
; GENERAL INFORMATION:
; APPLICANT: Chan, Andrew Chee-Yuen
; APPLICANT: Gordon, Nathaniel C.
; APPLICANT: Kelley, Robert F.
; APPLICANT: Koehler, Michael F.T.
; APPLICANT: Starovasinik, Melissa A.
; TITLE OF INVENTION: BLVS ANTAGONISTS AND USES THEREOF
; FILE REFERENCE: 11669.174USC1
; CURRENT APPLICATION NUMBER: US/11/291,698A
; CURRENT FILING DATE: 2005-11-30
; PRIOR APPLICATION NUMBER: PCT/US04/17682
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-291-698A-38
```

```
Query Match      22.3%; Score 63; DB 7; Length 175;
Best Local Similarity 50.0%; Pred. No. 0.63;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
```

```
QY      7 OCSQNEVFDLSLHACIPCOL 26
DB      21 QCNQTECFDPLVNCVSCLE 40
```

```
RESULT 6
US-10-953-349-20717
; Sequence 20717, Application US/10953349
```

```
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: ENCODED THEREBY
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20717
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-20717
```

```
Query Match      22.1%; Score 62.5; DB 6; Length 308;
Best Local Similarity 34.8%; Pred. No. 1.3;
Matches 16; Conservative 5; Mismatches 20; Indels 5; Gaps 1;
```

```
QY      6 GOCQNEVFDLSLHACIPCOLRCSSTNPPLTCORYCNASVTNSVKG 51
DB      67 GNCSGNGICNMSTGVC-----SCSENYFSPSCENTCVASTTCSGGS 107
```

```
RESULT 7
US-11-293-697-2874
; Sequence 2874, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2874
; LENGTH: 985
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-2874
```

```
Query Match      22.1%; Score 62.5; DB 7; Length 985;
Best Local Similarity 21.4%; Pred. No. 4;
Matches 12; Conservative 10; Mismatches 15; Indels 19; Gaps 1;
```

```
QY      3 QMAGCQNEVFDLSLHACIPC-----QLRCSSTNPPLTCOR 39
DB      34 QQPEKCDNNQYFDISALSCVPCGANGRDAGTSCVCLPGFQWISNNGPAILCKK 89
```

```
RESULT 8
US-10-496-758-2
; Sequence 2, Application US/10496758
; Publication No. US20060089311A1
; GENERAL INFORMATION:
; APPLICANT: Geneset
; TITLE OF INVENTION: TREATMENT OF METABOLIC DISORDERS WITH RYZN AGONISTS AND ANTAGONISTS
; FILE REFERENCE: 163.WO1
; CURRENT APPLICATION NUMBER: US/10/496,758
; CURRENT FILING DATE: 2004-05-26
; PRIOR APPLICATION NUMBER: 60/334,152
; PRIOR FILING DATE: 2003-11-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-496-758-2
```

Query Match 21.6%; Score 61; DB 6; Length 247;
Best Local Similarity 30.0%; Pred. No. 16;
Matches 12; Conservative 7; Mismatches 19; Indels 2; Gaps 1;

Qy 10 QNEYPDSLHACIPCOLRCSSTPPLTCORYCNASVTNSV 49
Db 29 QOKFYDHLRDCISCASICQH--PKQCAVYFENKLRSPV 66

RESULT 9

US-10-449-902-41231
; Sequence 41231, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41231
; LENGTH: 1182
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-41231

Query Match 20.7%; Score 58.5; DB 6; Length 1182;
Best Local Similarity 52.0%; Pred. No. 15;
Matches 13; Conservative 2; Mismatches 7; Indels 3; Gaps 2;

Qy 18 LHAC-IPOC--LRGSSNPPLACOR 39
Db 597 LHECISPCSKPLPCSHCEPMTCNR 621

RESULT 10

US-10-953-349-22125
; Sequence 22125, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22125
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-22125

Query Match 20.3%; Score 57.5; DB 6; Length 282;
Best Local Similarity 36.2%; Pred. No. 4.8;
Matches 17; Conservative 5; Mismatches 14; Indels 11; Gaps 2;

Qy 9 SONEYPDSLHACIPCOLR-----CSSNTPPLTCORYCNASVTNSV 50
Db 203 SSNTYTDVFQAAVVKFLQLHLDPASSNTLP-----ANGSITQSLK 243

RESULT 11

US-10-953-349-22124

; Sequence 22124, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22124
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-22124

Query Match 20.3%; Score 57.5; DB 6; Length 341;
Best Local Similarity 36.2%; Pred. No. 5.8;
Matches 17; Conservative 5; Mismatches 14; Indels 11; Gaps 2;

Qy 9 SONEYPDSLHACIPCOLR-----CSSNTPPLTCORYCNASVTNSV 50
Db 262 SSNTYTDVFQAAVVKFLQLHLDPASSNTLP-----ANGSITQSLK 302

RESULT 12

US-10-953-349-22123
; Sequence 22123, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22123
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-22123

Query Match 20.3%; Score 57.5; DB 6; Length 360;
Best Local Similarity 36.2%; Pred. No. 6.1;
Matches 17; Conservative 5; Mismatches 14; Indels 11; Gaps 2;

Qy 9 SONEYPDSLHACIPCOLR-----CSSNTPPLTCORYCNASVTNSV 50
Db 281 SSNTYTDVFQAAVVKFLQLHLDPASSNTLP-----ANGSITQSLK 321

RESULT 13

US-10-449-902-35358
; Sequence 35358, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791

```

; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 35358
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-35358

Query Match
Best Local Similarity 20.3%; Score 57.5; DB 6; Length 576;
Best Local Similarity 25.9%; Pred. No. 9.7;
Matches 14; Conservative 12; Mismatches 19; Indels 9; Gaps 2;

Qy
1 MLOMGQCSQNE--YFDSLHACIPCOLRCSSNTPPLTQ-----RYCNASV 45
Db
259 LVTLLGACTEASALVYELLPNGSLIEDRLNCVDNTPPLTWQVRIQITTEICSA 312

RESULT 14
US-10-449-902-52038
; Sequence 52038, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 52038
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-52038

Query Match
Best Local Similarity 20.3%; Score 57.5; DB 6; Length 645;
Best Local Similarity 25.9%; Pred. No. 11;
Matches 14; Conservative 12; Mismatches 19; Indels 9; Gaps 2;

Qy
1 MLOMGQCSQNE--YFDSLHACIPCOLRCSSNTPPLTQ-----RYCNASV 45
Db
328 LVTLLGACTEASALVYELLPNGSLIEDRLNCVDNTPPLTWQVRIQITTEICSA 381

RESULT 15
US-10-449-902-43388
; Sequence 43388, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 43388
; LENGTH: 807
; TYPE: PRT
; ORGANISM: Oryza sativa
```

```

US-10-449-902-43388

Query Match
Best Local Similarity 20.3%; Score 57.5; DB 6; Length 807;
Best Local Similarity 27.8%; Pred. No. 14;
Matches 15; Conservative 10; Mismatches 20; Indels 9; Gaps 2;

Qy
1 MLOMGQCSQNE--YFDSLHACIPCOLRCSSNTPPLTQ-----RYCNASV 45
Db
498 LVTLLVGCGEASGLVYEFLLPNGSLIEDRLNACESTSPPLTWQVRIQITTEICSA 551

RESULT 16
US-10-505-928-436
; Sequence 436, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; APPLICANT: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: Patentin 3.2
; SEQ ID NO 436
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-436

Query Match
Best Local Similarity 19.3%; Score 54.5; DB 6; Length 419;
Best Local Similarity 35.0%; Pred. No. 17;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

Qy
7 QCSQNEYPDSLHACIPCOLRCSSNTP--PLTCQRYCNAS 44
Db
327 QCGANREFDENTCQCV--CKRTCPRNQPLNPKACECTES 365

RESULT 17
US-10-505-928-864
; Sequence 864, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; APPLICANT: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: Patentin 3.2
; SEQ ID NO 864
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-864

Query Match
Best Local Similarity 19.3%; Score 54.5; DB 6; Length 419;
Best Local Similarity 35.0%; Pred. No. 17;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

Qy
7 QCSQNEYPDSLHACIPCOLRCSSNTP--PLTCQRYCNAS 44
Db
327 QCGANREFDENTCQCV--CKRTCPRNQPLNPKACECTES 365

RESULT 18
US-11-346-806-3
; Sequence 3, Application US/11346806
; Publication No. US20060121025A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: VEGF-RELATED PROTEIN
; FILE REFERENCE: P0963R1D1
; CURRENT APPLICATION NUMBER: US/11/346,806
; CURRENT FILING DATE: 2006-02-03
; PRIOR APPLICATION NUMBER: US/09/313,299
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: US 08/706,054
; PRIOR FILING DATE: 1996-08-30
; PRIOR APPLICATION NUMBER: US 60/003,491
; PRIOR FILING DATE: 1995-09-08
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 3
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: Human
; LOCATION: 1-419
; OTHER INFORMATION: Sequence source: VRF
; US-11-346-806-3

Query Match      19.3%; Score 54.5; DB 7; Length 419;
Best Local Similarity 35.0%; Pred. No. 17;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

Oy      7  GCSQNEYPDSLHACIPQLRCSSNTP--PLTCQRYCNA 44
Db      327  QCGANREFDENTCQCV-CRITCPRMQPLNPKACECTES 365

RESULT 19
US-11-293-697-2712
; Sequence 2712, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2712
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-293-697-2712

Query Match      19.1%; Score 54; DB 7; Length 298;
Best Local Similarity 34.0%; Pred. No. 14;
Matches 17; Conservative 3; Mismatches 16; Indels 14; Gaps 2;

Oy      14  FDSLHACIPQ---LRCSNTPPLTCORYCNA-----SVTVNSV 49
Db      61  FDYVLPPIQCQSHLVCSNCRPKLTCCTCGPLGISTNLMEVANSV 110

RESULT 20
US-10-449-902-33792
; Sequence 33792, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A02051-US
```

```

; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33792
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Oryza sativa
; US-10-449-902-33792

Query Match      18.9%; Score 53.5; DB 6; Length 84;
Best Local Similarity 34.1%; Pred. No. 4.5;
Matches 15; Conservative 4; Mismatches 18; Indels 7; Gaps 2;

Oy      5  AGQCSQNEYPDSLHACIPQLRCSSNTPPLT-----CORYCN 42
Db      31  AGRGSNTQYKKACLTFCKKCAKCLC-VPFTYGNKAGACPCYNN 73

RESULT 21
US-10-449-902-28786
; Sequence 28786, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A02051-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28786
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Oryza sativa
; US-10-449-902-28786

Query Match      18.9%; Score 53.5; DB 6; Length 272;
Best Local Similarity 47.6%; Pred. No. 14;
Matches 10; Conservative 2; Mismatches 4; Indels 5; Gaps 1;

Oy      6  GQCSQNEYPDSL-----HAC 21
Db      26  GSCSWDSYFDILKDTETHHAC 46

RESULT 22
US-10-449-902-49738
; Sequence 49738, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A02051-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
```



```
; APPLICANT: KHARE, Reena; BULLOCK, Sean A.
; TITLE OF INVENTION: RECEPTORS AND MEMBRANE-ASSOCIATED PROTEINS
; FILE REFERENCE: PF-1381 PCT
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: US/10/504,973
; PRIOR FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: US 60/358,279
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/364,338
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/375,657
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/376,669
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/379,837
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/379,853
; PRIOR FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PERL Program
; SEQ ID NO: 6
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 7509361CD1
US-10-504-973-6
```

```
Query Match      18.7%; Score 53; DB 6; Length 247;
Best Local Similarity 33.3%; Pred. No. 15;
Matches 14; Conservative 5; Mismatches 19; Indels 4; Gaps 2;
```

```
OY      8 CSONE---YFDSLHACIPQQLRCSSNTPPLTCORCNASVT 46
DB      127 CRKNQYRHWSNENLFCQCFNCSL-CLNGTHTLSCQENQNTVCT 167
```

```
RESULT 28
US-10-449-902-40143
; Sequence 40143, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A02051-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 40143
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-40143
```

```
Query Match      18.7%; Score 53; DB 6; Length 398;
Best Local Similarity 30.0%; Pred. No. 24;
Matches 12; Conservative 9; Mismatches 17; Indels 2; Gaps 1;
```

```
OY      1 MLOMAGCCSQ--NEYDLSLHACIPQQLRCSSNTPPLTQ 38
DB      77 LVTLLIGSCREARGLVYFLPKGSLIEDRLACLNNTPPLTQ 116
```

```
RESULT 29
US-10-449-902-38182
```

```
; Sequence 38182, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A02051-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 38182
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-38182
```

```
Query Match      18.6%; Score 52.5; DB 6; Length 502;
Best Local Similarity 27.7%; Pred. No. 35;
Matches 13; Conservative 6; Mismatches 13; Indels 15; Gaps 1;
```

```
OY      3 OMAGCCSONEYFDSLHACIPQQLR-----CSSNTP 34
DB      312 RMAGVCTENSTSDSEIQCHPRSTQSPKPGGVVRESPPVCSSDASP 358
```

```
RESULT 30
US-10-449-902-44810
; Sequence 44810, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A02051-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 44810
; LENGTH: 577
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-44810
```

```
Query Match      18.6%; Score 52.5; DB 6; Length 577;
Best Local Similarity 27.7%; Pred. No. 40;
Matches 13; Conservative 6; Mismatches 13; Indels 15; Gaps 1;
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```
OY      3 OMAGCCSONEYFDSLHACIPQQLR-----CSSNTP 34
DB      282 RMAGVCTENSTSDSEIQCHPRSTQSPKPGGVVRESPPVCSSDASP 328
```

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RESULT 31
US-10-953-349-18161
; Sequence 18161, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
```

;; TITLE OF INVENTION: ENCODED THERBY
;; FILE REFERENCE: 2750-1579PUS2
;; CURRENT APPLICATION NUMBER: US/10/953,349
;; CURRENT FILING DATE: 2004-09-30
;; NUMBER OF SEQ ID NOS: 40252
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 18161
;; LENGTH: 95
;; TYPE: PRT
;; ORGANISM: Glycine max
US-10-953-349-18161

Query Match 18.4%; Score 52; DB 6; Length 95;
Best Local Similarity 44.4%; Pred. No. 7.8;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 24 COLRCSSNTPPLTCORYC 41
DB 40 CRYRCSLHSPKICSRAC 57

RESULT 32
US-10-953-349-18160
; Sequence 18160, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18160
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18160

Query Match 18.4%; Score 52; DB 6; Length 102;
Best Local Similarity 44.4%; Pred. No. 8.3;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 24 COLRCSSNTPPLTCORYC 41
DB 47 CRYRCSLHSPKICSRAC 64

RESULT 33
US-10-953-349-18159
; Sequence 18159, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18159
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18159

Query Match 18.4%; Score 52; DB 6; Length 115;
Best Local Similarity 44.4%; Pred. No. 9.4;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 24 COLRCSSNTPPLTCORYC 41

DB 60 CRYRCSLHSPKICSRAC 77

RESULT 34
US-10-449-902-31482
; Sequence 31482, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31482
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-31482

Query Match 18.4%; Score 52; DB 6; Length 286;
Best Local Similarity 28.9%; Pred. No. 23;
Matches 13; Conservative 8; Mismatches 20; Indels 4; Gaps 1;

OY 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASYTNS 48
DB 22 CRIAHHLQHRVHCPTCOLHSTRFPLPATFISOPLSLSLSL 66

RESULT 35
US-11-174-307B-3284
; Sequence 3284, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
; FILE REFERENCE: 2750-1601PUS2
; CURRENT APPLICATION NUMBER: US/11/174,307B
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,671
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,781
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,651
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 3284
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-11-174-307B-3284

Query Match 18.4%; Score 52; DB 7; Length 513;
Best Local Similarity 40.0%; Pred. No. 41;
Matches 12; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

OY 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTC 37
DB 217 CITEBQLGCLLHNCFLQWRLSQCSPPLTC 246

RESULT 36

```
US-10-953-349-12782
; Sequence 12782, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12782
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-12782

Query Match      18.0%; Score 51; DB 6; Length 111;
Best Local Similarity 53.3%; Pred. No. 12;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy      21 CIPCOLRCSSNTPPL 35
Db      25 CLPLSFACSSPPPL 39

RESULT 37
US-10-953-349-2499
; Sequence 2499, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2499
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-2499

Query Match      18.0%; Score 51; DB 6; Length 197;
Best Local Similarity 32.6%; Pred. No. 21;
Matches 14; Conservative 5; Mismatches 22; Indels 2; Gaps 1;

Qy      9 SONEYFDSLHACIPCOLRCSSNTPPLTCORYCNASTNSVKG 51
Db      34 SYGHYLGSL--FVVRQARTSQEAWFLKSHKFCSTSTTSSENG 74

RESULT 38
US-10-953-349-38340
; Sequence 38340, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38340
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-38340

Query Match      18.0%; Score 51; DB 6; Length 348;
Best Local Similarity 28.1%; Pred. No. 37;
Matches 16; Conservative 10; Mismatches 25; Indels 6; Gaps 2;

Qy      1 MLOMAGCSONEYFDSLHACIPCOLRCSSNTP---PLT---CORYCNASTNSVKG 51
Db      79 LLEBAGRTYPLEKVEQVETCILIGLMCVDDPNKRPTLLDIERTLVDTNTDRG 135

RESULT 39
US-10-953-349-38339
; Sequence 38339, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38339
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-38339

Query Match      18.0%; Score 51; DB 6; Length 357;
Best Local Similarity 28.1%; Pred. No. 38;
Matches 16; Conservative 10; Mismatches 25; Indels 6; Gaps 2;

Qy      1 MLOMAGCSONEYFDSLHACIPCOLRCSSNTP---PLT---CORYCNASTNSVKG 51
Db      88 LLEBAGRTYPLEKVEQVETCILIGLMCVDDPNKRPTLLDIERTLVDTNTDRG 144

RESULT 40
US-10-953-349-38338
; Sequence 38338, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38338
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-38338

Query Match      18.0%; Score 51; DB 6; Length 442;
Best Local Similarity 28.1%; Pred. No. 47;
Matches 16; Conservative 10; Mismatches 25; Indels 6; Gaps 2;

Qy      1 MLOMAGCSONEYFDSLHACIPCOLRCSSNTP---PLT---CORYCNASTNSVKG 51
Db      173 LLEBAGRTYPLEKVEQVETCILIGLMCVDDPNKRPTLLDIERTLVDTNTDRG 229

RESULT 41
US-10-953-349-10968
; Sequence 10968, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
```



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; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10968
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-10-953-349-10968

Query Match
Best Local Similarity 18.0%; Score 51; DB 6; Length 645;
Pred. No. 69;
Matches 11; Conservative 2; Mismatches 3; Indels 8; Gaps 2;

QY 22 IPCQ-----LRCSNTPP---LTC 37
Db 7 LPDGDGVCMRCKSNPPRESLTC 30

RESULT 42
US-10-953-349-10967
; Sequence 10967, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10967
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-10-953-349-10967

Query Match
Best Local Similarity 18.0%; Score 51; DB 6; Length 660;
Pred. No. 70;
Matches 11; Conservative 2; Mismatches 3; Indels 8; Gaps 2;

QY 22 IPCQ-----LRCSNTPP---LTC 37
Db 22 LPDGDGVCMRCKSNPPRESLTC 45

RESULT 43
US-10-449-902-44069
; Sequence 44069, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44069
; LENGTH: 868
; TYPE: PRT
; ORGANISM: Oryza sativa
; US-10-449-902-44069
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Query Match
Best Local Similarity 18.0%; Score 51; DB 6; Length 868;
Pred. No. 92;
Matches 12; Conservative 6; Mismatches 7; Indels 4; Gaps 2;

QY 24 QLRCSNTPPLTCQRYCNASVTNS-VXG 51
Db 375 CRLSCLSN---CACRAYASANTSDAKG 400

RESULT 44
US-10-449-902-36200
; Sequence 36200, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36200
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Oryza sativa
; US-10-449-902-36200

Query Match
Best Local Similarity 17.8%; Score 50.5; DB 6; Length 364;
Pred. No. 45;
Matches 15; Conservative 8; Mismatches 16; Indels 7; Gaps 3;

QY 7 QCSNVEYFDSLHACIP--QQLRCSNTPPLTCQRYCNASVTNSVK 50
Db 25 QMSKYYLLPLRYNNVPMWC---CTSCNPPIVCAY--APIRSTIK 65

RESULT 45
US-10-953-349-2983
; Sequence 2983, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2983
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-10-953-349-2983

Query Match
Best Local Similarity 17.8%; Score 50.5; DB 6; Length 463;
Pred. No. 57;
Matches 14; Conservative 2; Mismatches 12; Indels 3; Gaps 2;

QY 23 PCQLRCSNTPPLT--CQRYCNASVTNSYKG 51
Db 229 PC-YRCLFPTPTPTACQRCSDSGVLGVVPG 258

RESULT 46
```

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US-10-953-349-2982
; Sequence 2982, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2982
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-2982

Query Match      17.8%; Score 50.5; DB 6; Length 464;
Best Local Similarity 45.2%; Pred. No. 57;
Matches 14; Conservative 2; Mismatches 12; Indels 3; Gaps 2;

OY      23 PCQLRCSSTNPPLT--CORYCNASTNSVKG 51
          ||| | | | | | | | : | |
Db       230 PC-YRLFPPTPTACQRCSDSGVLGVPG 259

RESULT 47
US-10-953-349-2981
; Sequence 2981, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2981
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-2981

Query Match      17.8%; Score 50.5; DB 6; Length 483;
Best Local Similarity 45.2%; Pred. No. 59;
Matches 14; Conservative 2; Mismatches 12; Indels 3; Gaps 2;

OY      23 PCQLRCSSTNPPLT--CORYCNASTNSVKG 51
          ||| | | | | | | | : | |
Db       249 PC-YRLFPPTPTACQRCSDSGVLGVPG 278

RESULT 48
US-10-449-902-54639
; Sequence 54639, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54639
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-54639

Query Match          17.7%; Score 50; DB 6; Length 351;
Best Local Similarity 39.3%; Pred. No. 50;
Matches 11; Conservative 4; Mismatches 9; Indels 4; Gaps 1;

Oy      24  COLRCSSNTPTPLTC---QRYCNASVTN  47
      |||::|::|::|::|::|::|::|::|::|
Db      211 CILSCSNNSPFFVALELRRSCQSSFTN  238

RESULT 49
US-11-293-697-3438
; Sequence 3438, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3438
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3438

Query Match          17.7%; Score 50; DB 7; Length 420;
Best Local Similarity 31.0%; Pred. No. 60;
Matches 13; Conservative 5; Mismatches 18; Indels 6; Gaps 2;

Oy      3  QMAGCCSQNEFYFDSLHACIPQLRCSSNTPTLCQRYCNAS  44
      |||::|::|::|::|::|::|::|::|::|
Db      344 QFCGCLRNRYGCDVRSALDPPDWVC---PP--CRGICNCS  379

RESULT 50
US-11-024-544A-22
; Sequence 22, Application US/11024544A
; Publication No. US20060094086A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours and Company, Inc.
; APPLICANT: Yadav, Narendra
; APPLICANT: Xue, Zhixiong
; APPLICANT: Zhang, Hongxiang
; TITLE OF INVENTION: DIACYLGYCEROL ACYLTRANSFERASES FOR ALTERATION OF POLYUNSATURATED
; FILE REFERENCE: C12717
; CURRENT APPLICATION NUMBER: US/11/024,544A
; CURRENT FILING DATE: 2004-12-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Aspergillus nidulans FGSC A4
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank Accession No. EAA57945
; DATABASE ENTRY DATE: 2004-09-09
; RELEVANT RESIDUES: (1)..(458)
US-11-024-544A-22

Query Match          17.7%; Score 50; DB 7; Length 458;
Best Local Similarity 45.0%; Pred. No. 65;

```

Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 10 ONEYFDSLHACTPCOLRCS 29
| : : : : :
Db 74 QDVVIGAILFALVPCQLCS 93

RESULT 51
US-11-190-750-136
; Sequence 136, Application US/11190750
; Publication No. US20060094088A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours and Company, Inc.
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Yadav, Narendra
; APPLICANT: Zhang, Hongxiang
; TITLE OF INVENTION: ACYTRANSFERASE REGULATION TO INCREASE THE PERCENT OF
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN TOTAL LIPIDS AND OILS OF
; FILE REFERENCE: CL2718
; CURRENT APPLICATION NUMBER: US/11/190,750
; CURRENT FILING DATE: 2005-07-27
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 136
; LENGTH: 458
; TYPE: PR1
; ORGANISM: Aspergillus nidulans FGSC A4 [GenBank Accession No. EAA57945]
US-11-190-750-136

Query Match 17.7%; Score 50; DB 7; Length 458;
Best Local Similarity 45.0%; Pred. No. 65;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 10 ONEYFDSLHACTPCOLRCS 29
| : : : : :
Db 74 QDVVIGAILFALVPCQLCS 93

RESULT 52
US-11-264-784-88
; Sequence 88, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 88
; LENGTH: 458
; TYPE: PR1
; ORGANISM: Aspergillus nidulans FGSC A4 [GenBank Accession No. EAA57945]
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: DGAT1
US-11-264-784-88

Query Match 17.7%; Score 50; DB 7; Length 458;
Best Local Similarity 45.0%; Pred. No. 65;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 10 ONEYFDSLHACTPCOLRCS 29
| : : : : :
Db 74 QDVVIGAILFALVPCQLCS 93

RESULT 53
US-11-264-737-129
; Sequence 129, Application US/11264737
; Publication No. US20060110806A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter J.
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Ragghianti, James John
; APPLICANT: Seip, John E.
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn Qun
; TITLE OF INVENTION: DCCSAHEXAENOIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3160 US NA
; CURRENT APPLICATION NUMBER: US/11/264,737
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 129
; LENGTH: 458
; TYPE: PR1
; ORGANISM: Aspergillus nidulans FGSC A4 [GenBank Accession No. EAA57945]
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: DGAT1
US-11-264-737-129

Query Match 17.7%; Score 50; DB 7; Length 458;
Best Local Similarity 45.0%; Pred. No. 65;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 10 ONEYFDSLHACTPCOLRCS 29
| : : : : :
Db 74 QDVVIGAILFALVPCQLCS 93

RESULT 54
US-11-265-761-101
; Sequence 101, Application US/11265761
; Publication No. US20060115881A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours and Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ECOSAPENTAENOIC ACID PRODUCING STRAINS OF YARROWIA
; FILE REFERENCE: CL2698 USA
; CURRENT APPLICATION NUMBER: US/11/265,761
; CURRENT FILING DATE: 2005-11-02
; PRIOR APPLICATION NUMBER: US 60/624812
; PRIOR FILING DATE: 2004-11-04
; NUMBER OF SEQ ID NOS: 414
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 101
; LENGTH: 458

```

; TYPE: PRT
; ORGANISM: Aspergillus nidulans FGSC A4 [GenBank Accession No. EAA57945]
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: DGA11
US-11-265-761-101

Query Match      17.7%; Score 50; DB 7; Length 458;
Best Local Similarity 45.0%; Pred. No. 65;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Cy      10 ONEYFDSLHACIPCOLRCS 29
      1: : : : : : : : : : : :
      74 QDVVIGAILFALVPCQLCS 93

RESULT 55
US-10-505-928-146
; Sequence 146, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 146
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-146

Query Match      17.7%; Score 50; DB 6; Length 592;
Best Local Similarity 32.6%; Pred. No. 84;
Matches 14; Conservative 9; Mismatches 14; Indels 6; Gaps 3;

Cy      6 GGCSSQNEY-FDSLHACIPCOL---RCSNTPPLTCQRYCNAA 43
      145 GGCSSRIWGLARQGYRCINCKLVHRC-HGLVPLTCRHMDS 186

RESULT 56
US-10-449-902-43722
; Sequence 43722, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USBS THEREOF
; FILE REFERENCE: MOA-A020511-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43722
; LENGTH: 801
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-43722

Query Match      17.7%; Score 50; DB 6; Length 801;
Best Local Similarity 32.4%; Pred. No. 11e+02;
Matches 12; Conservative 6; Mismatches 13; Indels 6; Gaps 1;
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Cy      8 CSQNEYFDSLHACIPCOLRCSNTPPLTCQRYCNAS 44
      404 CPPPEYFANLLFGLV-----NNVPLPSCKSKSNPS 434

RESULT 57
US-11-174-307B-2182
; Sequence 2182, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
; TITLE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS
; FILE REFERENCE: 2750-1601PUS2
; CURRENT APPLICATION NUMBER: US/11/174,307B
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,671
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,781
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,651
; NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 2182
; LENGTH: 1617
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 21536812; NR Description: unknown [Arabidopsis thaliana]
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 7239512; NR Description: Strong similarity to the
; OTHER INFORMATION: higher plant tyrosine-specific protein phosphatases (PPs) from A.
; OTHER INFORMATION: thaliana gi|3413424 expressed during embryogenesis. [Arabidopsis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 53793176; NR Description: tyrosine-specific
; OTHER INFORMATION: protein phosphatase-like protein [Oryza sativa (japonica
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 34912696; NR Description: P0686E09.18 (Oryza
; OTHER INFORMATION: sativa (japonica cultivar-group)] >gi|13365580[dbj|BAB39125.1]
US-11-174-307B-2182

Query Match      17.7%; Score 50; DB 7; Length 1617;
Best Local Similarity 36.0%; Pred. No. 2.3e+02;
Matches 9; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

Cy      20 ACIPCOLRCSNTPPLTCQRYCNAS 44
      82 ACTCTCTCTATTCATCTTTCAT 106

RESULT 58
US-11-174-307B-2458
; Sequence 2458, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
; TITLE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS
; FILE REFERENCE: 2750-1601PUS2
; CURRENT APPLICATION NUMBER: US/11/174,307B
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,671
```

```
/ PRIOR FILING DATE: 2004-06-30
/ PRIOR APPLICATION NUMBER: 60/583,781
/ PRIOR FILING DATE: 2004-06-30
/ PRIOR APPLICATION NUMBER: 60/583,651
/ PRIOR FILING DATE: 2004-06-30
/ NUMBER OF SEQ ID NOS: 5544
/ SEQ ID NO 2458
/ LENGTH: 1682
/ TYPE: PRT
/ ORGANISM: Arabidopsis thaliana
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: Pfam Name: 20G-FelI_Oxy, Pfam Description: 20G-Fe(II)
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: GI Number: 50933567, NR Description:
/ OTHER INFORMATION: ethylene-forming-enzyme-like protein [Oryza sativa]
/ OTHER INFORMATION: [japonica cultivar-group] >gi|24413984|dbj|BAC22235.1
/ OTHER INFORMATION: ethylene-forming-enzyme-like protein [Oryza sativa]
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: GI Number: 50252393, NR Description: putative
/ OTHER INFORMATION: iron/ascorbate-dependent oxidoreductase [Oryza sativa]
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: GI Number: 31115140, NR Description: iron/ascorbate-dependent
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: GI Number: 34898470, NR Description: ESTs
/ OTHER INFORMATION: D47168(S13332), D46350(S10967) correspond to a region of the
/ OTHER INFORMATION: predicted gene, similar to Prunus armeniaca
/ OTHER INFORMATION: ethylene-forming-enzyme-like dioxygenase. (U97530) [Oryza sativa]
/ US-11-174-307B-2458

Query Match          17.7%; Score 50; DB 7; Length 1682;
Best Local Similarity 37.0%; Pred. No. 2,4e+02;
Matches 10; Conservative 2; Mismatches 15; Indels 0; Gaps 0;

Qy 20 ACIPCOLRCSNPPPLTCORYNASVT 46
Db 4 ACCACTATCTCTCTCTCTCAATCT 30

RESULT 59
US-11-174-307B-5090
/ Sequence 5090, Application US/11174307B
/ Publication No. US20060143729A1
/ GENERAL INFORMATION:
/ APPLICANT: ALEXANDROV, Nikolai
/ APPLICANT: BROVER, Vyacheslav
/ TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
/ FILE REFERENCE: 2750-1601PUS2
/ CURRENT APPLICATION NUMBER: US/11/174,307B
/ CURRENT FILING DATE: 2005-06-30
/ PRIOR APPLICATION NUMBER: 60/583,671
/ PRIOR FILING DATE: 2004-06-30
/ PRIOR APPLICATION NUMBER: 60/583,781
/ PRIOR FILING DATE: 2004-06-30
/ PRIOR APPLICATION NUMBER: 60/583,651
/ PRIOR FILING DATE: 2004-06-30
```

```
/ NUMBER OF SEQ ID NOS: 5544
/ SEQ ID NO 5090
/ LENGTH: 152
/ TYPE: PRT
/ ORGANISM: Glycine max
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: GI Number: 22330130, NR Description: integral membrane
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: GI Number: 56784709, NR Description: integral membrane
/ OTHER INFORMATION: protein-like [Oryza sativa] [japonica cultivar-group]
/ OTHER INFORMATION: gi|56784036|dbj|BAD82664.1| integral membrane protein-like [Oryza
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: GI Number: 38604002, NR Description: At2g37200 [Arabidopsis
/ OTHER INFORMATION: [japonica cultivar-group] >gi|38454082|gb|AA20735.1| At2g37200 [Arabidopsis
/ OTHER INFORMATION: thaliana] >gi|30687069|ref|NP_181257.2| integral membrane protein,
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: GI Number: 50898970, NR Description: integral membrane
/ OTHER INFORMATION: protein-like [Oryza sativa] [japonica cultivar-group]
/ OTHER INFORMATION: >gi|47497809|dbj|BAD19907.1| integral membrane protein-like [Oryza
/ US-11-174-307B-5090

Query Match          17.5%; Score 49.5; DB 7; Length 152;
Best Local Similarity 35.9%; Pred. No. 25;
Matches 14; Conservative 2; Mismatches 16; Indels 7; Gaps 1;

Qy 2 LOMAGGCGNQNEFSLHACTPCQLRCSNPPPLTCOR 40
Db 93 LSLAAGCTASTADLLEA-----GSHCPKLCGRY 124

RESULT 60
US-11-289-102-328
/ Sequence 328, Application US/11289102
/ Publication No. US20060121511A1
/ GENERAL INFORMATION:
/ APPLICANT: Lee, Hyerim
/ APPLICANT: Shaw, Peter M.
/ APPLICANT: Clark, Edwin
/ TITLE OF INVENTION: BIOMARKERS AND METHODS FOR DETERMINING SENSITIVITY TO
/ FILE REFERENCE: 10338 NP
/ CURRENT APPLICATION NUMBER: US/11/289,102
/ CURRENT FILING DATE: 2005-11-29
/ PRIOR APPLICATION NUMBER: US 60/631,993
/ PRIOR FILING DATE: 2004-11-30
/ NUMBER OF SEQ ID NOS: 395
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 328
/ LENGTH: 324
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-11-289-102-328

Query Match          17.5%; Score 49.5; DB 7; Length 324;
Best Local Similarity 30.0%; Pred. No. 53;
Matches 12; Conservative 8; Mismatches 17; Indels 3; Gaps 1;

Qy 14 PSLHACTPCQ---LRCSNPPPLTCORYNASVTNSVK 50
Db 84 FDYVLPPIIQCOAGHVCNQCRKLSCCPTCGALTPSR 123

RESULT 61
US-10-953-349-21867
/ Sequence 21867, Application US/10953349
```

```
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nikolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 21867
LENGTH: 327
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-21867

Query Match      17.5%; Score 49.5; DB 6; Length 327;
Best Local Similarity 30.4%; Pred. No. 54;
Matches 14; Conservative 9; Mismatches 18; Indels 5; Gaps 2;

Oy      7  OCSQ--NEYFDSLHACIPQQLRCSSNTPPLTCQRYCNASVTNSVK 50
Db      5  OCTQSIPEYDNNSSSVLNCDSRDSKDT--OCQVYLSGEMISITK 47

RESULT 62
US-10-953-349-21866
Sequence 21866, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nikolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 21866
LENGTH: 506
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-21866

Query Match      17.5%; Score 49.5; DB 6; Length 506;
Best Local Similarity 30.4%; Pred. No. 83;
Matches 14; Conservative 9; Mismatches 18; Indels 5; Gaps 2;

Oy      7  OCSQ--NEYFDSLHACIPQQLRCSSNTPPLTCQRYCNASVTNSVK 50
Db      184 OCTQSIPEYDNNSSSVLNCDSRDSKDT--OCQVYLSGEMISITK 226

RESULT 63
US-10-505-928-397
Sequence 397, Application US/10505928
Publication No. US20060088532A1
GENERAL INFORMATION:
APPLICANT: Ludwig Institute for Cancer Research et al.
TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28967/39178
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE: PatentIn 3.2
SEQ ID NO 397
LENGTH: 971
TYPE: PRT
ORGANISM: Homo sapiens
US-10-505-928-397
```

```
Query Match      17.5%; Score 49.5; DB 6; Length 971;
Best Local Similarity 33.3%; Pred. No. 1.6e+02;
Matches 16; Conservative 3; Mismatches 16; Indels 13; Gaps 3;

Oy      8  CSQNEYFDSLHACT-----PCQLRCSS-----NTPPLTCQRYCNA 43
Db      326 CEYNPVEVSWL-TCLADVREPCQLGCRNLTYCTNFNNRFTFLFRSCNA 372

RESULT 64
US-10-449-902-41144
Sequence 41144, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 41144
LENGTH: 1016
TYPE: PRT
ORGANISM: Oryza sativa
US-10-449-902-41144

Query Match      17.5%; Score 49.5; DB 6; Length 1016;
Best Local Similarity 34.0%; Pred. No. 1.6e+02;
Matches 17; Conservative 11; Mismatches 11; Indels 11; Gaps 4;

Oy      8  CSQNEYFDSLHACT-----PCQLRCSSNTPPLTCQRYCNA 48
Db      6  CASRKGKALVHSCSSSIPIKIRPTS--PPLSGEADLPFCRPNASVTNA 53

RESULT 65
US-11-291-698A-132
Sequence 132, Application US/11291698A
Publication No. US20060135430A1
GENERAL INFORMATION:
APPLICANT: Chan, Andrew Chee-Yuen
APPLICANT: Gordon, Nathaniel C.
APPLICANT: Kelley, Robert F.
APPLICANT: Koehler, Michael F.T.
APPLICANT: Starovassnik, Melissa A.
TITLE OF INVENTION: BLYS ANTAGONISTS AND USES THEREOF
FILE REFERENCE: 11669.174USCI
CURRENT APPLICATION NUMBER: US/11/291,698A
CURRENT FILING DATE: 2005-11-30
PRIOR APPLICATION NUMBER: PCT/US04/17682
PRIOR FILING DATE: 2004-06-04
PRIOR APPLICATION NUMBER: US 60/476,414
PRIOR FILING DATE: 2003-06-05
PRIOR APPLICATION NUMBER: US 60/476,531
PRIOR FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: US 60/476,481
PRIOR FILING DATE: 2003-06-05
NUMBER OF SEQ ID NOS: 216
SOFTWARE: PatentIn version 3.3
SEQ ID NO 132
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Clone 91
```

US-11-291-698A-132

Query Match 17.3%; Score 49; DB 7; Length 17;
Best Local Similarity 53.3%; Pred. No. 3.3;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 12 EXFDSLHACIPCOL 26
Db 1 ECFDALVHRWPCDL 15

RESULT 66

US-10-953-349-10623
; Sequence 10623, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349

; NUMBER OF SEQ ID NOS: 40252

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 10623

; LENGTH: 343

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

US-10-953-349-10623

RESULT 67

US-10-953-349-10622
; Sequence 10622, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349

; NUMBER OF SEQ ID NOS: 40252

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 10622

; LENGTH: 369

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

US-10-953-349-10622

RESULT 68

US-11-217-557-4
; Sequence 4, Application US/11217557
; Publication No. US20060127927A1
; GENERAL INFORMATION:

; APPLICANT: Korneiluk, Robert G.

; APPLICANT: Mackenzie, Alexander E.

; APPLICANT: Baird, Stephen

; TITLE OF INVENTION: Mammalian IAP Gene Family, Primers,

; FILE REFERENCE: 07891/003007

; CURRENT APPLICATION NUMBER: US/11/217,557

; PRIOR FILING DATE: 2005-09-01

; PRIOR FILING DATE: 2000-09-01

; PRIOR FILING DATE: 1995-12-22

; PRIOR FILING DATE: 1995-08-04

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 497

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-217-557-4

Query Match 17.3%; Score 49; DB 7; Length 497;

Best Local Similarity 34.2%; Pred. No. 94;

Matches 13; Conservative 7; Mismatches 12; Indels 6; Gaps 2;

Qy 1 MLOMAGCCONEYPDS--LHACIPCOLRCSNTPPLT 36

Db 330 LLEQKQ-----EYNNHHLTHSLSECLVRTTEKTSPLT 363

RESULT 69

US-11-174-307B-1540
; Sequence 1540, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai

; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY

; FILE REFERENCE: 2750-1601PUS2

; CURRENT APPLICATION NUMBER: US/11/174,307B

; NUMBER OF SEQ ID NOS: 5544

; SEQ ID NO 1540

; LENGTH: 820

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

; FEATURE: NAME/KEY: misc_feature

; LOCATION: OTHER INFORMATION: sativa (japonica cultivar-group) >g1|21902069|dbj|BAC05617.1|

US-11-174-307B-1540

Query Match 17.3%; Score 49; DB 7; Length 820;

Best Local Similarity 28.6%; Pred. No. 1.5e+02;

Matches 8; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

Qy 21 CIPCOLRCSNTPPLTCORYNASVTNS 48

Db 17 CATCTCTCATGCTCTTTCATATTT 44

RESULT 70

US-11-174-307B-2106

; Sequence 2106, Application US/11174307B

; Publication No. US20060143729A1

```

; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai
; TITLE OF INVENTION: BROWER, Vacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
; FILE REFERENCE: 2750-1601PUS2
; CURRENT APPLICATION NUMBER: US/11/174,307B
; PRIOR FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,671
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,781
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,651
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 2106
; LENGTH: 1116
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Pfram Name: zf-C3HC4; Pfram Description: Zinc finger, C3HC4
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 21537318; NR Description: unknown [Arabidopsis thaliana]
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 6642645; NR Description: putative RING zinc finger
; OTHER INFORMATION: protein [Arabidopsis thaliana] >[15231414|ref|NP_187376.1| zinc
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 61097975; NR Description: similar to RING finger
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 50747306; NR Description: PREDICTED: similar to
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 61097975; NR Description: similar to RING finger
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 41617082; NR Description: TPA: HDC06237
; US-11-174-307B-2106

Query Match          17.3%; Score 49; DB 7; Length 1116;
Best Local Similarity 36.0%; Pred. No. 2.1e+02;
Matches 9; Conservative 2; Mismatches 14; Indels 0; Gaps 0;

Qy          20 ACIPQRCSSNTPLTCORXCNAS 44
Db          1 ACCACCTTGCTGTTCTCTCTAT 25

RESULT 71
US-11-178-724-22
; Sequence 22, Application US/11/178724
; Publication No. US20060128619A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN R.
; APPLICANT: YOUNG, LESLEY L.
; APPLICANT: MCKENZIE, GRAHAME J.
; TITLE OF INVENTION: THERAPEUTIC USE OF MODULATORS OF NOTCH
; FILE REFERENCE: 674525-2021
; CURRENT APPLICATION NUMBER: US/11/178,724
; PRIOR FILING DATE: 2005-07-11
; PRIOR APPLICATION NUMBER: PCT/GB04/00021
; PRIOR FILING DATE: 2004-01-09
; PRIOR APPLICATION NUMBER: GB 0300428.0
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 43
;
```

```

; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 22
; LENGTH: 1238
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-178-724-22

Query Match          17.3%; Score 49; DB 7; Length 1238;
Best Local Similarity 25.6%; Pred. No. 2.3e+02;
Matches 11; Conservative 8; Mismatches 18; Indels 6; Gaps 1;

Qy          5 AGCGSQNEYPDSL-----LHACIPQRCSSNTPLTCORXC 41
Db          169 AGMNPEDRMKSLHPSGHVAHLEQIRVRCDENYATCNKFC 211

RESULT 72
US-11-071-796A-21
; Sequence 21, Application US/11/071796A
; Publication No. US20060140943A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: SOLARI, ROBERTO CELESTE ERCOLE
; APPLICANT: DALIMAN, MARGARET JANE
; APPLICANT: LAMB, JONATHAN ROBERT
; APPLICANT: HOYNE, GERARD FRANCIS
; APPLICANT: BRIEND, EMMANUEL CYRILLE PASCAL
; TITLE OF INVENTION: IMMUNOTHERAPY USING MODULATORS OF NOTCH SIGNALLING
; FILE REFERENCE: 674525-2018
; CURRENT APPLICATION NUMBER: US/11/071,796A
; PRIOR FILING DATE: 2005-03-03
; PRIOR APPLICATION NUMBER: PCT/GB03/03874
; PRIOR FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: GB 0220658.9
; PRIOR FILING DATE: 2002-09-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 21
; LENGTH: 1238
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-071-796A-21

Query Match          17.3%; Score 49; DB 7; Length 1238;
Best Local Similarity 25.6%; Pred. No. 2.3e+02;
Matches 11; Conservative 8; Mismatches 18; Indels 6; Gaps 1;

Qy          5 AGCGSQNEYPDSL-----LHACIPQRCSSNTPLTCORXC 41
Db          169 AGMNPEDRMKSLHPSGHVAHLEQIRVRCDENYATCNKFC 211

RESULT 73
US-11-174-307B-1388
; Sequence 1388, Application US/11/174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai
; APPLICANT: BROWER, Vacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
; FILE REFERENCE: 2750-1601PUS2
; CURRENT APPLICATION NUMBER: US/11/174,307B
; PRIOR FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,671
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,781
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,651
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 1388
; LENGTH: 1882
;
```


QY 6 GQCSQNE---YFDSLHLACIPQQLR-CSSNTPELTQRYC 411

Db 12 GLCRANENRFYNSVIGKCRPFKYSGCCGGENNFTSKQEC 511

RESULT 77
US-10-953-349-3386
; Sequence 3386, Application US/10953349
; Publication No. US20060107345A1

```

? APPLICANT: ALEXANDROV, Nickolai et al.
? TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
? TITLE OF INVENTION: ENCODED THERBY
? FILE REFERENCE: 2750-1579PUS2
? CURRENT APPLICATION NUMBER: US/10/953,349
? CURRENT FILING DATE: 2004-09-30
? NUMBER OF SEQ ID NOS: 40252
? SOFTWARE: PatentIn version 3.3
? SEQ ID NO 3386
? LENGTH: 115
? TYPE: PRT
? ORGANISM: Arabidopsis thaliana
? US-10-953-349-3386

```

```
QY      16 SLHACIPQLR--CSSNTPPLTCQRNCNAS    44  
          | : : ||| | : |||| | ||  
Db       8 SSLSSILSAKLKRCCKSPSPSLTCLRLDTAS   38
```

RESULT 78
US-10-953-349-3385
; Sequence 3385, Application US/10953349
; Publication No. US20060107345A1

```

APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCODED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 3385
LENGTH: 147
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-10-953-349-3385

```

```
QY      16 SLHACIPQQLR--CSSNTPPLTCQRYCNAS 44
      |||:::||| |||::||| |||
Db      40 SSLSSILSAKLRCKCKSPSPSLTCLRLDNAS 70
```

RESULT 79
US-10-449-902-43991
; Sequence 43991, Application US/10449902
; Publication No. US20060123505A1

1. APPLICANT: National Institute of Agrobiological Sciences.
2. APPLICANT: Bio-oriented Technology Research Advancement Institution
3. APPLICANT: The Institute of Physical and Chemical Research.
4. APPLICANT: Foundation for Advancement of International Science.
5. TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
6. FILE REFERENCE: MOA-A0205Y1-US
7. CURRENT APPLICATION NUMBER: US/10/0449,902

```

? CURRENT FILING DATE: 2003-05-29
? PRIOR APPLICATION NUMBER: JP 2002-203263E
? PRIOR FILING DATE: 2002-05-30
? PRIOR APPLICATION NUMBER: JP 2002-383870
? PRIOR FILING DATE: 2002-12-11
? NUMBER OF SEQ ID NOS: 56791
? SOFTWARE: Patentln Ver. 2.1
? SEQ ID NO 43991
?
? LENGTH: 147
?
? TYPE: PRT
? ORGANISM: Oryza sativa
?
? US-10-43991-2002-43991
?

```

| | | | | |
|--------------------------|--------|---------------|-------|------------------|
| Query Match | 17.0% | Score 48; | DB 6; | Length 147; |
| Best Local Similarity | 29.8%; | Pred. No. 37; | | |
| Matches 14; Conservative | 3; | Mismatches | 30; | Indels 0; Gaps 0 |

```

QY      2 LQMGCCSQNEFYDLSLHACIPCCQLRCSNTPLTCQRYCNASVTNS 48
      | : | | | | | | | | | | | | | | | | | | | |
DB      55 LDIANGCEHKSPSFSRTHASFMQLQPCSLLSIVSTIDPCQCSSTQS 101

```

RESULT 80
US-10-953-349-3384
; Sequence 3384, Application US/10953349
; Publication No. US20060107345A1

```

; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3384
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-10-953-349-3384

```

```

QY      16 SLHACIPQLR--CSSNTPPLTCQRYCNAS 44
      |||:::|||||::|||
Db      92 SLSLSISAKLRCKCKSPSPBITCLRDTAS 122

```

RESULT 81
US-11-337-518-1
; Sequence 1, Application US/11337518
; Publication No. US20060128947A1

APPLICANT: Dorin, Glen J.
 APPLICANT: Arve, Bo H.
 APPLICANT: Pattison, Gregory J.
 APPLICANT: Halenbeck, Robert F.
 APPLICANT: Johnson, Kirk
 APPLICANT: Chen, Bao-Lu
 APPLICANT: Bana, Ralsharan K.
 APPLICANT: Hora, Maninder S.
 APPLICANT: Madani, Haasan
 APPLICANT: Tsang, Michael
 APPLICANT: Gustafson, Mark E.
 APPLICANT: Bild, Gary S.
 APPLICANT: Johnson, Gary V.
 TITLE OF INVENTION: Formulation, Solubilization, Purification, and Refolding of Tissue-
 TITLE OF INVENTION: Pathway Inhibitor
 FILE REFERENCE: 012441.00013
 CURRENT APPLICATION NUMBER: US/11/337, 518
 CURRENT FILING DATE: 2006-01-24

```

; PRIOR APPLICATION NUMBER: US/09/996,588
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 08/477,677
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/473,668
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: PCT/US96/09980
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 09/973,211
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: US 09/443,099
; PRIOR FILING DATE: 1999-11-18
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-337-518-1
```

```

Query Match      17.0%; Score 48; DB 7; Length 276;
Best Local Similarity 30.0%; Pred. No. 70;
Matches 12; Conservative 7; Mismatches 17; Indels 4; Gaps 2;
```

```
Qy      6 GGCQNE---YFDSLHACIPCOLR-CSSNTPPLTCORYC 41
Db      196 GICRANENRFYNSVIGKCRPFYSGCGGNNFTSKQEC 235
```

```

RESULT 82
US-11-287-121A-1
; Sequence 1, Application US/11287121A
; Publication No. US2006011296A1
; GENERAL INFORMATION:
; APPLICANT: Dey, Laetitia
; APPLICANT: Ley, Arthur C.
; APPLICANT: Ladner, Robert C.
; TITLE OF INVENTION: PLASMIN-INHIBITORY THERAPIES
; FILE REFERENCE: 10280-122001
; CURRENT APPLICATION NUMBER: US/11/287,121A
; CURRENT FILING DATE: 2005-11-22
; PRIOR APPLICATION NUMBER: US 60/630,226
; PRIOR FILING DATE: 2004-11-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-287-121A-1
```

```

Query Match      17.0%; Score 48; DB 7; Length 304;
Best Local Similarity 30.0%; Pred. No. 76;
Matches 12; Conservative 7; Mismatches 17; Indels 4; Gaps 2;
```

```
Qy      6 GGCQNE---YFDSLHACIPCOLR-CSSNTPPLTCORYC 41
Db      224 GICRANENRFYNSVIGKCRPFYSGCGGNNFTSKQEC 263
```

```

RESULT 83
US-10-449-902-29741
; Sequence 29741, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
```

```

; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 29741
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-29741
```

```

Query Match      17.0%; Score 48; DB 6; Length 343;
Best Local Similarity 32.4%; Pred. No. 86;
Matches 12; Conservative 3; Mismatches 14; Indels 8; Gaps 2;
```

```
Qy      21 CIPCOLR-CSSN-----TPPLTCORYCNASTVNSV 49
Db      236 CAPCTLALCCHNKPNPTTLTPSPACPCFGCSISRLV 272
```

```

RESULT 84
US-10-449-902-35921
; Sequence 35921, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 35921
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-35921
```

```

Query Match      17.0%; Score 48; DB 6; Length 354;
Best Local Similarity 20.4%; Pred. No. 89;
Matches 10; Conservative 13; Mismatches 24; Indels 2; Gaps 1;
```

```
Qy      4 MAGQCSQNEFYFDSLHACIPCO--LRSSNTPPLTCORYCNASTVNSV 50
Db      109 MSHCKSGKFWATLQACIPIMELIMERSREPRVYDNCISGIDSAWK 157
```

```

RESULT 85
US-10-449-902-37039
; Sequence 37039, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
```

```
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 37039
/ LENGTH: 386
/ TYPE: PRT
/ ORGANISM: Oryza sativa
US-10-449-902-37039

Query Match      17.0%; Score 48; DB 6; Length 386;
Best Local Similarity 32.4%; Pred. No. 97;
Matches 12; Conservative 3; Mismatches 14; Indels 8; Gaps 2;

Oy      21 CIPCOLR-CSSN-----TPELTQRCYNASVNSV 49
Db      279 CAPCTIALCHNKNPPTLTTPSPACPCFCRGSISRVL 315

RESULT 86
US-11-293-697-2797
/ Sequence 2797, Application US/11293697
/ Publication No. US20060105376A1
/ GENERAL INFORMATION:
/ APPLICANT: HELIX RESEARCH INSTITUTE
/ TITLE OF INVENTION: Novel full length cDNA
/ FILE REFERENCE: HI-A0106
/ CURRENT APPLICATION NUMBER: US/11/293, 697
/ CURRENT FILING DATE: 2005-12-05
/ PRIOR APPLICATION NUMBER: US/10/108, 260
/ PRIOR FILING DATE: 2002-03-28
/ NUMBER OF SEQ ID NOS: 5458
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2797
/ LENGTH: 392
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-293-697-2797

Query Match      17.0%; Score 48; DB 7; Length 392;
Best Local Similarity 33.3%; Pred. No. 98;
Matches 15; Conservative 1; Mismatches 23; Indels 6; Gaps 1;

Oy      2 LOMAGCCSNEYFDSLH-----ACIPQLRCSSNTPELTQRY 40
Db      175 LQVLANKQNRDPDKLKQYENPACBGRMLTFPTYMFQIPRY 219

RESULT 87
US-10-449-902-35730
/ Sequence 35730, Application US/10449902
/ Publication No. US20060123505A1
/ GENERAL INFORMATION:
/ APPLICANT: National Institute of Agrobiological Sciences.
/ APPLICANT: Bio-oriented Technology Research Advancement Institution.
/ APPLICANT: The Institute of Physical and Chemical Research.
/ APPLICANT: Foundation for Advancement of International Science.
/ TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
/ FILE REFERENCE: MOA-A020511-US
/ CURRENT APPLICATION NUMBER: US/10/449, 902
/ CURRENT FILING DATE: 2003-05-29
/ PRIOR APPLICATION NUMBER: JP 2002-203269
/ PRIOR FILING DATE: 2002-05-30
/ PRIOR APPLICATION NUMBER: JP 2002-383870
/ PRIOR FILING DATE: 2002-12-11
/ NUMBER OF SEQ ID NOS: 56791
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 35730
/ LENGTH: 405
/ TYPE: PRT
/ ORGANISM: Oryza sativa
US-10-449-902-35730

Query Match      17.0%; Score 48; DB 6; Length 405;
Best Local Similarity 26.5%; Pred. No. 1e+02;
Matches 13; Conservative 6; Mismatches 24; Indels 6; Gaps 1;
```

```
Oy      3 QMAGCCSNEYFDSLHACIPQLRCSSNTPELTQRCYNASVNSVG 51
Db      217 QFCGDLRYMRGENVLEAKKNPDWICP-----VCRGICNCSICRTKGG 259

RESULT 88
US-10-449-902-56162
/ Sequence 56162, Application US/10449902
/ Publication No. US20060123505A1
/ GENERAL INFORMATION:
/ APPLICANT: National Institute of Agrobiological Sciences.
/ APPLICANT: Bio-oriented Technology Research Advancement Institution.
/ APPLICANT: The Institute of Physical and Chemical Research.
/ APPLICANT: Foundation for Advancement of International Science.
/ TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
/ FILE REFERENCE: MOA-A020511-US
/ CURRENT APPLICATION NUMBER: US/10/449, 902
/ CURRENT FILING DATE: 2003-05-29
/ PRIOR APPLICATION NUMBER: JP 2002-203269
/ PRIOR FILING DATE: 2002-05-30
/ PRIOR APPLICATION NUMBER: JP 2002-383870
/ PRIOR FILING DATE: 2002-12-11
/ NUMBER OF SEQ ID NOS: 56791
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 56162
/ LENGTH: 405
/ TYPE: PRT
/ ORGANISM: Oryza sativa
US-10-449-902-56162

Query Match      17.0%; Score 48; DB 6; Length 405;
Best Local Similarity 26.5%; Pred. No. 1e+02;
Matches 13; Conservative 6; Mismatches 24; Indels 6; Gaps 1;

Oy      3 QMAGCCSNEYFDSLHACIPQLRCSSNTPELTQRCYNASVNSVG 51
Db      217 QFCGDLRYMRGENVLEAKKNPDWICP-----VCRGICNCSICRTKGG 259

RESULT 89
US-10-449-902-36732
/ Sequence 36732, Application US/10449902
/ Publication No. US20060123505A1
/ GENERAL INFORMATION:
/ APPLICANT: National Institute of Agrobiological Sciences.
/ APPLICANT: Bio-oriented Technology Research Advancement Institution.
/ APPLICANT: The Institute of Physical and Chemical Research.
/ APPLICANT: Foundation for Advancement of International Science.
/ TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
/ FILE REFERENCE: MOA-A020511-US
/ CURRENT APPLICATION NUMBER: US/10/449, 902
/ CURRENT FILING DATE: 2003-05-29
/ PRIOR APPLICATION NUMBER: JP 2002-203269
/ PRIOR FILING DATE: 2002-05-30
/ PRIOR APPLICATION NUMBER: JP 2002-383870
/ PRIOR FILING DATE: 2002-12-11
/ NUMBER OF SEQ ID NOS: 56791
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 36732
/ LENGTH: 450
/ TYPE: PRT
/ ORGANISM: Oryza sativa
US-10-449-902-36732

Query Match      17.0%; Score 48; DB 6; Length 450;
Best Local Similarity 32.4%; Pred. No. 1.1e+02;
Matches 12; Conservative 3; Mismatches 14; Indels 8; Gaps 2;

Oy      21 CIPCOLR-CSSN-----TPELTQRCYNASVNSV 49
Db      343 CAPCTIALCHNKNPPTLTTPSPACPCFCRGSISRVL 379
```

```
RESULT 90
US-10-449-902-38759
; Sequence 38759, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38759
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-38759

Query Match          17.0%; Score 48; DB 6; Length 450;
Best Local Similarity 32.4%; Pred. No. 1.1e+02;
Matches 12; Conservative 3; Mismatches 14; Indels 8; Gaps 2;

OY 21 CIPCOLR-CSSN-----TPPLTCORYCNASVTNSV 49
DB 343 CAPCTLALCHNKPNPTTLTPSPACPFCRGSISRIV 379

RESULT 91
US-10-449-902-55688
; Sequence 55688, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55688
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-55688

Query Match          17.0%; Score 48; DB 6; Length 450;
Best Local Similarity 32.4%; Pred. No. 1.1e+02;
Matches 12; Conservative 3; Mismatches 14; Indels 8; Gaps 2;

OY 21 CIPCOLR-CSSN-----TPPLTCORYCNASVTNSV 49
DB 343 CAPCTLALCHNKPNPTTLTPSPACPFCRGSISRIV 379

RESULT 92
US-10-515-429-43
; Sequence 43, Application US/10515429
; Publication No. US20060105387A1
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; GENERAL INFORMATION:
; APPLICANT: Prior, Christopher P.
; APPLICANT: Turner, Andrew J.
; APPLICANT: Sadeghi, Homayoun
; TITLE OF INVENTION: Transferrin Fusion Protein Libraries
; FILE REFERENCE: 054710-5007-WO
; CURRENT APPLICATION NUMBER: US/10/515,429
; PRIOR FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: PCT/US03/26779
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 10/384,060
; PRIOR FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 60/485,404
; PRIOR FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 686
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-515-429-43

Query Match          17.0%; Score 48; DB 6; Length 686;
Best Local Similarity 34.1%; Pred. No. 1.7e+02;
Matches 14; Conservative 3; Mismatches 12; Indels 12; Gaps 3;

OY 6 GGCSONEYFDSLHACIP-----COL-RSSNTPLPTC 37
DB 476 GTCNPEYFS--EGCAPSPNSRLCQLCGSGGIPPEKC 513

RESULT 93
US-10-449-902-47388
; Sequence 47388, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47388
; LENGTH: 775
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-47388

Query Match          17.0%; Score 48; DB 6; Length 775;
Best Local Similarity 31.0%; Pred. No. 1.9e+02;
Matches 13; Conservative 8; Mismatches 15; Indels 6; Gaps 2;

OY 1 MLQMGQCSQNEY-----FDSLHACIPCOLRCSSTPLPTCQ 38
DB 516 WHHLIGACP--EYGLVYEVYMWNGSLIEDRLFCRSGTPLPMWQ 555

RESULT 94
US-11-221-332-86
; Sequence 86, Application US/11221332
; Publication No. US20060121498A1
; GENERAL INFORMATION:
; APPLICANT: Eirik Therapeutics
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; TITLE OF INVENTION: Enzymes involved in apoptosis
; FILE REFERENCE: 8912/2042
; CURRENT APPLICATION NUMBER: US/11/221,332
; CURRENT FILING DATE: 2005-09-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/00957
; PRIOR FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: GB0305267.7
; PRIOR FILING DATE: 2003-05-07
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 86
; LENGTH: 952
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-221-332-86

Query Match      17.0%; Score 48; DB 7; Length 952;
Best Local Similarity 72.7%; Pred. No. 2.4e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      26 LRCSSNTPLT 36
      :|||:|||||
Db      275 IQCLSNTPPLT 285

RESULT 95
US-10-505-928-94
; Sequence 94, Application US/10505928
; Publication No. US2006008532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO: 94
; LENGTH: 969
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-94

Query Match      17.0%; Score 48; DB 6; Length 969;
Best Local Similarity 37.0%; Pred. No. 2.4e+02;
Matches 10; Conservative 1; Mismatches 16; Indels 0; Gaps 0;

Qy      8 CSQNEYPDSLHACIPCOLRCSSNTPP 34
      |||||:|||||
Db      832 CEPGYFDSLRICGCHHTCGTCVGP 858

RESULT 96
US-11-289-102-377
; Sequence 377, Application US/11289102
; Publication No. US2006012151A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Hyerim
; APPLICANT: Shaw, Peter M.
; APPLICANT: Clark, Edwin
; TITLE OF INVENTION: BIOMARKERS AND METHODS FOR DETERMINING SENSITIVITY TO
; MICROTUBULE-STABILIZING AGENTS
; FILE REFERENCE: 10338 NP
; CURRENT APPLICATION NUMBER: US/11/289,102
; CURRENT FILING DATE: 2005-11-29
; PRIOR APPLICATION NUMBER: US 60/631,993
; PRIOR FILING DATE: 2004-11-30
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 377
; LENGTH: 1190

; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-289-102-377

Query Match      17.0%; Score 48; DB 7; Length 1190;
Best Local Similarity 44.4%; Pred. No. 2.9e+02;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy      34 PLTCORCNCASVTNSVKG 51
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Db      290 PTNCKTYCRANKTKSSQG 307

RESULT 97
US-11-174-307B-1760
; Sequence 1760, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
; FILE REFERENCE: 2750-1601PUS2
; CURRENT APPLICATION NUMBER: US/11/174,307B
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,671
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,781
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,651
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO: 1760
; LENGTH: 1305
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Pfam Name: TMP1T; Pfam Description: TMP1T-like protein
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Pfam Name: TMP1T; Pfam Description: TMP1T-like protein
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 50758114; NR Description: PREDICTED: similar to
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 57870649; NR Description: Transmembrane protein
; OTHER INFORMATION: induced by tumor necrosis factor alpha [Mus musculus]
; OTHER INFORMATION: gi|58219512|ref|NP_001010945.1| transmembrane protein induced by
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 34871732; NR Description: similar to transmembrane
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 29769387; NR Description: transmembrane protein
; OTHER INFORMATION: induced by tumor necrosis factor alpha [Mus musculus]
; OTHER INFORMATION: >gi|28435931|gb|AAH46757.1| Transmembrane protein induced by tumo
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 58701915; NR Description: Unknown (protein for
US-11-174-307B-1760

Query Match      17.0%; Score 48; DB 7; Length 1305;
Best Local Similarity 29.0%; Pred. No. 3.2e+02;
Matches 9; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

Qy      21 CIPCOLRCSSNTPLTCORCNCASVTNSVKG 51
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Db 394 CTTGACAGCTACTTCATCCGACAGAAAG 424

RESULT 98

US-11-174-307B-2708
Sequence 2708, Application US/11174307B
Publication No. US20060143729A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nikolai
APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
TITLE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS
FILE REFERENCE: 2750-1601PUS2
CURRENT APPLICATION NUMBER: US/11/174,307B
PRIOR FILING DATE: 2005-06-30
PRIOR APPLICATION NUMBER: 60/583,671
PRIOR FILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: 60/583,781
PRIOR FILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: 60/583,651
PRIOR FILING DATE: 2004-06-30
NUMBER OF SEQ ID NOS: 5544
SEQ ID NO 2708
LENGTH: 1324
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
LOCATION:
OTHER INFORMATION: Pfam Name: Pro_Ca; Pfam Description: Carbonic anhydrase
FEATURE:
NAME/KEY: misc_feature
LOCATION:
OTHER INFORMATION: GI Number: 6016709; NR Description: carbonic anhydrase,
OTHER INFORMATION: chloroplast precursor [Arabidopsis thaliana]
OTHER INFORMATION: >gi115810273|gb|AA07024.1| putative carbonic anhydrase,
OTHER INFORMATION: chloroplast precursor [Arabidopsis thaliana]
FEATURE:
NAME/KEY: misc_feature
LOCATION:
OTHER INFORMATION: GI Number: 45451864; NR Description: chloroplast carbonic
FEATURE:
NAME/KEY: misc_feature
LOCATION:
OTHER INFORMATION: GI Number: 23397049; NR Description: putative carbonic
OTHER INFORMATION: anhydrase [Arabidopsis thaliana] >gi123397027|gb|AA031799.1|
OTHER INFORMATION: putative carbonic anhydrase [Arabidopsis thaliana]
OTHER INFORMATION: >gi112642852|gb|AA00368.1| putative carbonic anhydrase 2
FEATURE:
NAME/KEY: misc_feature
LOCATION:
OTHER INFORMATION: GI Number: 438449; NR Description: carbonic anhydrase
FEATURE:
NAME/KEY: misc_feature
LOCATION:
OTHER INFORMATION: GI Number: 20259533; NR Description: putative carbonic
OTHER INFORMATION: anhydrase, chloroplast precursor [Arabidopsis thaliana]
OTHER INFORMATION: >gi130678347|ref|NP_850490.1| carbonic anhydrase 1, chloroplast
US-11-174-307B-2708

Query Match 17.0%; Score 48; DB 7; Length 1324;
Best Local Similarity 29.0%; Pred. No. 3.3e+02;
Matches 9; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

Db 445 CTTGACAGCTACTTCATCCGACAGAAAG 475

Query 21 CTPCQLRSSNTPPLTCORRCNANASVYNSVG 51
US-11-174-307B-2656
Sequence 2656, Application US/11174307B
Publication No. US20060143729A1

GENERAL INFORMATION:

APPLICANT: ALEXANDROV, Nikolai
APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
TITLE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS
FILE REFERENCE: 2750-1601PUS2
CURRENT APPLICATION NUMBER: US/11/174,307B
PRIOR FILING DATE: 2005-06-30
PRIOR APPLICATION NUMBER: 60/583,671
PRIOR FILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: 60/583,781
PRIOR FILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: 60/583,651
PRIOR FILING DATE: 2004-06-30
NUMBER OF SEQ ID NOS: 5544
SEQ ID NO 2656
LENGTH: 1524
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
LOCATION:
OTHER INFORMATION: Pfam Name: Chal_sti_synt_C; Pfam Description: Chalcone and
FEATURE:
NAME/KEY: misc_feature
LOCATION:
OTHER INFORMATION: Pfam Name: MMTV_SAg; Pfam Description: Mouse mammary tumour
FEATURE:
NAME/KEY: misc_feature
LOCATION:
OTHER INFORMATION: GI Number: 50920373; NR Description: Putative fiddlehead-like
OTHER INFORMATION: protein [Oryza sativa (japonica cultivar-group)]
OTHER INFORMATION: >gi124960748|gb|AA05442.1| Putative fiddlehead-like protein [Oryz
FEATURE:
NAME/KEY: misc_feature
LOCATION:
OTHER INFORMATION: GI Number: 3142289; NR Description: Strong similarity to
OTHER INFORMATION: beta-keto-CoA synthase gbJ7088 from Simmondsia chinensis.
OTHER INFORMATION: [Arabidopsis thaliana] gi17488037|pir|T00951 probable
FEATURE:
NAME/KEY: misc_feature
LOCATION:
OTHER INFORMATION: GI Number: 1045614; NR Description: beta-ketoacyl-CoA synthase
FEATURE:
NAME/KEY: misc_feature
LOCATION:
OTHER INFORMATION: GI Number: 23297625; NR Description: beta-ketoacyl-CoA
OTHER INFORMATION: synthase [Arabidopsis thaliana] >gi11017945|db|BAB11304.1|
OTHER INFORMATION: beta-ketoacyl-CoA synthase [Arabidopsis thaliana]
OTHER INFORMATION: >gi115983491|gb|AA111613.1| AT5G43760/MOD19_11 [Arabidopsis
FEATURE:
NAME/KEY: misc_feature
LOCATION:
OTHER INFORMATION: GI Number: 50932775; NR Description: putative beta-ketoacyl
OTHER INFORMATION: synthase [Oryza sativa (japonica cultivar-group)]
OTHER INFORMATION: >gi150080251|gb|AA169586.1| putative beta-ketoacyl synthase [Oryza
US-11-174-307B-2656

Query Match 17.0%; Score 48; DB 7; Length 1524;
Best Local Similarity 34.4%; Pred. No. 3.8e+02;
Matches 11; Conservative 2; Mismatches 19; Indels 0; Gaps 0;

Db 161 ACGTCCTCCCAATATATCTCTCCGACCTTTCCG 192

Query 20 ACIPCQLRSSNTPPLTCORRCNANASVYNSVG 51
US-11-174-307B-2652

Search completed: July 10, 2006, 16:43:10
Job time : 13.8 secs

; Sequence 2652, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
; TITLE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS
; FILE REFERENCE: 2750-1601PUS2
; CURRENT APPLICATION NUMBER: US/11/174,307B
; PRIOR FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,671
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,781
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,651
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 2652
; LENGTH: 1587
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Pfam Name: Chal_sti_synt_C; Pfam Description: Chalcone and
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Pfam Name: MMTV_SAG; Pfam Description: Mouse mammary tumour
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 50920373; NR Description: Putative fiddlehead-like
; OTHER INFORMATION: protein [Oryza sativa (japonica cultivar-group)]
; OTHER INFORMATION: >gi|24960748|gb|AA065442.1| Putative fiddlehead-like protein [Ory
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 3142289; NR Description: Strong similarity to
; OTHER INFORMATION: beta-keto-CoA synthase gbj37088 from Simmondsia chinensis.
; OTHER INFORMATION: [Arabidopsis thaliana] gi|7488037|pir|T00951 probable
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 1045614; NR Description: beta-ketoacyl-CoA synthase
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 23297625; NR Description: beta-ketoacyl-CoA
; OTHER INFORMATION: synthase [Arabidopsis thaliana] >gi|10177945|dbj|BAB11304.1|
; OTHER INFORMATION: beta-ketoacyl-CoA synthase [Arabidopsis thaliana]
; OTHER INFORMATION: >gi|15983491|gb|AA11613.1| AT5943760/MQD19_11 [Arabidopsis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 50932775; NR Description: putative beta-ketoacyl
; OTHER INFORMATION: synthase [Oryza sativa (japonica cultivar-group)]
; OTHER INFORMATION: >gi|50080251|gb|AA069586.1| putative beta-ketoacyl synthase [Oryz
; US-11-174-307B-2652

Query Match 17.0%; Score 48; DB 7; Length 1587;

Best Local Similarity 32.4%; Pred No. 3.9e+02;
Matches 11; Conservative 4; Mismatches 17; Indels 2; Gaps 1;

Oy 20 ACIPQQLR--CSSNTPLTTCORYCNASVTSYKG 51
db 426 ACCTCAAGCCTTGTTCTTCTACCGATGTTTAGG 459

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:42:11 ; Search time 47.4 Seconds
(without alignments)
498.396 Million cell updates/sec

Title: US-10-077-137A-1_COPY_1_51

Perfect score: 283
Sequence: 1 MLOWAGQCSQNEFYDPLHA.....TPPLTCORYCNASVTNSVKG 51

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications AA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------------|
| 1 | 283 | 100.0 | 184 | 4 | US-10-077-438-1 |
| 2 | 283 | 100.0 | 184 | 4 | US-10-077-438-7 |
| 3 | 283 | 100.0 | 184 | 4 | US-10-077-137-1 |
| 4 | 283 | 100.0 | 184 | 4 | US-10-077-137-7 |
| 5 | 283 | 100.0 | 184 | 4 | US-10-068-725-2 |
| 6 | 283 | 100.0 | 184 | 4 | US-10-151-882-47 |
| 7 | 283 | 100.0 | 184 | 4 | US-10-115-192-8 |
| 8 | 283 | 100.0 | 184 | 4 | US-10-008-063-7 |
| 9 | 283 | 100.0 | 184 | 4 | US-10-152-363A-27 |
| 10 | 283 | 100.0 | 184 | 4 | US-10-216-074-11 |
| 11 | 283 | 100.0 | 184 | 4 | US-10-087-080-39 |
| 12 | 283 | 100.0 | 184 | 4 | US-10-742-634-9 |
| 13 | 283 | 100.0 | 184 | 5 | US-10-626-914-6 |
| 14 | 283 | 100.0 | 184 | 5 | US-10-485-489-6 |
| 15 | 283 | 100.0 | 184 | 5 | US-10-861-049-27 |
| 16 | 283 | 100.0 | 184 | 5 | US-10-989-826-46 |
| 17 | 283 | 100.0 | 184 | 5 | US-10-742-634-9 |
| 18 | 283 | 100.0 | 184 | 5 | US-10-967-527A-8 |
| 19 | 283 | 100.0 | 184 | 5 | US-10-501-841-4 |
| 20 | 283 | 100.0 | 184 | 6 | US-11-021-874-27 |
| 21 | 283 | 100.0 | 184 | 6 | US-11-242-294-27 |
| 22 | 283 | 100.0 | 184 | 6 | US-11-800-992-8 |
| 23 | 283 | 100.0 | 184 | 6 | US-11-069-473-4 |
| 24 | 283 | 100.0 | 184 | 6 | US-10-115-192-12 |
| 25 | 274 | 96.8 | 288 | 5 | US-10-469-469-120 |
| 26 | 269 | 95.1 | 51 | 3 | US-09-854-864-6 |
| 27 | 269 | 95.1 | 51 | 3 | US-09-855-158-6 |

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| 28 | 269 | 95.1 | 181 | 3 | US-09-854-864-5 | Sequence 5, Appli |
| 29 | 269 | 95.1 | 181 | 3 | US-09-855-158-5 | Sequence 5, Appli |
| 30 | 269 | 95.1 | 283 | 3 | US-09-854-864-9 | Sequence 9, Appli |
| 31 | 269 | 95.1 | 283 | 3 | US-09-855-158-9 | Sequence 9, Appli |
| 32 | 263 | 92.9 | 207 | 4 | US-10-077-438-3 | Sequence 3, Appli |
| 33 | 263 | 92.9 | 207 | 4 | US-10-077-137-3 | Sequence 3, Appli |
| 34 | 249 | 88.0 | 58 | 3 | US-09-854-864-21 | Sequence 21, Appli |
| 35 | 249 | 88.0 | 58 | 3 | US-09-855-158-21 | Sequence 21, Appli |
| 36 | 230 | 81.3 | 40 | 5 | US-10-967-527A-9 | Sequence 9, Appli |
| 37 | 201 | 71.0 | 34 | 3 | US-09-854-864-7 | Sequence 7, Appli |
| 38 | 201 | 71.0 | 34 | 3 | US-09-855-158-7 | Sequence 7, Appli |
| 39 | 201 | 71.0 | 81 | 3 | US-09-854-864-13 | Sequence 13, Appli |
| 40 | 201 | 71.0 | 81 | 3 | US-09-855-158-13 | Sequence 13, Appli |
| 41 | 181 | 64.0 | 185 | 3 | US-09-854-864-11 | Sequence 11, Appli |
| 42 | 181 | 64.0 | 185 | 3 | US-09-855-158-11 | Sequence 11, Appli |
| 43 | 181 | 64.0 | 185 | 4 | US-10-216-074-17 | Sequence 17, Appli |
| 44 | 181 | 64.0 | 185 | 5 | US-10-967-527A-10 | Sequence 10, Appli |
| 45 | 181 | 64.0 | 281 | 3 | US-09-854-864-10 | Sequence 10, Appli |
| 46 | 181 | 64.0 | 281 | 3 | US-09-855-158-10 | Sequence 10, Appli |
| 47 | 158 | 53.8 | 42 | 4 | US-10-145-206-197 | Sequence 197, App |
| 48 | 104 | 36.7 | 117 | 3 | US-09-854-864-12 | Sequence 12, Appli |
| 49 | 104 | 36.7 | 117 | 3 | US-09-855-158-12 | Sequence 12, Appli |
| 50 | 71.5 | 25.3 | 249 | 4 | US-10-087-192-1647 | Sequence 1647, Ap |
| 51 | 71.5 | 25.3 | 249 | 5 | US-10-967-527A-21 | Sequence 21, Appli |
| 52 | 71.5 | 25.3 | 249 | 6 | US-11-200-992-20 | Sequence 20, Appli |
| 53 | 70.5 | 24.9 | 1548 | 4 | US-10-180-903-2 | Sequence 2, Appli |
| 54 | 69.5 | 24.6 | 5374 | 4 | US-10-028-248A-75 | Sequence 75, Appli |
| 55 | 69.5 | 24.6 | 5374 | 4 | US-10-107-782-75 | Sequence 75, Appli |
| 56 | 69.5 | 24.6 | 5376 | 4 | US-10-028-248A-74 | Sequence 74, Appli |
| 57 | 69.5 | 24.6 | 5376 | 4 | US-10-107-782-74 | Sequence 74, Appli |
| 58 | 68.5 | 24.2 | 332 | 4 | US-10-152-363A-62 | Sequence 62, Appli |
| 59 | 68.5 | 24.2 | 332 | 6 | US-11-242-294-62 | Sequence 62, Appli |
| 60 | 67.5 | 23.9 | 37 | 3 | US-09-779-050A-45 | Sequence 45, Appli |
| 61 | 67.5 | 23.9 | 48 | 5 | US-10-967-527A-20 | Sequence 20, Appli |
| 62 | 67.5 | 23.9 | 59 | 3 | US-09-854-864-20 | Sequence 20, Appli |
| 63 | 67.5 | 23.9 | 59 | 3 | US-09-855-158-20 | Sequence 20, Appli |
| 64 | 67.5 | 23.9 | 166 | 3 | US-09-854-864-15 | Sequence 15, Appli |
| 65 | 67.5 | 23.9 | 166 | 3 | US-09-855-158-15 | Sequence 15, Appli |
| 66 | 67.5 | 23.9 | 166 | 4 | US-10-293-818-6 | Sequence 6, Appli |
| 67 | 67.5 | 23.9 | 166 | 6 | US-11-079-418-6 | Sequence 6, Appli |
| 68 | 67.5 | 23.9 | 171 | 5 | US-10-684-149-18 | Sequence 18, Appli |
| 69 | 67.5 | 23.9 | 245 | 6 | US-11-200-992-9 | Sequence 9, Appli |
| 70 | 67.5 | 23.9 | 265 | 5 | US-10-626-914-17 | Sequence 17, Appli |
| 71 | 67.5 | 23.9 | 265 | 5 | US-10-485-489-19 | Sequence 19, Appli |
| 72 | 67.5 | 23.9 | 265 | 5 | US-10-861-049-36 | Sequence 36, Appli |
| 73 | 67.5 | 23.9 | 265 | 6 | US-11-021-874-36 | Sequence 36, Appli |
| 74 | 67.5 | 23.9 | 265 | 6 | US-11-069-473-9 | Sequence 9, Appli |
| 75 | 67.5 | 23.9 | 291 | 3 | US-09-779-050A-43 | Sequence 43, Appli |
| 76 | 67.5 | 23.9 | 292 | 5 | US-10-967-527A-19 | Sequence 19, Appli |
| 77 | 67.5 | 23.9 | 293 | 3 | US-09-879-919-22 | Sequence 22, Appli |
| 78 | 67.5 | 23.9 | 293 | 3 | US-09-854-864-14 | Sequence 14, Appli |
| 79 | 67.5 | 23.9 | 293 | 3 | US-09-855-158-14 | Sequence 14, Appli |
| 80 | 67.5 | 23.9 | 293 | 3 | US-09-961-376-2 | Sequence 2, Appli |
| 81 | 67.5 | 23.9 | 293 | 3 | US-09-779-050A-42 | Sequence 42, Appli |
| 82 | 67.5 | 23.9 | 293 | 3 | US-09-302-863-2 | Sequence 2, Appli |
| 83 | 67.5 | 23.9 | 293 | 3 | US-09-855-158-2 | Sequence 2, Appli |
| 84 | 67.5 | 23.9 | 293 | 4 | US-10-087-192-1650 | Sequence 1650, Ap |
| 85 | 67.5 | 23.9 | 293 | 4 | US-10-084-971-2 | Sequence 2, Appli |
| 86 | 67.5 | 23.9 | 293 | 4 | US-10-068-725-4 | Sequence 4, Appli |
| 87 | 67.5 | 23.9 | 293 | 4 | US-10-151-882-46 | Sequence 46, Appli |
| 88 | 67.5 | 23.9 | 293 | 4 | US-10-293-818-2 | Sequence 2, Appli |
| 89 | 67.5 | 23.9 | 293 | 4 | US-10-008-063-8 | Sequence 8, Appli |
| 90 | 67.5 | 23.9 | 293 | 4 | US-10-152-363A-22 | Sequence 22, Appli |
| 91 | 67.5 | 23.9 | 293 | 4 | US-10-266-951-22 | Sequence 22, Appli |
| 92 | 67.5 | 23.9 | 293 | 4 | US-10-258-368-1 | Sequence 1, Appli |
| 93 | 67.5 | 23.9 | 293 | 4 | US-10-618-797-4 | Sequence 4, Appli |
| 94 | 67.5 | 23.9 | 293 | 4 | US-10-742-634-7 | Sequence 7, Appli |
| 95 | 67.5 | 23.9 | 293 | 4 | US-10-748-112-27 | Sequence 27, Appli |
| 96 | 67.5 | 23.9 | 293 | 5 | US-10-684-149-4 | Sequence 4, Appli |
| 97 | 67.5 | 23.9 | 293 | 5 | US-10-626-914-3 | Sequence 3, Appli |
| 98 | 67.5 | 23.9 | 293 | 5 | US-10-485-489-3 | Sequence 3, Appli |
| 99 | 67.5 | 23.9 | 293 | 5 | US-10-861-049-25 | Sequence 25, Appli |
| 100 | 67.5 | 23.9 | 293 | 5 | US-10-742-634-7 | Sequence 7, Appli |


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977 51 18.0 957 4 US-10-425-114-54541 Sequence 54541, A
978 51 18.0 999 5 US-10-732-923-14198 Sequence 14198, A
979 51 18.0 1043 4 US-10-424-599-28311 Sequence 28311,
980 51 18.0 1857 4 US-10-437-963-152007 Sequence 152007,
981 50.5 17.8 74 4 US-10-425-115-262946 Sequence 262946,
982 50.5 17.8 99 3 US-09-950-933A-83 Sequence 83, App1
983 50.5 17.8 119 4 US-10-767-701-55749 Sequence 55749, A
984 50.5 17.8 139 4 US-10-437-963-152280 Sequence 152280,
985 50.5 17.8 159 4 US-10-425-115-265606 Sequence 265606,
986 50.5 17.8 162 3 US-09-798-788-12 Sequence 12, App1
987 50.5 17.8 162 4 US-10-218-102-422 Sequence 422, App
988 50.5 17.8 182 4 US-10-424-599-213191 Sequence 213191,
989 50.5 17.8 191 3 US-09-950-933A-66 Sequence 66, App1
990 50.5 17.8 191 4 US-10-424-599-213188 Sequence 213188,
991 50.5 17.8 198 4 US-10-425-115-208386 Sequence 208386,
992 50.5 17.8 209 4 US-10-425-115-219536 Sequence 219536,
993 50.5 17.8 237 4 US-10-282-122A-59188 Sequence 59188, A
994 50.5 17.8 435 4 US-10-237-790-10 Sequence 10, App1
995 50.5 17.8 464 5 US-10-739-930-5983 Sequence 5983, Ap
996 50.5 17.8 520 4 US-10-408-765A-570 Sequence 570, App
997 50.5 17.8 541 4 US-10-425-114-72556 Sequence 72556, A
998 50.5 17.8 575 3 US-09-796-753-2 Sequence 2, App1
999 50.5 17.8 626 4 US-10-437-963-190192 Sequence 190192,
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ALIGNMENTS

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RESULT 1
US-10-077-438-1
; Sequence 1, Application US/10077438
; Publication No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRF
; ORGANISM: homo sapien
US-10-077-438-1

Query Match 100.0%; Score 283; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Publication No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRF
; ORGANISM: homo sapien
US-10-077-438-7
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Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MLOMAGCSONEYFDSLHACIPCOLRCSNTPTLCORYNASVTNSVKG 51
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US-10-077-137-1
; Sequence 1, Application US/10077137
; Publication No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRF
; ORGANISM: homo sapien
US-10-077-137-1

Query Match 100.0%; Score 283; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4
US-10-077-137-7
; Sequence 7, Application US/10077137
; Publication No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-7

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Best Local Similarity 100.0%; Pred. No. 2.5e-25;
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Db 1 MLOMAGCQSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTVSVKG 51

RESULT 5
US-10-068-725-2
; Sequence 2, Application US/10068725
; Publication No. US20030012783A1
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne
; TITLE OF INVENTION: Antibodies That Bind Both BCMA and TACI
; FILE REFERENCE: 01-04
; CURRENT APPLICATION NUMBER: US/10/068,725
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/270,274
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/283,447
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-725-2

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Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MLOMAGCQSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTVSVKG 51

RESULT 6
US-10-151-882-47
; Sequence 47, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554
; CURRENT APPLICATION NUMBER: US/10/151,882
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-882-47

Query Match 100.0%; Score 283; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 7
US-10-115-192-8
; Sequence 8, Application US/10115192
; Publication No. US20030082175A1
; GENERAL INFORMATION:
; APPLICANT: Apotech R & D S.A.
; TITLE OF INVENTION: Apr1l Receptor (BCMA) and Uses Thereof
; FILE REFERENCE: A083PCT
; CURRENT APPLICATION NUMBER: US/10/115,192
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 60/215688
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/181807
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/157933
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-115-192-8

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Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MLOMAGCQSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTVSVKG 51

RESULT 8
US-10-008-063-7
; Sequence 7, Application US/10008063
; Publication No. US20030092164A1
; GENERAL INFORMATION:

APPLICANT: Gross, Jane A.
APPLICANT: Xu, Wenfeng
APPLICANT: Henne, Randal M.
APPLICANT: Grant, Francis J.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
FILE REFERENCE: 00-103
CURRENT APPLICATION NUMBER: US/10/008,063
CURRENT FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 184
TYPE: PRT
ORGANISM: Homo sapiens
US-10-008-063-7

Query Match 100.0%; Score 283; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MLOMAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASTNSVKG 51

RESULT 9
US-10-152-363A-27
Sequence 27, Application US/10152363A
Publication No. US20030103966A1
GENERAL INFORMATION:
APPLICANT: Rixon, Mark W.
APPLICANT: Gross, Jane A.
TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
FILE REFERENCE: 01-20
CURRENT APPLICATION NUMBER: US/10/152,363A
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: 60/293,343
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 27
LENGTH: 184
TYPE: PRT
ORGANISM: Homo sapiens
US-10-152-363A-27

Query Match 100.0%; Score 283; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MLOMAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASTNSVKG 51

RESULT 10
US-10-216-074-11
Sequence 11, Application US/10216074
Publication No. US20030148445A1
GENERAL INFORMATION:
APPLICANT: Shu, Hong-Bing
TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
FILE REFERENCE: 2879-72
METHODS OF USE THEREOF
CURRENT APPLICATION NUMBER: US/10/216,074
CURRENT FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US/09/565,423
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: UNKNOWN
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/132,892
PRIOR FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 17

SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 184
TYPE: PRT
ORGANISM: Homo sapiens
US-10-216-074-11

Query Match 100.0%; Score 283; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLOMAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASTNSVKG 51
DB 1 MLOMAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASTNSVKG 51

RESULT 11
US-10-087-080-39
Sequence 39, Application US/10087080
Publication No. US20030235820A1
GENERAL INFORMATION:
APPLICANT: Markowitz, David H.
APPLICANT: Eos Biotechnology, Inc.
APPLICANT: Case Western Reserve University
TITLE OF INVENTION: No. US20030235820A1 Methods of Diagnosis of Metastatic Colorectal
TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for
FILE REFERENCE: 018501-000840US
CURRENT APPLICATION NUMBER: US/10/087,080
CURRENT FILING DATE: 2002-10-25
PRIOR APPLICATION NUMBER: US 60/272,206
PRIOR FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: US 60/281,149
PRIOR FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: US 60/284,555
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 39
LENGTH: 184
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: tumor necrosis factor receptor superfamily, member
US-10-087-080-39

Query Match 100.0%; Score 283; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MLOMAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASTNSVKG 51

RESULT 12
US-10-742-634-9
Sequence 9, Application US/10742634
Publication No. US20040208824A1
GENERAL INFORMATION:
APPLICANT: Parmelee, David
APPLICANT: Yeh, Ren-Hwa
APPLICANT: Galperina, Olga
APPLICANT: Hilbert, David
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: Neutrokin-alpha Conjugate, Neutrokin-alpha Complex, and Uses The
FILE REFERENCE: 1488.181002
CURRENT APPLICATION NUMBER: US/10/742,634
CURRENT FILING DATE: 2003-12-22
PRIOR APPLICATION NUMBER: US 60/435,262
PRIOR FILING DATE: 2002-12-23

;; PRIOR APPLICATION NUMBER: US 60/467,198
;; PRIOR FILING DATE: 2003-05-02
;; NUMBER OF SEQ ID NOS: 17
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 9
;; LENGTH: 184
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-742-634-9

Query Match 100.0%; Score 283; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MLOMAGCCSNEFYDSLHACIPQCLRCSSNTPPLTCQRYCNASVTSYVG 51

RESULT 13
US-10-626-914-6
;; Sequence 6, Application US/10626914
;; Publication No. US20050043516A1
;; GENERAL INFORMATION:
;; PatIn Docket Preview
;; APPLICANT: CHUNTHARAPAI, ANAN
;; APPLICANT: GREML, IOBAL
;; APPLICANT: KIM, KYUNG JIN
;; APPLICANT: YAN, MINHONG
;; TITLE OF INVENTION: TACT Antibodies and Uses Thereof
;; FILE REFERENCE: P1942R1
;; CURRENT APPLICATION NUMBER: US/10/626,914
;; CURRENT FILING DATE: 2003-07-25
;; PRIOR APPLICATION NUMBER: US 60/398,530
;; PRIOR FILING DATE: 2002-07-25
;; NUMBER OF SEQ ID NOS: 17
;; SEQ ID NO 6
;; LENGTH: 184
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-626-914-6

Query Match 100.0%; Score 283; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLOMAGCCSNEFYDSLHACIPQCLRCSSNTPPLTCQRYCNASVTSYVG 51
Db 1 MLOMAGCCSNEFYDSLHACIPQCLRCSSNTPPLTCQRYCNASVTSYVG 51

RESULT 14
US-10-485-489-6
;; Sequence 6, Application US/10485489
;; Publication No. US20050070689A1
;; GENERAL INFORMATION:
;; APPLICANT: Dixit, Vishva
;; APPLICANT: Grewal, Iqbal
;; APPLICANT: Ridgway, John
;; APPLICANT: Yan, Minhong
;; TITLE OF INVENTION: TACTs and BR3 Polypeptides and Uses Thereof
;; FILE REFERENCE: 11669.175USWO
;; CURRENT APPLICATION NUMBER: US/10/485,489
;; CURRENT FILING DATE: 2004-01-30
;; PRIOR APPLICATION NUMBER: PCT/US02/23487
;; PRIOR FILING DATE: 2002-07-24
;; PRIOR APPLICATION NUMBER: US 60/310,114
;; PRIOR FILING DATE: 2001-08-03
;; PRIOR APPLICATION NUMBER: US 60/377,171
;; PRIOR FILING DATE: 2002-04-30
;; NUMBER OF SEQ ID NOS: 19
;; SEQ ID NO 6
;; LENGTH: 184
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-485-489-6

;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-485-489-6

Query Match 100.0%; Score 283; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLOMAGCCSNEFYDSLHACIPQCLRCSSNTPPLTCQRYCNASVTSYVG 51
Db 1 MLOMAGCCSNEFYDSLHACIPQCLRCSSNTPPLTCQRYCNASVTSYVG 51

RESULT 15
US-10-861-049-27
;; Sequence 27, Application US/10861049
;; Publication No. US20050095243A1
;; GENERAL INFORMATION:
;; APPLICANT: Andrew Chan
;; APPLICANT: Qian Gong
;; APPLICANT: Flavius Martin
;; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
;; FILE REFERENCE: P2040R1US
;; CURRENT APPLICATION NUMBER: US/10/861,049
;; CURRENT FILING DATE: 2004-06-04
;; PRIOR APPLICATION NUMBER: US 60/476,531
;; PRIOR FILING DATE: 2003-06-06
;; PRIOR APPLICATION NUMBER: US 60/476,481
;; PRIOR FILING DATE: 2003-06-05
;; PRIOR APPLICATION NUMBER: US 60/476,414
;; PRIOR FILING DATE: 2003-06-05
;; NUMBER OF SEQ ID NOS: 145
;; SEQ ID NO 27
;; LENGTH: 184
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-861-049-27

Query Match 100.0%; Score 283; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLOMAGCCSNEFYDSLHACIPQCLRCSSNTPPLTCQRYCNASVTSYVG 51
Db 1 MLOMAGCCSNEFYDSLHACIPQCLRCSSNTPPLTCQRYCNASVTSYVG 51

RESULT 16
US-10-989-826-46
;; Sequence 46, Application US/10989826
;; Publication No. US20050238650A1
;; GENERAL INFORMATION:
;; APPLICANT: Genentech, Inc.
;; APPLICANT: Crowley, Craig
;; APPLICANT: De Sauvage, Frederic J.
;; APPLICANT: Eaton, Daniel L.
;; APPLICANT: Ebens, Allen
;; APPLICANT: Polson, Andrew
;; APPLICANT: Smith, Victoria
;; TITLE OF INVENTION: Compositions and Methods for the Treatment of Tumor of
;; FILE REFERENCE: P5105R1US
;; CURRENT APPLICATION NUMBER: US/10/989,826
;; CURRENT FILING DATE: 2004-11-16
;; PRIOR APPLICATION NUMBER: US 60/520,842
;; PRIOR FILING DATE: 2003-11-17
;; PRIOR APPLICATION NUMBER: US 60/532,426
;; PRIOR FILING DATE: 2003-12-24
;; NUMBER OF SEQ ID NOS: 75
;; SEQ ID NO 46
;; LENGTH: 184
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-989-826-46

US-10-989-826-46

Query Match 100.0%; Score 283; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLOMAGQCSQNEYPDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVGK 51
DB 1 MLOMAGQCSQNEYPDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVGK 51

RESULT 17

US-10-742-634-9
; Sequence 9, Application US/10742634
; Publication No. US20050249671A9
; GENERAL INFORMATION:
; APPLICANT: Parmelee, David
; APPLICANT: Yen, Ren-Hwa
; APPLICANT: Galperina, Olga
; APPLICANT: Hilbert, David
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Neutrokin-alpha Conjugate, Neutrokin-alpha Complex, and Uses Th
; FILE REFERENCE: 1488.1810002
; CURRENT APPLICATION NUMBER: US/10/742,634
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: US 60/435,262
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/467,198
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-742-634-9

Query Match 100.0%; Score 283; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLOMAGQCSQNEYPDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVGK 51
DB 1 MLOMAGQCSQNEYPDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVGK 51

RESULT 18

US-10-967-527A-8
; Sequence 8, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Znf14, A Tumor Necrosis Factor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-967-527A-8

Query Match 100.0%; Score 283; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLOMAGQCSQNEYPDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVGK 51
DB 1 MLOMAGQCSQNEYPDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVGK 51

RESULT 19

US-10-501-841-4
; Sequence 4, Application US/10501841
; Publication No. US20060084055A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordenez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; TITLE OF INVENTION: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis
; FILE REFERENCE: 014058-014402PC
; CURRENT APPLICATION NUMBER: US/10/501,841
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 10/057,475
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: WO PCT/US03/02353
; PRIOR FILING DATE: 2003-01-22
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-501-841-4

Query Match 100.0%; Score 283; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLOMAGQCSQNEYPDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVGK 51
DB 1 MLOMAGQCSQNEYPDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVGK 51

RESULT 20

US-11-021-874-27
; Sequence 27, Application US/11021874
; Publication No. US20050163775A1
; GENERAL INFORMATION:
; APPLICANT: Andrew Chan
; APPLICANT: Qian Gong
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
; FILE REFERENCE: P2040R1P1
; CURRENT APPLICATION NUMBER: US/11/021,874
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US 10/861,049
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 27
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-874-27

Query Match 100.0%; Score 283; DB 6; Length 184;

Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLOMAGCGSONEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTSVKG 51
DB 1 MLOMAGCGSONEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTSVKG 51

RESULT 21
US-11-242-294-27
; Sequence 27, Application US/11242294
; Publication No. US20060034852A1
; GENERAL INFORMATION:
; APPLICANT: Rixom, Mark W.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/11/242,294
; PRIOR FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US/10/152,363
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-242-294-27

Query Match 100.0%; Score 283; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLOMAGCGSONEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTSVKG 51
DB 1 MLOMAGCGSONEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTSVKG 51

RESULT 22
US-11-200-992-8
; Sequence 8, Application US/11200992
; Publication No. US20060067933A1
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madsen, Karen
; APPLICANT: Yee, David P.
; TITLE OF INVENTION: SOLUBLE RECEPTOR BR43X2 AND METHODS OF USING
; FILE REFERENCE: 0558.0034.CNUS01
; CURRENT APPLICATION NUMBER: US/11/200,992
; CURRENT FILING DATE: 2005-08-10
; PRIOR APPLICATION NUMBER: 60/115,068
; PRIOR FILING DATE: 1999-01-07
; PRIOR APPLICATION NUMBER: 60/169,890
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/479,856
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-200-992-8

Query Match 100.0%; Score 283; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLOMAGCGSONEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTSVKG 51

DB 1 MLOMAGCGSONEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTSVKG 51

RESULT 23
US-11-069-473-4
; Sequence 4, Application US/11069473
; Publication No. US20060073146A1
; GENERAL INFORMATION:
; APPLICANT: AVI J. ASHKENAZI
; APPLICANT: KELLY H. DODGE
; APPLICANT: IOBAL GREWAL
; APPLICANT: KYUNG JIN KIM
; APPLICANT: SCOT A. MARSTERS
; APPLICANT: ROBERT M. PITTI
; TITLE OF INVENTION: MINHONG YAN
; TITLE OF INVENTION: USES OF AGONISTS AND ANTAGONISTS TO MODULATE ACTIVITY
; FILE REFERENCE: P1805R1
; CURRENT APPLICATION NUMBER: US/11/069,473
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US/09/724,341
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/182,938
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: US 60/226,986
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 4
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-069-473-4

Query Match 100.0%; Score 283; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLOMAGCGSONEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTSVKG 51
DB 1 MLOMAGCGSONEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTSVKG 51

RESULT 24
US-10-115-192-12
; Sequence 12, Application US/10115192
; Publication No. US20030082175A1
; GENERAL INFORMATION:
; APPLICANT: Apotech R & D S.A.
; APPLICANT: Biogen, Inc.
; TITLE OF INVENTION: April Receptor (BCMA) and Uses thereof
; FILE REFERENCE: A083PCT
; CURRENT APPLICATION NUMBER: US/10/115,192
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 60/215688
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/181807
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/157933
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 302
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-115-192-12

Query Match 100.0%; Score 283; DB 4; Length 302;
Best Local Similarity 100.0%; Pred. No. 4.1e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLOMAGCGSONEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTSVKG 51

Db 24 MLAGCSONEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVG 74

RESULT 25
US-10-469-469-120

```
; Sequence 120, Application US/10469469
; Publication No. US20060079493A1
; GENERAL INFORMATION:
; APPLICANT: FRITZ, LAWRENCE C.
; APPLICANT: BURROWS, FRANCIS J.
; TITLE OF INVENTION: METHODS FOR TREATING GENETICALLY-DEFINED PROLIFERATIVE
; TITLE OF INVENTION: DISORDERS WITH HSP90 INHIBITORS
; FILE REFERENCE: CON-0010-USN
; CURRENT APPLICATION NUMBER: US/10/469,469
; CURRENT FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: PCT/US02/06518
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: 60/272,751
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 120
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-469-469-120
```

Query Match 96.8%; Score 274; DB 5; Length 288;
Best Local Similarity 98.0%; Pred. No. 4.5e-24;
Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 2 LMAQCSONEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVG 51
Db 106 LMAQCSONEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVG 155

```
RESULT 26
US-09-854-864-6
; Sequence 6, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-6
```

Query Match 95.1%; Score 269; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.2e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 MAGCSONEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVG 51
Db 1 MAGCSONEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVG 48

```
RESULT 27
US-09-855-158-6
; Sequence 6, Application US/09855158
; Publication No. US20020086018A1
```

```
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BLY
; TITLE OF INVENTION: 3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-6
```

Query Match 95.1%; Score 269; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.2e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 MAGCSONEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVG 51
Db 1 MAGCSONEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVG 48

```
RESULT 28
US-09-854-864-5
; Sequence 5, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-5
```

Query Match 95.1%; Score 269; DB 3; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.1e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 MAGCSONEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVG 51
Db 1 MAGCSONEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVG 48

```
RESULT 29
US-09-855-158-5
; Sequence 5, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BLY
; TITLE OF INVENTION: 3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
```

```
/ CURRENT FILING DATE: 2001-09-11
/ PRIOR APPLICATION NUMBER: US 60/214,591
/ PRIOR FILING DATE: 2000-06-27
/ PRIOR APPLICATION NUMBER: US 60/204,039
/ PRIOR FILING DATE: 2000-05-12
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 5
/ LENGTH: 181
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-09-855-158-5
```

```
Query Match          95.1%; Score 269; DB 3; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.1e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 MAGGCGNNEYPDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSYKG 51
DB 1 MAGGCGNNEYPDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSYKG 48
```

```
RESULT 30
US-09-854-864-9
/ Sequence 9, Application US/09854864
/ Patent No. US20020081296A1
/ GENERAL INFORMATION:
/ APPLICANT: THEILL, LARS EYDE
/ APPLICANT: YU, GANG
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
/ FILE REFERENCE: BLYS/AGP-3, AND TACI
/ CURRENT APPLICATION NUMBER: US/09/854,864
/ CURRENT FILING DATE: 2001-09-11
/ PRIOR APPLICATION NUMBER: US 60/204,039
/ PRIOR FILING DATE: 2000-05-12
/ PRIOR APPLICATION NUMBER: US 60/214,591
/ PRIOR FILING DATE: 2000-06-27
/ NUMBER OF SEQ ID NOS: 31
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 9
/ LENGTH: 283
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-09-854-864-9
```

```
Query Match          95.1%; Score 269; DB 3; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.7e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 MAGGCGNNEYPDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSYKG 51
DB 1 MAGGCGNNEYPDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSYKG 48
```

```
RESULT 31
US-09-855-158-9
/ Sequence 9, Application US/09855158
/ Publication No. US20020086018A1
/ GENERAL INFORMATION:
/ APPLICANT: THEILL, LARS EYDE
/ APPLICANT: YU, GANG
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BI
/ FILE REFERENCE: A-686A
/ CURRENT APPLICATION NUMBER: US/09/855,158
/ CURRENT FILING DATE: 2001-09-11
/ PRIOR APPLICATION NUMBER: US 60/214,591
/ PRIOR FILING DATE: 2000-06-27
/ PRIOR APPLICATION NUMBER: US 60/204,039
/ PRIOR FILING DATE: 2000-05-12
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: PatentIn version 3.1
```

```
/ SEQ ID NO 9
/ LENGTH: 283
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-09-855-158-9
```

```
Query Match          95.1%; Score 269; DB 3; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.7e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 MAGGCGNNEYPDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSYKG 51
DB 1 MAGGCGNNEYPDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSYKG 48
```

```
RESULT 32
US-10-077-438-3
/ Sequence 3, Application US/10077438
/ Publication No. US20020165156A1
/ GENERAL INFORMATION:
/ APPLICANT: Mackay, Fabienne
/ APPLICANT: Browning, Jeffrey
/ APPLICANT: Ambrose, Christine
/ APPLICANT: Tschopp, Jurg
/ APPLICANT: Schneider, Pascal
/ APPLICANT: Thompson, Jeffrey
/ APPLICANT: Biogen, Inc.
/ APPLICANT: Apotech R&D S.A.
/ TITLE OF INVENTION: Baff Receptor (BCMA), An
/ FILE REFERENCE: A080PCT
/ CURRENT APPLICATION NUMBER: US/10/077,438
/ CURRENT FILING DATE: 2002-02-18
/ PRIOR APPLICATION NUMBER: 60/149,378
/ PRIOR FILING DATE: 1999-08-17
/ PRIOR APPLICATION NUMBER: 60/181,684
/ PRIOR FILING DATE: 2000-02-11
/ PRIOR APPLICATION NUMBER: 60/183,536
/ PRIOR FILING DATE: 2000-02-18
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 207
/ TYPE: PRF
/ ORGANISM: homo sapien
US-10-077-438-3
```

```
Query Match          92.9%; Score 263; DB 4; Length 207;
Best Local Similarity 71.8%; Pred. No. 6.5e-23;
Matches 51; Conservative 0; Mismatches 0; Indels 20; Gaps 1;
```

```
QY 1 MLOMAGGCGNNEYPDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSYKG 40
DB 39 MLOMAGGCGNNEYPDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSYKG 98
```

```
QY 41 CNASVTNSYKG 51
DB 99 CNASVTNSYKG 109
```

```
RESULT 33
US-10-077-137-3
/ Sequence 3, Application US/10077137
/ Publication No. US20020172674A1
/ GENERAL INFORMATION:
/ APPLICANT: Mackay, Fabienne
/ APPLICANT: Browning, Jeffrey
/ APPLICANT: Ambrose, Christine
/ APPLICANT: Tschopp, Jurg
/ APPLICANT: Schneider, Pascal
/ APPLICANT: Thompson, Jeffrey
/ APPLICANT: Biogen, Inc.
/ APPLICANT: Apotech R&D S.A.
```

```

; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-3

Query Match          92.9%; Score 263; DB 4; Length 207;
Best Local Similarity 71.8%; Pred. No. 6.5e-23;
Matches 51; Conservative 0; Mismatches 0; Indels 20; Gaps 1;

OY 1 MOWAGGCSQNEYFDSL-----LHACIPQRCSSNTPPLTCORY 40
DB 39 MOWAGGCSQNEYFDSLHACIPQRCSSNTPPLTCORHACIPQRCSSNTPPLTCORY 98
OY 41 CNASVTNSVKG 51
DB 99 CNASVTNSVKG 109

RESULT 34
US-09-854-864-21
; Sequence 21, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-21

Query Match          88.0%; Score 249; DB 3; Length 58;
Best Local Similarity 100.0%; Pred. No. 8.2e-22;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 CSQNEYFDSLHACIPQRCSSNTPPLTCORYCNASVTNSVKG 51
DB 1 CSQNEYFDSLHACIPQRCSSNTPPLTCORYCNASVTNSVKG 44

RESULT 35
US-09-855-158-21
; Sequence 21, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
```

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; TITLE OF INVENTION: 3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-21

Query Match          88.0%; Score 249; DB 3; Length 58;
Best Local Similarity 100.0%; Pred. No. 8.2e-22;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 CSQNEYFDSLHACIPQRCSSNTPPLTCORYCNASVTNSVKG 51
DB 1 CSQNEYFDSLHACIPQRCSSNTPPLTCORYCNASVTNSVKG 44

RESULT 36
US-10-967-527A-9
; Sequence 9, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Hollaway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Znftr14, A Tumor Necrosis Factor
; TITLE OF INVENTION: Receptor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 40
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(40)
; OTHER INFORMATION: cysteine rich
US-10-967-527A-9

Query Match          81.3%; Score 230; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 9.9e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GQCSQNEYFDSLHACIPQRCSSNTPPLTCORYCNASV 45
DB 1 GQCSQNEYFDSLHACIPQRCSSNTPPLTCORYCNASV 40

RESULT 37
US-09-854-864-7
; Sequence 7, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
```


;; PRIOR APPLICATION NUMBER: US 60/204,039
;; PRIOR FILING DATE: 2000-05-12
;; PRIOR APPLICATION NUMBER: US 60/214,591
;; PRIOR FILING DATE: 2000-06-27
;; NUMBER OF SEQ ID NOS: 31
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 7
;; LENGTH: 34
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-854-864-7

Query Match 71.0%; Score 201; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 2,2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 41
Db 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34

RESULT 38
US-09-855-158-7
;; Sequence 7, Application US/09855158
;; Publication No. US20020086018A1
;; GENERAL INFORMATION:
;; APPLICANT: THEILL, LARS EYDE
;; APPLICANT: YU, GANG
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BLI
;; FILE REFERENCE: A-686A
;; CURRENT APPLICATION NUMBER: US/09/855,158
;; CURRENT FILING DATE: 2001-09-11
;; PRIOR APPLICATION NUMBER: US 60/214,591
;; PRIOR FILING DATE: 2000-06-27
;; PRIOR APPLICATION NUMBER: US 60/204,039
;; PRIOR FILING DATE: 2000-05-12
;; NUMBER OF SEQ ID NOS: 30
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 7
;; LENGTH: 34
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-855-158-7

Query Match 71.0%; Score 201; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 2,2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 41
Db 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34

RESULT 39
US-09-854-864-13
;; Sequence 13, Application US/09854864
;; Patent No. US20020081296A1
;; GENERAL INFORMATION:
;; APPLICANT: THEILL, LARS EYDE
;; APPLICANT: YU, GANG
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
;; FILE REFERENCE: A-686B
;; CURRENT APPLICATION NUMBER: US/09/854,864
;; CURRENT FILING DATE: 2001-09-11
;; PRIOR APPLICATION NUMBER: US 60/204,039
;; PRIOR FILING DATE: 2000-05-12
;; PRIOR APPLICATION NUMBER: US 60/214,591
;; PRIOR FILING DATE: 2000-06-27
;; NUMBER OF SEQ ID NOS: 31
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 13

;; LENGTH: 81
;; TYPE: PRT
;; ORGANISM: Consensus
US-09-854-864-13

Query Match 71.0%; Score 201; DB 3; Length 81;
Best Local Similarity 100.0%; Pred. No. 5,2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 41
Db 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34

RESULT 40
US-09-855-158-13
;; Sequence 13, Application US/09855158
;; Publication No. US20020086018A1
;; GENERAL INFORMATION:
;; APPLICANT: THEILL, LARS EYDE
;; APPLICANT: YU, GANG
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BLI
;; FILE REFERENCE: A-686A
;; CURRENT APPLICATION NUMBER: US/09/855,158
;; CURRENT FILING DATE: 2001-09-11
;; PRIOR APPLICATION NUMBER: US 60/214,591
;; PRIOR FILING DATE: 2000-06-27
;; PRIOR APPLICATION NUMBER: US 60/204,039
;; PRIOR FILING DATE: 2000-05-12
;; NUMBER OF SEQ ID NOS: 30
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 13
;; LENGTH: 81
;; TYPE: PRT
;; ORGANISM: Consensus
US-09-855-158-13

Query Match 71.0%; Score 201; DB 3; Length 81;
Best Local Similarity 100.0%; Pred. No. 5,2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 41
Db 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34

RESULT 41
US-09-854-864-11
;; Sequence 11, Application US/09854864
;; Patent No. US20020081296A1
;; GENERAL INFORMATION:
;; APPLICANT: THEILL, LARS EYDE
;; APPLICANT: YU, GANG
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
;; FILE REFERENCE: A-686B
;; CURRENT APPLICATION NUMBER: US/09/854,864
;; CURRENT FILING DATE: 2001-09-11
;; PRIOR APPLICATION NUMBER: US 60/204,039
;; PRIOR FILING DATE: 2000-05-12
;; PRIOR APPLICATION NUMBER: US 60/214,591
;; PRIOR FILING DATE: 2000-06-27
;; NUMBER OF SEQ ID NOS: 31
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 11
;; LENGTH: 185
;; TYPE: PRT
;; ORGANISM: Murine
US-09-854-864-11

Query Match 64.0%; Score 181; DB 3; Length 185;
Best Local Similarity 70.8%; Pred. No. 2,7e-13;

Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY 4 MAGCSONEYFDSLHACTIPCOLRCSSNTPPLTCORYCNASTYNSVG 51
DB 1 MAQCCHSEYFDSLHACKPCHLRCSN--PPATCQPCDPSTSVSSVG 46

RESULT 42

US-09-855-158-11
; Sequence 11, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Murine
US-09-855-158-11

Query Match 64.0%; Score 181; DB 3; Length 185;
Best Local Similarity 70.8%; Pred. No. 2.7e-13;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY 4 MAGCSONEYFDSLHACTIPCOLRCSSNTPPLTCORYCNASTYNSVG 51
DB 1 MAQCCHSEYFDSLHACKPCHLRCSN--PPATCQPCDPSTSVSSVG 46

RESULT 43

US-10-216-074-17
; Sequence 17, Application US/10216074
; Publication No. US20030148445A1
; GENERAL INFORMATION:
; APPLICANT: SHU, Hong-Bing
; TITLE OF INVENTION: TAIL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/10/216,074
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-216-074-17

Query Match 64.0%; Score 181; DB 4; Length 185;
Best Local Similarity 70.8%; Pred. No. 2.7e-13;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY 4 MAGCSONEYFDSLHACTIPCOLRCSSNTPPLTCORYCNASTYNSVG 51
DB 1 MAQCCHSEYFDSLHACKPCHLRCSN--PPATCQPCDPSTSVSSVG 46

RESULT 44

US-10-967-527A-10
; Sequence 10, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Zcnfr14, A Tumor Necrosis Factor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 185
; TYPE: PRT
; ORGANISM: mus musculus
US-10-967-527A-10

Query Match 64.0%; Score 181; DB 5; Length 185;
Best Local Similarity 70.8%; Pred. No. 2.7e-13;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY 4 MAGCSONEYFDSLHACTIPCOLRCSSNTPPLTCORYCNASTYNSVG 51
DB 1 MAQCCHSEYFDSLHACKPCHLRCSN--PPATCQPCDPSTSVSSVG 46

RESULT 45

US-09-854-864-10
; Sequence 10, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-854-864-10

Query Match 64.0%; Score 181; DB 3; Length 281;
Best Local Similarity 70.8%; Pred. No. 4e-13;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY 4 MAGCSONEYFDSLHACTIPCOLRCSSNTPPLTCORYCNASTYNSVG 51
DB 1 MAQCCHSEYFDSLHACKPCHLRCSN--PPATCQPCDPSTSVSSVG 46

RESULT 46

US-09-855-158-10
; Sequence 10, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG

```

; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-158-10

Query Match          64.0%; Score 181; DB 3; Length 281;
Best Local Similarity 70.8%; Pred. No. 4e-13;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY      4  MAGCCSONEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVGK 51
Db      1  MAQQCFHSEYFDSLHACKPCILRCSN--PPATCPCDPSVTNSVGK 46
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 47
US-10-145-206-197
; Sequence 197, Application US/10145206
; Publication No. US20030195156A1
; GENERAL INFORMATION:
; APPLICANT: MIN, HOSUNG
; APPLICANT: HSU, HAILING
; APPLICANT: ZIONG, FEI
; TITLE OF INVENTION: PEPTIDES AND RELATED MOLECULES THAT BIND TO TALL-1
; FILE REFERENCE: A-743
; CURRENT APPLICATION NUMBER: US/10/145,206
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,196
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 197
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Human
US-10-145-206-197

Query Match          55.8%; Score 158; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MLOMAGCCSONEYFDSLHACIPCOLRC 28
Db      15  MLOMAGCCSONEYFDSLHACIPCOLRC 42
      |||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 48
US-09-854-864-12
; Sequence 12, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
```

```

; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: human-murine Consensus
US-09-854-864-12

Query Match          36.7%; Score 104; DB 3; Length 117;
Best Local Similarity 69.8%; Pred. No. 0.0002;
Matches 30; Conservative 1; Mismatches 2; Indels 10; Gaps 6;

QY      9  SONEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVGK 51
Db      2  ACEYFDSLHAC-PC-LRCS----PPTCQ-YC--SVT-SVGK 34
      :|:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 49
US-09-855-158-12
; Sequence 12, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: human-murine Consensus
US-09-855-158-12

Query Match          36.7%; Score 104; DB 3; Length 117;
Best Local Similarity 69.8%; Pred. No. 0.0002;
Matches 30; Conservative 1; Mismatches 2; Indels 10; Gaps 6;

QY      9  SONEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVGK 51
Db      2  ACEYFDSLHAC-PC-LRCS----PPTCQ-YC--SVT-SVGK 34
      :|:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 50
US-10-087-192-1647
; Sequence 1647, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1647
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-087-192-1647
```

| | | | | |
|--------------------------|--------|----------------|-----------|-------------|
| Query Match | 25.3% | Score 71.5; | DB 4; | Length 249; |
| Best Local Similarity | 35.3%; | Pred. No. 2.9; | | |
| Matches 12; Conservative | 8; | Mismatches 13; | Indels 1; | Gaps 1; |

Dy 8 CSQNEYFBDLLHACIPQLRCSNTPLPTCQRVC 41
 |:::| | | | : |
Db 6 CEKDQYWBSSRKSCVSCALTCGRS-QRCTDFC 38

RESULT 51

```

US-10-967-527A-21
Sequence 21, Application US/10967527A
Publication No. US20050256041A1
GENERAL INFORMATION:
APPLICANT: Fox, Brian A.
APPLICANT: Holloway, James L.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: znfnf14, A Tumor Necro
TITLE OF INVENTION: Receptor
FILE REFERENCE: 03-17
CURRENT APPLICATION NUMBER: US/10/967,527A
CURRENT FILING DATE: 2004-10-18
PRIOR APPLICATION NUMBER: 60/511,698
PRIOR FILING DATE: 2003-10-16
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 249
TYPE: PRF
ORGANISM: mus musculus
US-10-967-527A-21

```

| | | | | |
|-----------------------|-----------------|----------------|-----------|-------------|
| Query Match | 25.3% | Score 71.5; | DB 5; | Length 249; |
| Best Local Similarity | 35.3%; | Pred. No. 2.9; | | |
| Matches 12; | Conservative 8; | Mismatches 13; | Indels 1; | Gaps 1 |

```

Qy      8 CSONEYPFDLLHACIPQQLRCSNTPTLTQRYC 41
      |:::|:::|:::|:::|:::|:::|:::|
Db      6 CPKDQYWDSSRKSKVSCALTCSPRS-QRTCTDFC 38

```

RESULT 52

```

US-11-200-992-20
? Sequence 20, Application US/11/200992
? Publication NO. US20060067933A1
? GENERAL INFORMATION:
? APPLICANT: Gross, Jane A.
? APPLICANT: Xu, Wenfeng
? APPLICANT: Madden, Karen
? APPLICANT: Yee, David P.
? TITLE OF INVENTION: SOLUBLE RECEPTOR BR43X2 AND METHODS OF USING
? FILE REFERENCE: 05558, 0034, CNU501
? CURRENT APPLICATION NUMBER: US/11/200, 992
? PRIORITY FILING DATE: 2005-08-10
? PRIOR APPLICATION NUMBER: 60/115,068
? PRIOR FILING DATE: 1999-01-07
? PRIOR APPLICATION NUMBER: 60/169,890
? PRIOR FILING DATE: 1999-12-09
? PRIOR APPLICATION NUMBER: 09/479,856
? PRIOR FILING DATE: 2000-01-07
? NUMBER OF SEQ ID NOS: 60
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 20
? LENGTH: 249
? TYPE: PRT
? ORGANISM: Mus musculus
? US-11-200-992-20

```

| | | | | |
|-----------------------|--------------|----------------|----------------|-------------|
| Query Match | 25.3% | Score 71.5; | DB 6; | Length 249; |
| Best Local Similarity | 35.3%; | Pred. No. 2.9; | | |
| Matches 12; | Conservative | 8; | Mismatches 13; | Indels 1; |
| | | | Gaps | 1 |

```

QY      8 CSQNEYFSLHACIPQRLRCSNTPPLTCQRYC 41
        |:::|::|::|::|::|
Db      6 CEKDQYMSRSRKSCTVSCALTCQGRS-QRCCTDFC 38

```

RESULT 53
US-10-180-903-2
; Sequence 2, Application US/10180503
; Publication No. US20030093824A1
; GENERAL INFORMATION:

Qy 7 QCSQNEYFDSLHACIPCCQLRCSNTTP-----LTCQRICNASVTNSVK 50
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1151 ECAAVEYWDGSHRCQPCHKKCSRSGSPSEDQCYTCPREFLLNTTCVK 1199

```

RESULT 54
US-10-028-248A-75
; Sequence 75, Application US/10028248A
; Publication No. US20030235882A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard
; APPLICANT: Patturajan, Meera
; APPLICANT: Vernet, Corine
; APPLICANT: Casman, Stacie
; APPLICANT: Malyankar, Uriel
; APPLICANT: Shenoy, Suresh
; APPLICANT: Spytek, Kimberly
; APPLICANT: Gangoli, Esha
; APPLICANT: Miller, Charles
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Smithson, Glenda
; APPLICANT: Zernusen, Bryan
; APPLICANT: Liu, Xiaohong
; APPLICANT: Colman, Steven
; APPLICANT: Tchernev, Veilzar
; APPLICANT: Si, Jingsheng
; APPLICANT: Edinger, Shlomlt
; APPLICANT: Stone, David
; APPLICANT: Sciore, Paul
; APPLICANT: Miller, Isabelle
; APPLICANT: Rothenberg, Mark
; TITLE OF INVENTION: No. US20030235882A1 Nuclieic Acids and Polypeptides and Methods c
; FILE REFERENCE: 21402-222
; CURRENT FILING DATE: 2001-12-19
; CURRENT APPLICATION NUMBER: US/10/028,248A
; PRIOR APPLICATION NUMBER: 60/256619
; PRIOR FILING DATE: 2000-12-19

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; PRIOR APPLICATION NUMBER: 60/262959
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/272408
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/285189
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/308039
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 60/311266
; PRIOR FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: Patencin Ver. 2.1
; SEQ ID NO 75
; LENGTH: 5374
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-028-248A-75

Query Match      24.6%; Score 69.5; DB 4; Length 5374;
Best Local Similarity 36.8%; Pred. No. 1e+02;
Matches 14; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

QY      7  OCSONEYPDSLHACIP-CQLRCSSNTP--PLTCORYC 41
Db      3297  QCPYNSQFTDCLPSCVSCSNRCVTSFSPVSSCREGC 3334

RESULT 55
US-10-107-782-75
; Sequence 75, Application US/10107782
; Publication No. US20040018970A1
; GENERAL INFORMATION:
; APPLICANT: Boldog, Ferenc,
; APPLICANT: Casman, Stacie
; APPLICANT: Coleman, Steve,
; APPLICANT: Edinger, Shlomlt,
; APPLICANT: Gangolli, Esha,
; APPLICANT: Kekuda, Ramesh,
; APPLICANT: Li, Li,
; APPLICANT: Liu, Xiaohong,
; APPLICANT: Malpankar, Uriel,
; APPLICANT: Miller, Charles,
; APPLICANT: Millet, Isabelle,
; APPLICANT: Patuaraajan, Meera,
; APPLICANT: Rothenberg, Mark,
; APPLICANT: Scioe, Paul,
; APPLICANT: Shenoy, Suresh,
; APPLICANT: Shinkets, Richard,
; APPLICANT: Si, Jingsheng,
; APPLICANT: Smithson, Glenda,
; APPLICANT: Spytek, Kimberly,
; APPLICANT: Stone, David,
; APPLICANT: Taupier, Raymond, Jr.,
; APPLICANT: Tchernev, Vellizar,
; APPLICANT: Vernet, Corine,
; APPLICANT: Zernusen, Brian
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: 21402-222CIP
; CURRENT APPLICATION NUMBER: US/10/107,782
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 10/028,248
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256,619
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/262,959
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/272,408
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/285,189
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/308,039
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 60/311,266
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; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/279,344
; PRIOR FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: Curaseqelist version 0.1
; SEQ ID NO 75
; LENGTH: 5374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-107-782-75

Query Match      24.6%; Score 69.5; DB 4; Length 5374;
Best Local Similarity 36.8%; Pred. No. 1e+02;
Matches 14; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

QY      7  OCSONEYPDSLHACIP-CQLRCSSNTP--PLTCORYC 41
Db      3297  QCPYNSQFTDCLPSCVSCSNRCVTSFSPVSSCREGC 3334

RESULT 56
US-10-028-248A-74
; Sequence 74, Application US/10028248A
; Publication No. US20030235882A1
; GENERAL INFORMATION:
; APPLICANT: Shinkets, Richard
; APPLICANT: Patuaraajan, Meera
; APPLICANT: Vernet, Corine
; APPLICANT: Casman, Stacie
; APPLICANT: Malpankar, Uriel
; APPLICANT: Shenoy, Suresh
; APPLICANT: Spytek, Kimberly
; APPLICANT: Gangolli, Esha
; APPLICANT: Miller, Charles
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Smithson, Glenda
; APPLICANT: Zernusen, Bryan
; APPLICANT: Liu, Xiaohong
; APPLICANT: Coleman, Steven
; APPLICANT: Tchernev, Vellizar
; APPLICANT: Si, Jingsheng
; APPLICANT: Edinger, Shlomlt
; APPLICANT: Scioe, Paul
; APPLICANT: Shinkets, Richard
; APPLICANT: Rothenberg, Mark
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: 21402-222
; CURRENT APPLICATION NUMBER: US/10/028,248A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256619
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/262959
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/272408
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/285189
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/308039
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 60/311266
; PRIOR FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: Patencin Ver. 2.1
; SEQ ID NO 74
; LENGTH: 5376
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-028-248A-74
```

Query Match 24.6%; Score 69.5; DB 4; Length 5376;
Best Local Similarity 36.8%; Pred. No. 1e+02;
Matches 14; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

QY 7 QCSONEYFDSLHACIP-CQLRCSSNTP--PLTCORYC 41
DB 3299 QCPTNSQFTDCLPSCVPSCSNRCEVTSFVPSSCREGC 3336

RESULT 57

US-10-107-782-74
; Sequence 74, Application US/10107782
; Publication No. US20040018970A1
; GENERAL INFORMATION:
; APPLICANT: Boldog, Ferenc,
; APPLICANT: Casman, Stacie,
; APPLICANT: Coleman, Steve,
; APPLICANT: Edinger, Shlomo,
; APPLICANT: Gangoli, Esha,
; APPLICANT: Kekuda, Ramesh,
; APPLICANT: Li, Li,
; APPLICANT: Liu, Xiaohong,
; APPLICANT: Malyankar, Uriel,
; APPLICANT: Miller, Charles,
; APPLICANT: Millet, Isabelle,
; APPLICANT: Patwardhan, Meera,
; APPLICANT: Rothenberg, Mark,
; APPLICANT: Sciore, Paul,
; APPLICANT: Shenoy, Suresh,
; APPLICANT: Shimkets, Richard,
; APPLICANT: Si, Jingsheng,
; APPLICANT: Smithson, Glenda,
; APPLICANT: Spytek, Kimberly,
; APPLICANT: Stone, David,
; APPLICANT: Taupier, Raymond, Jr.,
; APPLICANT: Tchernev, Velizar,
; APPLICANT: Vernet, Corine,
; APPLICANT: Zettersen, Brian
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: 21402-222CIP
; CURRENT APPLICATION NUMBER: US/10/107,782
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 10/028,248
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256,619
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/262,959
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/272,408
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/285,189
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/308,039
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 60/311,266
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/279,344
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: Cuiaseqdist version 0.1
; SEQ ID NO 74
; LENGTH: 5376
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-107-782-74

Query Match 24.6%; Score 69.5; DB 4; Length 5376;
Best Local Similarity 36.8%; Pred. No. 1e+02;
Matches 14; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

QY 7 QCSONEYFDSLHACIP-CQLRCSSNTP--PLTCORYC 41

DB 3299 QCPTNSQFTDCLPSCVPSCSNRCEVTSFVPSSCREGC 3336

RESULT 58
US-10-152-363A-62
; Sequence 62, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.,
; APPLICANT: Gross, Jane A.,
; TITLE OF INVENTION: TACT-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 62
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein.
US-10-152-363A-62

Query Match 24.2%; Score 68.5; DB 4; Length 332;
Best Local Similarity 27.9%; Pred. No. 8.6;
Matches 12; Conservative 10; Mismatches 20; Indels 1; Gaps 1;

QY 1 MLQWAGCSQNEYPDSLHACIPQQLRCSSNTPPLTCORYCNA 43
DB 17 VLAMRSCPEQYWDPLIGTCMCKTICNHOS-QRTCAAFERS 58

RESULT 59
US-11-242-294-62
; Sequence 62, Application US/11242294
; Publication No. US20060034852A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.,
; APPLICANT: Gross, Jane A.,
; TITLE OF INVENTION: TACT-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/11/242,294
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US/10/152,363
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 62
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein.
US-11-242-294-62

Query Match 24.2%; Score 68.5; DB 6; Length 332;
Best Local Similarity 27.9%; Pred. No. 8.6;
Matches 12; Conservative 10; Mismatches 20; Indels 1; Gaps 1;

QY 1 MLQWAGCSQNEYPDSLHACIPQQLRCSSNTPPLTCORYCNA 43
DB 17 VLAMRSCPEQYWDPLIGTCMCKTICNHOS-QRTCAAFERS 58

RESULT 60
US-09-779-050A-45
; Sequence 45, Application US/09779050A
; Patent No. US20020160416A1

```
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-779-050A-45

Query Match      23.9%; Score 67.5; DB 3; Length 37;
Best Local Similarity 30.6%; Pred. No. 1.3;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY      8 CSONEYFDSLHACIPQOLRCSSNTPPLTCORYCNA 43
DB      2 CPEEQYWDPLGTGCMSCKTICNHQS-QRTCAAFCRS 36

RESULT 61
US-10-967-527A-20
; Sequence 20, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Znftrf4, A Tumor Necrosis Factor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 48
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(48)
; OTHER INFORMATION: cysteine rich
; US-10-967-527A-20

Query Match      23.9%; Score 67.5; DB 5; Length 48;
Best Local Similarity 30.6%; Pred. No. 1.7;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY      8 CSONEYFDSLHACIPQOLRCSSNTPPLTCORYCNA 43
DB      13 CPEEQYWDPLGTGCMSCKTICNHQS-QRTCAAFCRS 47

RESULT 62
US-09-854-864-20
; Sequence 20, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; PRIOR APPLICATION NUMBER: US/09/854,864
; CURRENT APPLICATION NUMBER: US/09/854,864
```

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; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-854-864-20

Query Match      23.9%; Score 67.5; DB 3; Length 59;
Best Local Similarity 30.6%; Pred. No. 2;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY      8 CSONEYFDSLHACIPQOLRCSSNTPPLTCORYCNA 43
DB      1 CPEEQYWDPLGTGCMSCKTICNHQS-QRTCAAFCRS 35

RESULT 63
US-09-855-158-20
; Sequence 20, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-855-158-20

Query Match      23.9%; Score 67.5; DB 3; Length 59;
Best Local Similarity 30.6%; Pred. No. 2;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY      8 CSONEYFDSLHACIPQOLRCSSNTPPLTCORYCNA 43
DB      1 CPEEQYWDPLGTGCMSCKTICNHQS-QRTCAAFCRS 35

RESULT 64
US-09-854-864-15
; Sequence 15, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
```


Best Local Similarity 30.6%; Pred. No. 5.9;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 8 CSONEYFDSLHACIPCOLRCSSNTPLTCQRCYCN 43
DB 6 CPEEQYWDPLGTGCMCKTTCNHQS-QRTCAAFCRS 40

RESULT 69

US-11-200-992-9
; Sequence 9, Application US/11200992
; Publication No. US20060067933A1
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen
; APPLICANT: Yee, David P.
; TITLE OF INVENTION: SOLUBLE RECEPTOR BR43X2 AND METHODS OF USING
; FILE REFERENCE: 05558.0034.CNDS01
; CURRENT APPLICATION NUMBER: US/11/200,992
; CURRENT FILING DATE: 2005-08-10
; PRIOR APPLICATION NUMBER: 60/115,068
; PRIOR FILING DATE: 1999-01-07
; PRIOR APPLICATION NUMBER: 60/169,890
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/479,856
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-200-992-9

Query Match 23.9%; Score 67.5; DB 6; Length 245;
Best Local Similarity 30.6%; Pred. No. 8.4;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 8 CSONEYFDSLHACIPCOLRCSSNTPLTCQRCYCN 43
DB 30 CPEEQYWDPLGTGCMCKTTCNHQS-QRTCAAFCRS 64

RESULT 70

US-10-626-914-17
; Sequence 17, Application US/10626914
; Publication No. US20050043516A1
; GENERAL INFORMATION:
; Patin Docket Preview
; APPLICANT: CHUNTHARAPAI, ANAN
; APPLICANT: GREWAL, IOBAL
; APPLICANT: KIM, KYUNG JIN
; APPLICANT: YAN, MINHONG
; TITLE OF INVENTION: TACT Anticodifies and Uses Thereof
; FILE REFERENCE: P1942R1
; CURRENT APPLICATION NUMBER: US/10/626,914
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 60/398,530
; PRIOR FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 17
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-626-914-17

Query Match 23.9%; Score 67.5; DB 5; Length 265;
Best Local Similarity 30.6%; Pred. No. 9.1;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 8 CSONEYFDSLHACIPCOLRCSSNTPLTCQRCYCN 43

DB 34 CPEEQYWDPLGTGCMCKTTCNHQS-QRTCAAFCRS 68

RESULT 71

US-10-485-489-19
; Sequence 19, Application US/10485489
; Publication No. US20050070689A1
; GENERAL INFORMATION:
; APPLICANT: Dixit, Vishva
; APPLICANT: Grewal, Iobal
; APPLICANT: Ridgway, John
; APPLICANT: Yan, Minhong
; TITLE OF INVENTION: TACTs and BR3 Polypeptides and Uses Thereof
; FILE REFERENCE: 11669.175USWO
; CURRENT APPLICATION NUMBER: US/10/485,489
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: PCT/US02/23487
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US 60/310,114
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/377,171
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 19
; SEQ ID NO 19
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-489-19

Query Match 23.9%; Score 67.5; DB 5; Length 265;
Best Local Similarity 30.6%; Pred. No. 9.1;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 8 CSONEYFDSLHACIPCOLRCSSNTPLTCQRCYCN 43
DB 34 CPEEQYWDPLGTGCMCKTTCNHQS-QRTCAAFCRS 68

RESULT 72

US-10-861-049-36
; Sequence 36, Application US/10861049
; Publication No. US20050095243A1
; GENERAL INFORMATION:
; APPLICANT: Andrew Chan
; APPLICANT: Qian Gong
; APPLICANT: Flavius Martin
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
; FILE REFERENCE: P2040R1US
; CURRENT APPLICATION NUMBER: US/10/861,049
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 36
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-861-049-36

Query Match 23.9%; Score 67.5; DB 5; Length 265;
Best Local Similarity 30.6%; Pred. No. 9.1;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 8 CSONEYFDSLHACIPCOLRCSSNTPLTCQRCYCN 43
DB 34 CPEEQYWDPLGTGCMCKTTCNHQS-QRTCAAFCRS 68

RESULT 73


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; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/26,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/016,812
; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 22
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-879-919-22

Query Match      23.9%; Score 67.5; DB 3; Length 293;
Best Local Similarity 30.6%; Pred. No. 10;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY      8 CSONEYFDSLHACIPCOLRCSNTPTLCORYCNA 43
DB      34 CPEEQYWDPLGTGCMCKTICNHQS-QRTCAAFCRS 68

RESULT 78
US-09-854-864-14
; Sequence 14, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentln version 3.1
; SEQ ID NO 14
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-854-864-14

Query Match      23.9%; Score 67.5; DB 3; Length 293;
Best Local Similarity 30.6%; Pred. No. 10;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY      8 CSONEYFDSLHACIPCOLRCSNTPTLCORYCNA 43
DB      34 CPEEQYWDPLGTGCMCKTICNHQS-QRTCAAFCRS 68

RESULT 79
US-09-855-158-14
; Sequence 14, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
```

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; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentln version 3.1
; SEQ ID NO 14
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-855-158-14

Query Match      23.9%; Score 67.5; DB 3; Length 293;
Best Local Similarity 30.6%; Pred. No. 10;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY      8 CSONEYFDSLHACIPCOLRCSNTPTLCORYCNA 43
DB      34 CPEEQYWDPLGTGCMCKTICNHQS-QRTCAAFCRS 68

RESULT 80
US-09-961-376-2
; Sequence 2, Application US/09961376
; Patent No. US20020106736A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR17
; FILE REFERENCE: PF524P1
; CURRENT APPLICATION NUMBER: US/09/961,376
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/254,874
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/235,991
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/533,822
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/188,208
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-961-376-2

Query Match      23.9%; Score 67.5; DB 3; Length 293;
Best Local Similarity 30.6%; Pred. No. 10;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY      8 CSONEYFDSLHACIPCOLRCSNTPTLCORYCNA 43
DB      34 CPEEQYWDPLGTGCMCKTICNHQS-QRTCAAFCRS 68

RESULT 81
US-09-779-050A-42
; Sequence 42, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOTLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
```

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; PRIOR FILING DATE:2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-42

```

| | | | | | | | |
|-----------------------|-------|--------------|------|------------|----|--------|-----|
| Query Match | 23.9% | Score | 67.5 | DB | 3 | Length | 293 |
| Best Local Similarity | 30.6% | Pred. | No. | 10 | | | |
| Matches | 11 | Conservative | 9 | Mismatches | 15 | Indels | 1 |
| | | | | | | Gaps | 1 |

```

QY      8 CSONEYFDLSLHACIPQQLRCSSTNPPLTCORYCNA 43
        | : : | | | : : | : : | : : | : :
Db     34 CPBEQYWDPLIGTCWCKTICNHQS-QRTCAAFCRS 68

```

RESULT 82
US-09-302-863-2

```

; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G
; APPLICANT: Ding, Wawan S

```

```

; FILE REFERENCE: 2519
; CURRENT APPLICATION NUMBER: US/09/302,863
; CURRENT FILING DATE: 1999-04-30

```

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; SOFTWARE: PatentIn Ver. 2.0
; SEO ID NO 2
; LENGTH: 293

```

ORGANISM: Human
US-09-302-863-2

| | | | | |
|--------------------------|-------|---------------|-------|-------------------|
| Query Match | 23.9% | Score 67.5; | DB 3; | Length 293; |
| Best Local Similarity | 30.6% | Pred. No. 10; | | |
| Matches 11; Conservative | | 9; Mismatches | 15; | Indels 1; Gaps 1; |

QY 8 CSONEYFDSLILHACIPQLRCSSTNPPLTCORYCNA 433
| : : | | | : : : : : : : : :
Db 34 CPBEQYWDPDLIGTMCSCSKTICNHOS-QRTCAAFCRS 68

RESULT 83
US-09-855-564-2

/ ; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G

FILE REFERENCE: 2519
CURRENT APPLICATION NUMBER: US/09/855,564
CURRENT FILING DATE: 09/08/05

PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 5
SEQUENCE: Data not available

LENGTH: 293
TYPE: PRT
ORGANISM: HUMANS

| | | | | |
|-----------------------|-------|--------------|-------|-------------|
| Query Match | 23.9% | Score 67.5; | DB 3; | Length 293; |
| Post-Topic Classifier | 30.6% | Prod No. 10; | | |

QY 8 CSQNEYFDSLHACIPQQLRCSNTPPLTCQRYCNA 43

Db 34 CPBEEQWDPPLGTCSCKTICNHQS-QRTCAAFCRS 68

RESULT 84
US-10-087-192-1650
SECURITY 1650

```

; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K

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```

; TITLE OF INVENTION:  CANCER
;
; FILE REFERENCE:  529452000122
;
; CURRENT APPLICATION NUMBER:  US/10/087,192

```

;; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586

```

; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1650

```

ORGANISM: Homo sapiens
US-10-087-192-1650

| | | | | |
|-----------------------|--------------|--------------|------------|------------|
| Query March | 23.9% | Score 67.5 | DB 4 | Length 293 |
| Best Local Similarity | 30.6% | Pred. NO. 10 | | |
| Matches 11 | Conservative | 9 | Mismatches | 15 |
| | | | Indels | 1 |
| | | | Gaps | 1 |

```
Qy      8 CSQNEYFDSLIIHACIPQRLCSSNTPLTCORYCNA 43
      34 CPBEQYMDPLLGTCMSCKTIQNHQS-QRTCAFCRS 68
Db
```

RESULT 85
US-10-084-971-2

GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
PROJECT OR INVENTION OR DEVELOPMENT: [REDACTED] and Methods and Apparatus

CURRENT APPLICATION NUMBER: US/10/084,971
CURRENT FILING DATE: 2002-03-01
PRIORITY INFORMATION ATTACHED: NO
PUBLICATION NUMBER: WO/00/623,822

PRIOR APPLICATION NUMBER: 60/126,599
 PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-26
 PRIOR APPLICATION NUMBER: 60/488,308

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; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1

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; TYPE: PRT
; ORGANISM: Homo sapiens
ITS-10-084-971-2

```

| | | | | |
|--------------------------|-------|---------------|-------|-------------|
| Query Match | 23.9% | Score 67.5; | DB 4; | Length 293; |
| Best Local Similarity | 30.6% | Pred. No. 10; | | |
| Matches 11: Conservative | 9: | Mismatches | 15: | Indels |
| | | | 1: | Gaps |

| | | | |
|----|----|---------------------------------------|----|
| QY | 8 | CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNA | 43 |
| | | : : : : : : : : : : | |
| Db | 34 | CPPEQYWDPIIGTCMSSCKTICNHQS-ORTCAAFCRS | 68 |

RESULT 86
US-10-068-725-4

US-10-066-123-4
; Sequence 4, Application US/10068725
; Publication No. US20030012783A1

```

; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne
; TITLE OF INVENTION: Antibodies That Bind Both BCMA and TRACI
; FILE REFERENCE: 01-04
; CURRENT APPLICATION NUMBER: US/10/068,725
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/270,274
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/283,447
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-725-4

Query Match      23.9%; Score 67.5; DB 4; Length 293;
Best Local Similarity 30.6%; Pred. No. 10;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF54
; CURRENT APPLICATION NUMBER: US/10/151,882
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-882-46

RESULT 87
US-10-151-882-46
; Sequence 46, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF54
; CURRENT APPLICATION NUMBER: US/10/151,882
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-882-46

Query Match      23.9%; Score 67.5; DB 4; Length 293;
Best Local Similarity 30.6%; Pred. No. 10;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; FILE REFERENCE: 44158/254623
; CURRENT APPLICATION NUMBER: US/10/293,816
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 09/782,857
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/290,333
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US 08/810,572
US-10-293-816-2

RESULT 88
US-10-293-816-2
; Sequence 2, Application US/10293816
; Publication No. US20030082173A1
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; FILE REFERENCE: 44158/254623
; CURRENT APPLICATION NUMBER: US/10/293,816
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 09/782,857
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/290,333
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US 08/810,572
US-10-293-816-2
```

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; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-816-2

Query Match      23.9%; Score 67.5; DB 4; Length 293;
Best Local Similarity 30.6%; Pred. No. 10;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenteng
; APPLICANT: Henne, Randal M.
; APPLICANT: Grant, Francis, J.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
; FILE REFERENCE: 00-103
; CURRENT APPLICATION NUMBER: US/10/008,063
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-008-063-8

RESULT 89
US-10-008-063-8
; Sequence 8, Application US/10008063
; Publication No. US20030092164A1
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenteng
; APPLICANT: Henne, Randal M.
; APPLICANT: Grant, Francis, J.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
; FILE REFERENCE: 00-103
; CURRENT APPLICATION NUMBER: US/10/008,063
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-008-063-8

Query Match      23.9%; Score 67.5; DB 4; Length 293;
Best Local Similarity 30.6%; Pred. No. 10;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

; GENERAL INFORMATION:
; APPLICANT: Rixson, Mark W.
; APPLICANT: Grose, Jane A.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-152-363A-2

RESULT 90
US-10-152-363A-2
; Sequence 2, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixson, Mark W.
; APPLICANT: Grose, Jane A.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-152-363A-2

Query Match      23.9%; Score 67.5; DB 4; Length 293;
Best Local Similarity 30.6%; Pred. No. 10;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
```

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QY      8 CSQNEYFDSLHACIPQLRCSSTNPPLTCQRYCMA 43
      | : : | | | : : : | : : | :
Db     34 CPEDGYMDPLLGTCMCKTICNHQS-QRTCAFCRS 68

```

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RESULT 91
US-10-268-951--22
Sequence 22, Application US/10268951
Publication No. US20030166864A1
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang, et al.
TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
FILE REFERENCE: PF253P2
CURRENT FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: US/10/268,951
PRIOR FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: 10/082,260
PRIOR FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/879,919
PRIOR FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 08/815,783
PRIOR FILING DATE: 1997-03-12
PRIOR APPLICATION NUMBER: 60/328,401
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/293,812
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,978
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/254,875
PRIOR FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: 60/241,952
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/211,537
PRIOR FILING DATE: 2000-06-15
Remaining Prior Application data removed - See File Wrapper or PALM
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
LENGTH: 293
TYPE: PRT
ORGANISM: Homo sapiens
US-10-268-951--22

```

| | | | | |
|--------------------------|-------|---------------|------------|------------|
| Query Match | 23.9% | Score 67.5 | DB 4 | Length 293 |
| Best Local Similarity | 30.6% | Pred. No. 10 | | |
| Matches 11; Conservative | | 9; Mismatches | 15; Indels | 1; Gaps |

```

RESULT 92
US-10-258-368-1
: Sequence 1, Application US/10258368
: Publication No. US20040013674A1
: GENERAL INFORMATION:
: APPLICANT: Ambrose, Christine
: APPLICANT: Thompson, Jeffrey
: APPLICANT: Schneider, Pascal
: APPLICANT: Rennett, Paul
: TITLE OF INVENTION: Taci As As Anti-Tumor Agent
: FILE REFERENCE: BIOG0130 NP of PCR/US01/406266
: CURRENT APPLICATION NUMBER: US/10/258,368
: PRIORITY FILING DATE: 2003-10-21
: PRIOR APPLICATION NUMBER: USSN 60/129,946
: PRIORITY FILING DATE: 2000-04-27
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 1
: LENGTH: 293
: TYPE: PRT
/
/
/

```

ORGANISM: Homo sapiens
US-10-258-368-1

| | | | | |
|--------------------------|--------|----------------|-----------|-------------|
| Query Match | 23.9% | Score 67.5; | DB 4; | Length 293; |
| Best Local Similarity | 30.6%; | Pred. No. 10; | | |
| Matches 11; Conservative | 9; | Mismatches 15; | Indels 1; | Gaps 1; |

```

QY      8 CSQNEYFDLSLHACIPQQLRCSSTNPPLTCQRYCNA 43
      | : : | | : : | : | : | :
DB      34 CPEEQYWDPLLTGTCMSCKTICNHQS-QRTCAAFCRS 68

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RESULT 93
US-10-618-797-4
; Sequence 4, Application US/10618797
; Publication No. US20040048296A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Ruben, Steven M
; TITLE OF INVENTION: Human Tumor Necrosis Factor TR20 and Methods Based Thereon
; FILE REFERENCE: PR527D1
; CURRENT APPLICATION NUMBER: US/10/618,797
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 09/848, 295
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/202,193
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 293
; TYPE: prt
; ORGANISM: human
US-10-618-797-4

```

| | | | | |
|--------------------------|-------|-------------------|-----------|-------------|
| Query Match | 23.9% | Score 67.5; | DB 4; | Length 293; |
| Best Local Similarity | 30.6% | Pred. No. 10; | | |
| Matches 11; Conservative | | 9; Mismatches 15; | Indels 1; | Gaps 1; |

```

QY      8 CSQNEYFDSLHACIPQQLRCSSTNPPLTCQRCA 43
Db      34 CPREQYWDPLLTGTCMCKTINC HQS-QRTCAAFCRS 68

```

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RESULT 94
US-10-742-634-7
; Sequence 7, Application US/10742634
; Publication No. US20040208824A1
; GENERAL INFORMATION:
; APPLICANT: Parmelee, David
; APPLICANT: Yeh, Ren-Hwa
; APPLICANT: Galperina, Olga
; APPLICANT: Hilbert, David
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Neutrokin-alpha Conjugate, and Uses Thereof
; FILE REFERENCE: 1468 1810002
; CURRENT APPLICATION NUMBER: US/10/742,634
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: US 60/435,262
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/467,198
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-742-634-7

```

| | | | | |
|--------------------------|-------|----------------|-----------|-------------|
| Query Match | 23.9% | Score 67.5; | DB 4; | Length 293; |
| Best Local Similarity | 30.6% | Pred. No. 10; | | |
| Matches 11; Conservative | 9; | Mismatches 15; | Indels 1; | Gaps 1; |

```

Oy      8  CSONEFFDLSILHACIPCOLRCSSNTPPLTCORYNCA 43
      | : | | | | | | | | | | | | | | | | | | | |
Db      34 CPEQOYNDPILGTCSMCKTICNHOS-QRTCAAFCS 68

RESULT 95
US-10-748-112-27
; Sequence 27, Application US/10748112
; Publication No. US20040208874A1
; GENERAL INFORMATION:
; APPLICANT: Khare, Sanjay D.
; TITLE OF INVENTION: COMBINATION THERAPY WITH CO-STIMULATORY FACTORS
; FILE REFERENCE: 06843, 0052-0000
; CURRENT APPLICATION NUMBER: US/10/748, 112
; CURRENT FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: US 60/437,405
; PRIOR FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-748-112-27

```

```

Query Match          23.9%; Score 67.5; DB 4; Length 293;
Best Local Similarity 30.6%; Pred.No.10;
Matches    11; Conservative     9; Mismatches   15; Indels      1; Gaps       1.;

OY           8 CSONEYPDSLHACIPCOLRCSSNTPPLTCORYCNA 43
| : | : || | : | : | : | : | : | : 
Db            34 CPBEOYPDLLGTGCMSCKKTICNHOS-QRTCAAFCKRS 68


RESULT_96
US-10-684-149-4
; Sequence 4, Application US/10684149
; Publication No. US20050009149A1
; GENERAL INFORMATION:
; APPLICANT: West, James W.
; APPLICANT: Brandt, Cameron S.
; TITLE OF INVENTION: Production of Homotrimeric Fusion
; FILE REFERENCE: 02-17
; CURRENT APPLICATION NUMBER: US/10/684,149
; PRIORITY FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/417,801
; PRIORITY FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 293
; TYPE: PRF
; ORGANISM: Human
US-10-684-149-4

Query Match          23.9%; Score 67.5; DB 5; Length 293;
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; Publication No. US20050043516A1
; GENERAL INFORMATION:
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 ; APPLICANT: GREVAL, IOBAL
 ; APPLICANT: KIM, KYONG JIN
 ; APPLICANT: YAN, MINHONG
 ; TITLE OF INVENTION: TACI Antibodies and Uses Thereof
 ; FILE REFERENCE: P1942R1
 ; CURRENT APPLICATION NUMBER: US/10/626,914
 ; CURRENT FILING DATE: 2003-07-25
 ; PRIOR APPLICATION NUMBER: US 60/398,530
 ; PRIOR FILING DATE: 2002-07-25
 ; NUMBER OF SEQ ID NOS: 17
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 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; US-10-626-914-3

[illegible]

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:41:39 ; Search time 27 Seconds
(without alignments)
165.336 Million cell updates/sec

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 segs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
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SUMMARIES

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| 893 | 47 | 16.6 | 224 | 2 | US-08-974-022-50 | Sequence 50, Appl1 | 966 | 47 | 16.6 | 642 | 2 | US-09-949-016-6048 | Sequence 6048, Ap |
| 894 | 47 | 16.6 | 224 | 2 | US-08-795-445A-50 | Sequence 50, Appl1 | 967 | 47 | 16.6 | 729 | 2 | US-09-919-497-51 | Sequence 51, Appl1 |
| 895 | 47 | 16.6 | 224 | 2 | US-08-795-447A-50 | Sequence 50, Appl1 | 968 | 47 | 16.6 | 733 | 2 | US-09-252-991A-23192 | Sequence 23192, A |
| 896 | 47 | 16.6 | 224 | 2 | US-08-974-186-50 | Sequence 50, Appl1 | 969 | 47 | 16.6 | 756 | 2 | US-09-699-266A-13 | Sequence 13, Appl1 |
| 897 | 47 | 16.6 | 224 | 2 | US-08-795-446B-50 | Sequence 50, Appl1 | 970 | 47 | 16.6 | 857 | 1 | US-08-659-251-2 | Sequence 2, Appl1 |
| 898 | 47 | 16.6 | 224 | 2 | US-08-706-945D-137 | Sequence 137, App | 971 | 47 | 16.6 | 857 | 1 | US-09-256-490-2 | Sequence 2, Appl1 |
| 899 | 47 | 16.6 | 224 | 2 | US-08-577-788C-51 | Sequence 51, Appl1 | 972 | 47 | 16.6 | 857 | 5 | PCT-US96-11445-2 | Sequence 2, Appl1 |
| 900 | 47 | 16.6 | 224 | 3 | US-09-613-591F-134 | Sequence 134, App | 973 | 47 | 16.6 | 861 | 2 | US-09-949-016-10418 | Sequence 10418, A |
| 901 | 47 | 16.6 | 237 | 2 | US-09-270-767-44305 | Sequence 44305, A | 974 | 47 | 16.6 | | | | |
| 902 | 47 | 16.6 | 237 | 2 | | | 975 | 47 | 16.6 | | | | |

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976 47 16.6 879 2 US-09-872-733A-16 Sequence 16, Appl
977 47 16.6 1015 2 US-08-537-210A-1 Sequence 1, Appl
978 47 16.6 1015 2 US-09-113-825-1 Sequence 1, Appl
979 47 16.6 1042 2 US-09-959-392-2 Sequence 2, Appl
980 47 16.6 1194 2 US-09-171-553B-5 Sequence 5, Appl
981 47 16.6 1455 2 US-08-726-012B-2 Sequence 2, Appl
982 47 16.6 1693 2 US-09-560-385A-4 Sequence 4, Appl
983 47 16.6 1693 2 US-09-560-385A-8 Sequence 8, Appl
984 47 16.6 1713 2 US-08-600-982-24 Sequence 24, Appl
985 47 16.6 1713 2 US-09-560-385A-6 Sequence 6, Appl
986 47 16.6 1713 2 US-09-538-092-1359 Sequence 1359, Ap
987 47 16.6 1713 5 PCT-US94-10261A-24 Sequence 24, Appl
988 47 16.6 1724 2 US-09-560-385A-2 Sequence 2, Appl
989 47 16.6 1924 3 US-09-866-557A-2 Sequence 2, Appl
990 47 16.6 2471 1 US-08-185-432-16 Sequence 16, Appl
991 47 16.6 2471 1 US-08-083-590A-19 Sequence 19, Appl
992 47 16.6 2471 2 US-08-532-384-19 Sequence 19, Appl
993 47 16.6 2471 2 US-08-899-232-1 Sequence 1, Appl
994 47 16.6 2471 2 US-09-121-457-1 Sequence 1, Appl
995 46.5 16.4 49 2 US-09-230-637-60 Sequence 60, Appl
996 46.5 16.4 68 2 US-09-910-009A-249 Sequence 249, App
997 46.5 16.4 69 1 US-08-358-160-125 Sequence 125, App
998 46.5 16.4 75 1 US-08-465-380-6 Sequence 6, Appl
999 46.5 16.4 75 1 US-08-465-380-41 Sequence 41, Appl
1000 46.5 16.4 75 1 US-08-480-478-35 Sequence 35, Appl
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ALIGNMENTS

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RESULT 1
US-09-565-423-11
; Sequence 11, Application US/09565423
; Patent No. 6475987
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; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TAL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565,423
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-565-423-11
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Query Match 100.0%; Score 283; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 4.4e-26;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 MLOMAGQCSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVGK 51
Db 1 MLOMAGQCSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVGK 51

RESULT 2
US-09-949-016-11115
; Sequence 1115, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
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; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1115
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11115
```

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Query Match 100.0%; Score 283; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 4.6e-26;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 MLOMAGQCSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVGK 51
Db 9 MLOMAGQCSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVGK 59
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RESULT 3
US-09-854-864-6
; Sequence 6, Application US/09854864
; Patent No. 6774106
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; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-6
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Query Match 95.1%; Score 269; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 5.2e-25;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 4 MAGQCSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVGK 51
Db 1 MAGQCSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVGK 48
```

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RESULT 4
US-09-854-864-5
; Sequence 5, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
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SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 181
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-864-5

Query Match
Best Local Similarity 100.0%; Score 269; DB 2; Length 181;
Pred. No. 2e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCORXCNAVSNTSVYKG 51
DB 1 MAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCORXCNAVSNTSVYKG 48

RESULT 5
US-09-854-864-9
Sequence 9, Application US/09854864
Patent No. 6774106
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
PRIOR FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-864-9

Query Match
Best Local Similarity 100.0%; Score 269; DB 2; Length 283;
Pred. No. 3.2e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCORXCNAVSNTSVYKG 51
DB 1 MAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCORXCNAVSNTSVYKG 48

RESULT 6
US-09-854-864-21
Sequence 21, Application US/09854864
Patent No. 6774106
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
PRIOR FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
SEQ ID NO 21
LENGTH: 58
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-864-21

Query Match
Best Local Similarity 100.0%; Score 249; DB 2; Length 58;
Pred. No. 1.4e-22;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCORXCNAVSNTSVYKG 51
DB 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCORXCNAVSNTSVYKG 44

RESULT 7
US-09-854-864-7
Sequence 7, Application US/09854864
Patent No. 6774106
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
PRIOR FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
LENGTH: 34
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-864-7

Query Match
Best Local Similarity 100.0%; Score 201; DB 2; Length 34;
Pred. No. 4e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCORXC 41
DB 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCORXC 34

RESULT 8
US-09-854-864-13
Sequence 13, Application US/09854864
Patent No. 6774106
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
PRIOR FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
SEQ ID NO 13
LENGTH: 81
TYPE: PRT
ORGANISM: Consensus
US-09-854-864-13

Query Match
Best Local Similarity 100.0%; Score 201; DB 2; Length 81;
Pred. No. 1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCORXC 41
DB 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCORXC 34

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RESULT 9
US-09-565-423-17
; Sequence 17, Application US/09565423
; Patent No. 6475987
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565,423
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-565-423-17

Query Match      64.0%; Score 181; DB 2; Length 185;
Best Local Similarity 70.8%; Pred. No. 5.7e-14;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY      4 MAGCSQNEYFDSLHACIPQCRGSSNTPPLTCQRYCNASVTNSYKG 51
Db      1 MAQCFHSEYFDSLHACKPCHLRCSN--PPATCQPCDPSTVTSYKG 46

RESULT 10
US-09-854-864-11
; Sequence 11, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACT
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Murine
US-09-854-864-11

Query Match      64.0%; Score 181; DB 2; Length 185;
Best Local Similarity 70.8%; Pred. No. 5.7e-14;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY      4 MAGCSQNEYFDSLHACIPQCRGSSNTPPLTCQRYCNASVTNSYKG 51
Db      1 MAQCFHSEYFDSLHACKPCHLRCSN--PPATCQPCDPSTVTSYKG 46

RESULT 11
US-09-854-864-10
; Sequence 10, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
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; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACT
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-854-864-10

Query Match      64.0%; Score 181; DB 2; Length 281;
Best Local Similarity 70.8%; Pred. No. 9e-14;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY      4 MAGCSQNEYFDSLHACIPQCRGSSNTPPLTCQRYCNASVTNSYKG 51
Db      1 MAQCFHSEYFDSLHACKPCHLRCSN--PPATCQPCDPSTVTSYKG 46

RESULT 12
US-09-854-864-12
; Sequence 12, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACT
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: human-murine Consensus
US-09-854-864-12

Query Match      36.7%; Score 104; DB 2; Length 117;
Best Local Similarity 69.8%; Pred. No. 4.9e-05;
Matches 30; Conservative 1; Mismatches 2; Indels 10; Gaps 6;

QY      9 SONEYFDSLHACIPQCRGSSNTPPLTCQRYCNASVTNSYKG 51
Db      2 AQCEYFDSLHAC-PC-LRCS----PPTCQ-YC--SVT-SYKG 34

RESULT 13
US-09-854-864-20
; Sequence 20, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACT
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
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PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
SEQ ID NO 20
LENGTH: 59
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-864-20

Query Match 23.9%; Score 67.5; DB 2; Length 59;
Best Local Similarity 30.6%; Pred. No. 1.5;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 8 CSONEYFDSLHACIPCOLRCSNTPLTCORCYNA 43
DB 1 CPEEQYWDPLGTGCMSCKTICNHQS-QRTCAFCRS 35

RESULT 14

US-08-810-572A-6
Sequence 6, Application US/08810572A
Patent No. 5969102
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,572A
FILING DATE: 28-FEB-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-810-572A-6

Query Match 23.9%; Score 67.5; DB 1; Length 166;
Best Local Similarity 30.6%; Pred. No. 1.5;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 8 CSONEYFDSLHACIPCOLRCSNTPLTCORCYNA 43

DB 34 CPEEQYWDPLGTGCMSCKTICNHQS-QRTCAFCRS 68

RESULT 15

US-09-290-333-6
Sequence 6, Application US/09290333
Patent No. 6316222
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/290,333
FILING DATE: 12-Apr-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-290-333-6

Query Match 23.9%; Score 67.5; DB 2; Length 166;
Best Local Similarity 30.6%; Pred. No. 1.5;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 8 CSONEYFDSLHACIPCOLRCSNTPLTCORCYNA 43
DB 34 CPEEQYWDPLGTGCMSCKTICNHQS-QRTCAFCRS 68

RESULT 16

US-09-782-857A-6
Sequence 6, Application US/09782857A
Patent No. 6500428
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
NUMBER OF SEQUENCES: 10

```

CORRESPONDENCE ADDRESS:
ADDRESSER: David A. Jackson, Esq.,
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/782,857A
FILING DATE: 14-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/810,572
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-782-857A-6

Query Match      23.9%; Score 67.5; DB 2; Length 166;
Best Local Similarity 30.6%; Pred. No. 1.5;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

Qy      8 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYCNA 43
Db      34 CPBEOYMDPLGTGCMSCKTICNHQS-QRTCAAFCRS 68

RESULT 17
US-09-854-864-15
Sequence 15, Application US/09854864
Patent No. 6774106
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/570, BCMA,
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
SEQ ID NO 15
LENGTH: 166
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-864-15
```

```

Query Match      23.9%; Score 67.5; DB 2; Length 166;
Best Local Similarity 30.6%; Pred. No. 1.5;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

Qy      8 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYCNA 43
Db      34 CPBEOYMDPLGTGCMSCKTICNHQS-QRTCAAFCRS 68

RESULT 18
US-08-810-572A-2
Sequence 2, Application US/08810572A
Patent No. 5969102
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
APPLICANT: von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: David A. Jackson, Esq.,
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,572A
FILING DATE: 28-FEB-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-810-572A-2

Query Match      23.9%; Score 67.5; DB 1; Length 293;
Best Local Similarity 30.6%; Pred. No. 2.8;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

Qy      8 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYCNA 43
Db      34 CPBEOYMDPLGTGCMSCKTICNHQS-QRTCAAFCRS 68

RESULT 19
US-09-290-333-2
Sequence 2, Application US/09290333
Patent No. 6316222
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
US-09-290-333-2
```

von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/290,333
FILING DATE: 12-Apr-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-290-333-2
Query Match 23.9%; Score 67.5; DB 2; Length 293;
Best Local Similarity 30.6%; Pred. No. 2.8;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
QY 8 CSONEYFDSLHACIPQRCSSNTPPLTCORYCNA 43
DB 34 CPBEQYWDPLGTGCMCKTICNHQS-QRTCAAFCRS 68
RESULT 20
US-09-782-857A-2
Sequence 2, Application US/09782857A
Patent No. 6500428
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/782,857A
FILING DATE: 14-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/810,572
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-782-857A-2
Query Match 23.9%; Score 67.5; DB 2; Length 293;
Best Local Similarity 30.6%; Pred. No. 2.8;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
QY 8 CSONEYFDSLHACIPQRCSSNTPPLTCORYCNA 43
DB 34 CPBEQYWDPLGTGCMCKTICNHQS-QRTCAAFCRS 68
RESULT 21
US-09-879-919-22
Sequence 22, Application US/09879919
Patent No. 6541224
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang, et al.
TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
FILE REFERENCE: PF253P1
CURRENT APPLICATION NUMBER: US/09/879,919
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,978
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/254,875
PRIOR FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: 60/241,952
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/211,537
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 08/815,783
PRIOR FILING DATE: 1997-03-12
PRIOR APPLICATION NUMBER: 60/016,812
PRIOR FILING DATE: 1996-03-14
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 22
LENGTH: 293
TYPE: PRT
ORGANISM: Homo sapiens
US-09-879-919-22

| | | | | |
|-----------------------|-----------------|----------------|-----------|-------------|
| Query Match | 23.9% | Score 67.5; | DB 2; | Length 293; |
| Best Local Similarity | 30.6% | Pred. No. 2.8; | | |
| Matches 11; | Conservative 9; | Mismatches 15; | Indels 1; | Gaps 1; |

```
QY      8 CSQNEYFDLSLHACIPQLRCSSTNPPLTCQRYCNA 43
      | : : : | | : : : : : : : : : :
Db     34 CPBEDYWDPLIGTSCMCKTICNHQS-QRTCAFCRS 68
```

```

RESULT 22
US-09-848-295-4
; Sequence 4, Application US/09848295
; Patent No. 6623941
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Tumor Necrosis Factor TR20 and Methods Based
; TITLE OF INVENTION: Theron
; FILE REFERENCE: P5527
; CURRENT APPLICATION NUMBER: US/09/848,295
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/202,193
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-848-295-4

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| | | | | |
|-----------------------|-----------------|----------------|-----------|-------------|
| Query Match | 23.9% | Score 67.5; | DB 2; | Length 293; |
| Best Local Similarity | 30.6%; | Pred. No. 2.8; | | |
| Matches 11; | Conservative 9; | Mismatches 15; | Indels 1; | Gaps 1. |

QY 8 CSQNEYFDSLHACIPQLRCSNTPLTTCORYCNA 43
| : : | | | : : : : : | : :
Db 34 CPBEOYWDPLIGTCMSCKTICNHOS-ORTCAAFCRS 68

RESULT 23
US-09-854-864-14
Sequence 14, Application US/09854864
Patent No. 6774106
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGF-3, AND TACI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 293
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-864-14

| | | | | |
|--------------------------|--------|----------------|-----------|-------------|
| Query Match | 23.9% | Score 67.5; | DB 2; | Length 293; |
| Best Local Similarity | 30.6%; | Pred. No. 2.8; | | |
| Matches 11; Conservative | 9; | Mismatches 15; | Indels 1; | Gaps 1 |

```

QY      8 CSQNEYFDSLHACIPQLRGCSNTPPLTQRYCNA 433
      | : : | | | | : : : : | : : :
Db      34 CPREQYWDPLLTGTCMSCKTICNHQS-ORTCAFCRS 688

```

RESULT 24
US-09-961-376-2
: Sequence 2, Application US/09961376

ORGANISM: Homo sapiens
US-09-961-376-2

| | | | | | | | |
|-----------------------|-------|--------------|------|------------|----|--------|-----|
| Query Match | 23.9% | Score | 67.5 | DB | 2 | Length | 293 |
| Best Local Similarity | 30.6% | Pred. No. | 2.8 | | | | |
| Matches | 11 | Conservative | 9 | Mismatches | 15 | Indels | 1 |
| | | | | | | Gaps | 1 |

```

09      CSQNEFSDSLHACIPCOLRCSNTPLTCORCYNA 43
Db      :|:|:| |:|:| |:|:|
          34 CPEQYMDPLGTCTWSCXTTICNHOS-ORTCAFCRS 68

RESULT 25
US-09-854-864-18
; Sequence 18, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLVS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 18
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-18
```

| | | | | |
|--------------------------|-------|---------------|----------|------------|
| Query Match | 23.9% | Score 67.5 | DB 2 | Length 397 |
| Best Local Similarity | 30.6% | Pred. No. 3.9 | | |
| Matches 11; Conservative | 9 | Mismatches 15 | Indels 1 | Gaps 1 |

QY 8 CSQNEYFDLSLHACIPQRLRCSNTPLTQRYCNA 433
| : : | | | : : : | : : | : :
Db 34 CPREQYWDPLIGTMSCKTICNHQS -ORTCAFCRS 688

RESULT 26
US-09-854-864-16
; Sequence 16, Application US/09854864
; Patent No. 6774106

```
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLXS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-854-864-16

Query Match      23.5%; Score 66.5; DB 2; Length 67;
Best Local Similarity 32.4%; Pred. No. 0.77;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy      8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 41
Db      1 CPEEQYWDPLGTGCMCKRTICNHQS-QRTCAFC 33

RESULT 27
US-10-104-047-2804
; Sequence 2804, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. 6943241el full length CDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2804
; LENGTH: 581
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-104-047-2804

Query Match      22.8%; Score 64.5; DB 2; Length 581;
Best Local Similarity 30.8%; Pred. No. 13;
Matches 12; Conservative 5; Mismatches 9; Indels 13; Gaps 1;

Qy      7 QCSQNEYFDSLHACIPCOL-----RCSNT 32
Db      336 QCSPGHYNTSIHRCIRCAMGSYQDPDFRONFCRCPGNT 374

RESULT 28
US-10-104-047-2834
; Sequence 2834, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length CDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2834
```

```
; LENGTH: 880
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-104-047-2834

Query Match      22.8%; Score 64.5; DB 2; Length 880;
Best Local Similarity 30.8%; Pred. No. 20;
Matches 12; Conservative 5; Mismatches 9; Indels 13; Gaps 1;

Qy      7 QCSQNEYFDSLHACIPCOL-----RCSNT 32
Db      635 QCSPGHYNTSIHRCIRCAMGSYQDPDFRONFCRCPGNT 673

RESULT 29
US-09-949-016-9626
; Sequence 9626, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9626
; LENGTH: 1106
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-9626

Query Match      22.3%; Score 63; DB 2; Length 1106;
Best Local Similarity 32.6%; Pred. No. 39;
Matches 14; Conservative 6; Mismatches 21; Indels 2; Gaps 1;

Qy      7 QCSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNAVYNSV 49
Db      898 KCSPEYWDDEADPGCKPCHVXCFHCWCPAEDQ--CQTCMNSL 938

RESULT 30
US-09-950-933A-82
; Sequence 82, Application US/09950933A
; Patent No. 6875907
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro, Pedro
; TITLE OF INVENTION: Antimicrobial Peptides and Methods of
; TITLE OF INVENTION: Use
; FILE REFERENCE: 35718/238472
; CURRENT APPLICATION NUMBER: US/09/950,933A
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/232,569
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-09-950-933A-82

Query Match      21.7%; Score 61.5; DB 2; Length 99;
Best Local Similarity 35.6%; Pred. No. 4.6;
Matches 16; Conservative 7; Mismatches 17; Indels 5; Gaps 2;
```



```
/ Patent No. 6638907
/ GENERAL INFORMATION:
/ APPLICANT: Kortessmaa, Jarkko
/ APPLICANT: Tryggvason, Karl
/ TITLE OF INVENTION: Laminin 8 and Methods for Its Use
/ FILE REFERENCE: 99, 274-D
/ CURRENT APPLICATION NUMBER: US/09/561,818A
/ CURRENT FILING DATE: 2000-04-28
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 4
/ LENGTH: 1792
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-09-561-818A-4

Query Match      20.5%; Score 58; DB 2; Length 1792;
Best Local Similarity 21.0%; Pred. No. 2.6e+02;
Matches 13; Conservative 13; Mismatches 20; Indels 16; Gaps 2;

QY      5 ACQCSNNEYFDSLHACIPQ-----LRCSNTPPLTCQRYCNASTNSV 49
DB      40 AEKCNAG-FFHTLSGECVPCDCNGNSNECLDSSGYCVHCQRRTTGBHCKCLDGYIGDSI 98
QY      50 KG 51
DB      99 RG 100

RESULT 36
US-09-561-818A-8
/ Sequence 8, Application US/09561818A
/ Patent No. 6638907
/ GENERAL INFORMATION:
/ APPLICANT: Kortessmaa, Jarkko
/ APPLICANT: Tryggvason, Karl
/ TITLE OF INVENTION: Laminin 8 and Methods for Its Use
/ FILE REFERENCE: 99, 274-D
/ CURRENT APPLICATION NUMBER: US/09/561,818A
/ CURRENT FILING DATE: 2000-04-28
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 8
/ LENGTH: 1800
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-09-561-818A-8

Query Match      20.5%; Score 58; DB 2; Length 1800;
Best Local Similarity 21.0%; Pred. No. 2.6e+02;
Matches 13; Conservative 13; Mismatches 20; Indels 16; Gaps 2;

QY      5 ACQCSNNEYFDSLHACIPQ-----LRCSNTPPLTCQRYCNASTNSV 49
DB      40 AEKCNAG-FFHTLSGECVPCDCNGNSNECLDSSGYCVHCQRRTTGBHCKCLDGYIGDSI 98
QY      50 KG 51
DB      99 RG 100

RESULT 37
US-09-561-818A-2
/ Sequence 2, Application US/09561818A
/ Patent No. 6638907
/ GENERAL INFORMATION:
/ APPLICANT: Kortessmaa, Jarkko
/ APPLICANT: Tryggvason, Karl
/ TITLE OF INVENTION: Laminin 8 and Methods for Its Use
/ FILE REFERENCE: 99, 274-D
/ CURRENT APPLICATION NUMBER: US/09/561,818A
/ CURRENT FILING DATE: 2000-04-28
/ NUMBER OF SEQ ID NOS: 28
```

```
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 2
/ LENGTH: 1816
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-09-561-818A-2

Query Match      20.5%; Score 58; DB 2; Length 1816;
Best Local Similarity 21.0%; Pred. No. 2.6e+02;
Matches 13; Conservative 13; Mismatches 20; Indels 16; Gaps 2;

QY      5 ACQCSNNEYFDSLHACIPQ-----LRCSNTPPLTCQRYCNASTNSV 49
DB      64 AEKCNAG-FFHTLSGECVPCDCNGNSNECLDSSGYCVHCQRRTTGBHCKCLDGYIGDSI 122
QY      50 KG 51
DB      123 RG 124

RESULT 38
US-09-561-818A-6
/ Sequence 6, Application US/09561818A
/ Patent No. 6638907
/ GENERAL INFORMATION:
/ APPLICANT: Kortessmaa, Jarkko
/ APPLICANT: Tryggvason, Karl
/ TITLE OF INVENTION: Laminin 8 and Methods for Its Use
/ FILE REFERENCE: 99, 274-D
/ CURRENT APPLICATION NUMBER: US/09/561,818A
/ CURRENT FILING DATE: 2000-04-28
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 6
/ LENGTH: 1824
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-09-561-818A-6

Query Match      20.5%; Score 58; DB 2; Length 1824;
Best Local Similarity 21.0%; Pred. No. 2.6e+02;
Matches 13; Conservative 13; Mismatches 20; Indels 16; Gaps 2;

QY      5 ACQCSNNEYFDSLHACIPQ-----LRCSNTPPLTCQRYCNASTNSV 49
DB      64 AEKCNAG-FFHTLSGECVPCDCNGNSNECLDSSGYCVHCQRRTTGBHCKCLDGYIGDSI 122
QY      50 KG 51
DB      123 RG 124

RESULT 39
US-09-848-295-2
/ Sequence 2, Application US/09848295
/ Patent No. 6623941
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Steven M.
/ APPLICANT: Ruben, Steven M.
/ TITLE OF INVENTION: Human Tumor Necrosis Factor TR20 and Methods Based
/ FILE REFERENCE: PF527
/ CURRENT APPLICATION NUMBER: US/09/848,295
/ CURRENT FILING DATE: 2001-05-04
/ PRIOR APPLICATION NUMBER: 60/202,193
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 142
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-09-848-295-2
```

```
Query Match      20.3%; Score 57.5; DB 2; Length 142;
Best Local Similarity 32.4%; Pred. No. 20;
Matches 12; Conservative 8; Mismatches 12; Indels 5; Gaps 1;

QY      8 CSQNEYFDSLHAC-IPCOLRCSNTPLTCORYCNAS 44
DB      4 CPEEQYMAALLGTCMECKKACIKNHQS-----QRTCAAS 35

RESULT 40
US-09-270-767-31650
; Sequence 31650, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31650
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-31650

Query Match      20.1%; Score 57; DB 2; Length 201;
Best Local Similarity 31.1%; Pred. No. 33;
Matches 14; Conservative 4; Mismatches 13; Indels 14; Gaps 3;

QY      7 QCSQNEYFDSLHAC-IPCOLRCSNTPLTCORYCN 42
DB      33 KCOENSSSF-----ACPKNKCSLECSGYQMDNSNGCPTCCRYCN 72

RESULT 41
US-09-270-767-46867
; Sequence 46867, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46867
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-46867

Query Match      20.1%; Score 57; DB 2; Length 201;
Best Local Similarity 31.1%; Pred. No. 33;
Matches 14; Conservative 4; Mismatches 13; Indels 14; Gaps 3;

QY      7 QCSQNEYFDSLHAC-IPCOLRCSNTPLTCORYCN 42
DB      33 KCOENSSSF-----ACPKNKCSLECSGYQMDNSNGCPTCCRYCN 72

RESULT 42
US-09-589-892B-11
; Sequence 11, Application US/09589892B
; Patent No. 6689583
; GENERAL INFORMATION:
; APPLICANT: Jenuwein, Thomas
; APPLICANT: Laidle, Gotz
; APPLICANT: O'Carroll, Donald
; APPLICANT: Eisenhaber, Frank
```

```
; APPLICANT: Rea, Stephen
; TITLE OF INVENTION: Chromatin-Regulator Genes
; FILE REFERENCE: 0652.1670001
; CURRENT APPLICATION NUMBER: US/09/589,892B
; CURRENT FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: US 08/945,988
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: PCT/EP96/01818
; PRIOR FILING DATE: 1996-05-02
; PRIOR APPLICATION NUMBER: DE 195 16 776.7
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 760
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-589-892B-11

Query Match      20.1%; Score 57; DB 2; Length 760;
Best Local Similarity 26.7%; Pred. No. 1.4e+02;
Matches 12; Conservative 8; Mismatches 23; Indels 2; Gaps 1;

QY      2 LQMAQCSQNEYFDSL--HACIPCOLRCSNTPLTCORYCNAS 44
DB      521 IQLKDDSSNHVYNYTRCDHPGHPDMMNCSCIQTONFCEKFCNCS 565

RESULT 43
US-10-094-749-2573
; Sequence 2573, Application US/10094749
; Patent No. 6979557
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 08435/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2573
; LENGTH: 824
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-2573

Query Match      20.1%; Score 57; DB 2; Length 824;
Best Local Similarity 36.8%; Pred. No. 1.5e+02;
Matches 14; Conservative 6; Mismatches 16; Indels 2; Gaps 1;

QY      8 CSQNEYFDSLHACIPCOLRCSNTPLTCORYCNASV 45
```

Db 393 CGKSAVAVSLRECV--KLPSDPVPLMAKVCIGSL 428

RESULT 44

US-08-276-967-2

Sequence 2, Application US/08276967

Patent No. 5851817

GENERAL INFORMATION:

APPLICANT: Hardy, Daniel M.

APPLICANT: Garbers, David L.

TITLE OF INVENTION: Species-Specific Egg-Binding Proteins of

TITLE OF INVENTION: Sperm

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P. O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/276,967

FILING DATE: Submitted Heterwith

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Kitchell, Barbara S.

REGISTRATION NUMBER: 33,928

REFERENCE/DOCKET NUMBER: UTSD:418\KIT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 713-787-1400

TELEFAX: 713-789-2679

TELEX: 79-0924

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 2476 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-276-967-2

Query Match 19.8%; Score 56; DB 1; Length 2476;

Best Local Similarity 31.6%; Pred. No. 6.3e+02;

Matches 12; Conservative 8; Mismatches 14; Indels 4; Gaps 2;

QY 8 CSQNEVFDLSLHACIP-CO---LRCSNTPPLTCORXC 41

Db 1851 CSNHSVYTCVPSCLPSCODPEGCTGAGAFSTCEBGC 1888

RESULT 45

US-10-037-417-6

Sequence 6, Application US/10037417

Patent No. 6903201

GENERAL INFORMATION:

APPLICANT: Kekuda, Ramesh

APPLICANT: Alsobrook II, John P

APPLICANT: Tchernev, Velizar T

APPLICANT: Liu, Xiaohong

APPLICANT: Spytek, Kimberly A

APPLICANT: Raturajan, Meera

APPLICANT: Grose, William M

APPLICANT: Lepley, Denise M

APPLICANT: Burgess, Catherine E

APPLICANT: Vernet, Corine A.M.

APPLICANT: Li, Li

APPLICANT: Gorman, Linda

APPLICANT: Edinger, Shlomit R

APPLICANT: Sciore, Paul

APPLICANT: Ellerman, Karen

APPLICANT: Malyskar, Uriel M

APPLICANT: Rothenberg, Mark

APPLICANT: Stone, David J

APPLICANT: Boldog, Ferenc L

APPLICANT: Guo, Xiaojia

APPLICANT: Shenoy, Suresh G

APPLICANT: Anderson, David W

APPLICANT: Padigaru, Muralidhara

APPLICANT: Taupier Jr, Raymond J

APPLICANT: Miller, Charles E

APPLICANT: Eissen, Andrew J

TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

FILE REFERENCE: 21402-235

CURRENT APPLICATION NUMBER: US/10/037,417

CURRENT FILING DATE: 2002-09-20

PRIOR APPLICATION NUMBER: 60/260,018

PRIOR FILING DATE: 2001-01-05

PRIOR APPLICATION NUMBER: 60/260,360

PRIOR FILING DATE: 2001-01-08

PRIOR APPLICATION NUMBER: 60/272,411

PRIOR FILING DATE: 2001-02-28

PRIOR APPLICATION NUMBER: 60/272,817

PRIOR FILING DATE: 2001-03-02

PRIOR APPLICATION NUMBER: 60/291,186

PRIOR FILING DATE: 2001-05-15

PRIOR APPLICATION NUMBER: 60/303,231

PRIOR FILING DATE: 2001-07-05

PRIOR APPLICATION NUMBER: 60/305,060

PRIOR FILING DATE: 2001-07-12

PRIOR APPLICATION NUMBER: 60/318,405

PRIOR FILING DATE: 2001-09-10

PRIOR APPLICATION NUMBER: 60/318,700

PRIOR FILING DATE: 2001-09-12

NUMBER OF SEQ ID NOS: 227

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 6

LENGTH: 3597

TYPE: PRT

ORGANISM: Homo sapiens

US-10-037-417-6

Query Match 19.8%; Score 56; DB 2; Length 3597;

Best Local Similarity 27.1%; Pred. No. 9.3e+02;

Matches 16; Conservative 5; Mismatches 20; Indels 18; Gaps 3;

QY 7 QCSQNEVFD--SLHACIPCOLR-----CSSNTPPLTCORXCNASTVNS 48

Db 1825 ECAPGFYRDVKGILFGRGVPCOCHGSHDRCLPSSGVCCOHTGNAHCER--COAGFVSS 1882

RESULT 46

US-10-037-417-2

Sequence 2, Application US/10037417

Patent No. 6903201

GENERAL INFORMATION:

APPLICANT: Kekuda, Ramesh

APPLICANT: Alsobrook II, John P

APPLICANT: Tchernev, Velizar T

APPLICANT: Liu, Xiaohong

APPLICANT: Spytek, Kimberly A

APPLICANT: Raturajan, Meera

APPLICANT: Grose, William M

APPLICANT: Lepley, Denise M

APPLICANT: Burgess, Catherine E

APPLICANT: Vernet, Corine A.M.

APPLICANT: Li, Li

APPLICANT: Gorman, Linda

APPLICANT: Edinger, Shlomit R

APPLICANT: Sciore, Paul

APPLICANT: Ellerman, Karen

APPLICANT: Malyskar, Uriel M

```

; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eisen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/10/037,417
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 3600
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-037-417-2
;
Query Match          19.8%; Score 56; DB 2; Length 3600;
Best Local Similarity 27.1%; Pred. No. 9.3e+02;
Matches 16; Conservative 5; Mismatches 20; Indels 18; Gaps 3;
```

```

Qy 7 QCSQNEYFDP---SLHACIPCOLR-----CSSNTPPLTCORYCNASVTNS 48
Db 1828 ECAPGFYRDVKGLFLGRVCVPCQCHGHSRCLPGSGVCVCQHNTGGAHGER-CQAGFVSS 1885

RESULT 47
US-09-949-016-10932
; Sequence 10932, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMEROPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10932
; LENGTH: 3647
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-10932
```

```

Query Match          19.6%; Score 55.5; DB 2; Length 3647;
Best Local Similarity 26.7%; Pred. No. 1.1e+03;
Matches 16; Conservative 6; Mismatches 19; Indels 19; Gaps 3;
```

```

Qy 7 QCSQNEYFDP---SLHACIPCO-----LRCSNTPPLTCORYCNASVTNS 48
Db 1778 ECAPGFYRDVKGLFLGRVCVPCQCHGHSRCLPGSGVCVCQHNTGGAHGER-CQAGFVSS 1836

RESULT 48
US-08-718-388-9
; Sequence 9, Application US/08718388
; Patent No. 6271362
; GENERAL INFORMATION:
; APPLICANT: MORIKAWA, MINORU
; APPLICANT: HARADA, NAOKI
; TITLE OF INVENTION: GENE ENCODING IgG Fc REGION-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/718,388
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 0230-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5405 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-718-388-9

Query Match          19.6%; Score 55.5; DB 2; Length 5405;
Best Local Similarity 33.3%; Pred. No. 1.1e+03;
Matches 12; Conservative 6; Mismatches 13; Indels 5; Gaps 2;
```

```

Qy 7 QCSQNEYFDSLHACT-PCQLRCSNTPPLTCORYC 41
Db 2732 ECPQNSHYE---LCADYCSLGSALSAPLQCPDGC 2763

RESULT 49
US-09-270-767-56958
; Sequence 56958, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-034
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56958
```

LENGTH: 142
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-56958

Query Match 19.4%; Score 55; DB 2; Length 142;
Best Local Similarity 29.2%; Pred. No. 40;
Matches 14; Conservative 8; Mismatches 20; Indels 6; Gaps 2;

QY 4 MAGCCSQNEYFDSLHACIPQCLRCSSNTPPLTCOR--YCNASVTNSV 49
DB 29 VATVCTGDIYDSDLGCVSRQVA---TPVAGCNRCQYATSTFVNAAV 72

RESULT 50
US-09-270-767-41714
Sequence 41714, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 41714
LENGTH: 392
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-41714

Query Match 19.4%; Score 55; DB 2; Length 392;
Best Local Similarity 29.2%; Pred. No. 1.2e+02;
Matches 14; Conservative 8; Mismatches 20; Indels 6; Gaps 2;

QY 4 MAGCCSQNEYFDSLHACIPQCLRCSSNTPPLTCOR--YCNASVTNSV 49
DB 279 VATVCTGDIYDSDLGCVSRQVA---TPVAGCNRCQYATSTFVNAAV 322

RESULT 51
US-09-902-540-11984
Sequence 11984, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217, 883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 11984
LENGTH: 991
TYPE: PRT
ORGANISM: Myxococcus xanthus
US-09-902-540-11984

Query Match 19.4%; Score 55; DB 2; Length 991;
Best Local Similarity 26.8%; Pred. No. 3.1e+02;
Matches 15; Conservative 9; Mismatches 24; Indels 8; Gaps 2;

QY 3 QNAGCCSQNEYFDSLHACIPQCLRCSSNTPPLTC-----ORCNASVTNSVKG 51
DB 453 QVVSACADPE-DTALRGCVRRVRAIINTPTGCSIQAPLPDAVNVAGVPLTLTG 507

RESULT 52

US-09-561-818A-12
Sequence 12, Application US/09561818A
Patent No. 6638907
GENERAL INFORMATION:
APPLICANT: Kortsema, Jarkko
APPLICANT: Tryggvason, Karl
TITLE OF INVENTION: Lamlnh 8 and Methods For Its Use
FILE REFERENCE: 99, 274-D
CURRENT APPLICATION NUMBER: US/09/561, 818A
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 1792
TYPE: PRT
ORGANISM: Mus musculus
US-09-561-818A-12

Query Match 19.4%; Score 55; DB 2; Length 1792;
Best Local Similarity 22.6%; Pred. No. 5.8e+02;
Matches 14; Conservative 10; Mismatches 22; Indels 16; Gaps 2;

QY 5 AAGCCSQNEYFDSLHACIPQCLRCSSNTPPLTCORRYCNASVTNSV 49
DB 40 AERCDAG-FFRTLSEBCAPCDGNSHCELDGSGFCLHCQRVTTGHECHCKLIDGYIGDSI 98

QY 50 KG 51
DB 99 KG 100

RESULT 53
US-09-561-818A-10
Sequence 10, Application US/09561818A
Patent No. 6638907
GENERAL INFORMATION:
APPLICANT: Kortsema, Jarkko
APPLICANT: Tryggvason, Karl
TITLE OF INVENTION: Lamlnh 8 and Methods For Its Use
FILE REFERENCE: 99, 274-D
CURRENT APPLICATION NUMBER: US/09/561, 818A
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 1816
TYPE: PRT
ORGANISM: Mus musculus
US-09-561-818A-10

Query Match 19.4%; Score 55; DB 2; Length 1816;
Best Local Similarity 22.6%; Pred. No. 5.9e+02;
Matches 14; Conservative 10; Mismatches 22; Indels 16; Gaps 2;

QY 5 AAGCCSQNEYFDSLHACIPQCLRCSSNTPPLTCORRYCNASVTNSV 49
DB 64 AERCDAG-FFRTLSEBCAPCDGNSHCELDGSGFCLHCQRVTTGHECHCKLIDGYIGDSI 122

QY 50 KG 51
DB 123 KG 124

RESULT 54
US-09-270-767-32231
Sequence 32231, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17

```

; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32231
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
; US-09-270-767-32231

Query Match      19.3%; Score 54.5; DB 2; Length 145;
Best Local Similarity 27.8%; Pred. No. 46;
Matches 15; Conservative 3; Mismatches 23; Indels 13; Gaps 2;

QY      7  OCSQNEVFDLSLHACIPCOLRCSSNTP--PLTCQRYCNAS 48
DB      12  OCHRTHTGTERPHVCTVCCGPARSYKLOQHMRHISGERPYKC-TYCEKSFYOS 64

RESULT 55
US-08-999-811-4
; Sequence 4, Application US/08999811
; Patent No. 5932540
; GENERAL INFORMATION:
; APPLICANT: HU, JING-SHAN
; APPLICANT: ROSEN, CRAIG A.
; APPLICANT: CAO, LIANG
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/999,811
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/207,550
; FILING DATE: 8-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,968
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MARKOWICZ, KAREN R.
; REGISTRATION NUMBER: 36,351
; REFERENCE/DOCKET NUMBER: 1488.1000004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-999-811-4

Query Match      19.3%; Score 54.5; DB 1; Length 350;
Best Local Similarity 35.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY      7  OCSQNEVFDLSLHACIPCOLRCSSNTP--PLTCQRYCNAS 44
DB      258  QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACACECTES 296
```

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RESULT 56
US-08-824-996-2
; Sequence 2, Application US/08824996B
; Patent No. 5935820
; GENERAL INFORMATION:
; APPLICANT: HU, JING-SHAN
; APPLICANT: ROSEN, CRAIG A.
; APPLICANT: CAO, LIANG
; TITLE OF INVENTION: Polynucleotides Encoding Vascular Endothelial Growth
; FILE REFERENCE: PFI12D1
; CURRENT APPLICATION NUMBER: US/08/824,996B
; CURRENT FILING DATE: 1997-03-27
; EARLIER APPLICATION NUMBER: 08/207,550
; EARLIER FILING DATE: 1994-03-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-824-996-2

Query Match      19.3%; Score 54.5; DB 1; Length 350;
Best Local Similarity 35.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY      7  OCSQNEVFDLSLHACIPCOLRCSSNTP--PLTCQRYCNAS 44
DB      258  QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACACECTES 296

RESULT 57
US-09-042-105-4
; Sequence 4, Application US/09042105
; Patent No. 6040157
; GENERAL INFORMATION:
; APPLICANT: HU, JING-SHAN
; APPLICANT: ROSEN, CRAIG A.
; APPLICANT: CAO, LIANG
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,105
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/207,550
; FILING DATE: 8-MAR-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,968
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: TO BE ASSIGNED
; FILING DATE: 24-DEC-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
```

NAME: ERIC K. STEFFE
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1000003/EKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-042-105-4

Query Match 19.3%; Score 54.5; DB 2; Length 350;
Best Local Similarity 35.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

Qy 7 OCSQNEYPDSLHACIPQCLRCSSNTP--PLTCQRYCNAS 44
Db 258 OCGANREFDENTQCV-CKRTCPRNQPLNPGKCAECTES 296

RESULT 58
US-08-510-133A-33
Sequence 33, Application US/08510133A
Patent No. 6221839
GENERAL INFORMATION:
APPLICANT: Aittalo, Kari
TITLE OF INVENTION: Receptor Ligand
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,133A
FILING DATE: 01-Aug-1995
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28113/32863
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-08-510-133A-33

Query Match 19.3%; Score 54.5; DB 2; Length 350;
Best Local Similarity 35.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

Qy 7 OCSQNEYPDSLHACIPQCLRCSSNTP--PLTCQRYCNAS 44
Db 258 OCGANREFDENTQCV-CKRTCPRNQPLNPGKCAECTES 296

RESULT 59
US-08-585-895-33
Sequence 33, Application US/08585895
Patent No. 6245330
GENERAL INFORMATION:
APPLICANT: Aittalo, Kari
TITLE OF INVENTION: Receptor Ligand
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/585,895
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28113/33072
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-585-895-33

Query Match 19.3%; Score 54.5; DB 2; Length 350;
Best Local Similarity 35.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

Qy 7 OCSQNEYPDSLHACIPQCLRCSSNTP--PLTCQRYCNAS 44
Db 258 OCGANREFDENTQCV-CKRTCPRNQPLNPGKCAECTES 296

RESULT 60
US-10-084-488-4
Sequence 4, Application US/10084488
Patent No. 6734285
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,488

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; FILING DATE: 28-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/623,725
; FILING DATE: 07-Sep-2000
; APPLICATION NUMBER: US 09/042,105
; FILING DATE: 13-MAR-1998
; APPLICATION NUMBER: US 09/107,997
; FILING DATE: 30-JUN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: MICHELE M. WALES
; REGISTRATION NUMBER: 43,975
; REFERENCE/DOCKET NUMBER: PF112PCT3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301)309-8504
; TELEFAX: (301)309-8439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-084-468-4
Query Match 19.3%; Score 54.5; DB 2; Length 350;
Best Local Similarity 35.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDSLHACIPQCLRCSSNTP--PLTCQRYCNAS 44
Db 258 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACECTES 296

RESULT 61
US-09-499-468-4
; Sequence 4, Application US/09499468
; Patent No. 6995132
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig
; APPLICANT: et al,
; TITLE OF INVENTION: Vascular Endothelial Growth Factor 2
; FILE REFERENCE: PF112U1
; CURRENT APPLICATION NUMBER: US/09/499,468
; CURRENT FILING DATE: 2000-02-07
; PRIOR APPLICATION NUMBER: 60/119,179
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 60/119,926
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: 60/137,796
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: 60/171,505
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 350
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-499-468-4
Query Match 19.3%; Score 54.5; DB 2; Length 350;
Best Local Similarity 35.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDSLHACIPQCLRCSSNTP--PLTCQRYCNAS 44
Db 258 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACECTES 296

RESULT 62
US-09-219-442-4
; Sequence 4, Application US/09219442
```

```

; Patent No. 6998386
; GENERAL INFORMATION:
; APPLICANT: HU, JING-SHAN
; APPLICANT: ROSEN, CRAIG A.
; APPLICANT: CAO, LIANG
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/219,442
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/999,811
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,968
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MARKOWICZ, KAREN R.
; REGISTRATION NUMBER: 36,351
; REFERENCE/DOCKET NUMBER: 1488.1000004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-219-442-4
Query Match 19.3%; Score 54.5; DB 2; Length 350;
Best Local Similarity 35.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDSLHACIPQCLRCSSNTP--PLTCQRYCNAS 44
Db 258 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACECTES 296

RESULT 63
US-08-999-811-2
; Sequence 2, Application US/08999811
; Patent No. 5932540
; GENERAL INFORMATION:
; APPLICANT: HU, JING-SHAN
; APPLICANT: ROSEN, CRAIG A.
; APPLICANT: CAO, LIANG
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/999,811
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/207,550
FILING DATE: 8-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MARKOWICZ, KAREN R.
REGISTRATION NUMBER: 36,351
REFERENCE/DOCKET NUMBER: 1488.1000004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-999-811-2

Query Match 19.3%; Score 54.5; DB 1; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYPDSLHACIPCOLRCSNTP--PLTCQRYCNAS 44
Db 327 QCGANREFDENTQCV-CKRTCPRNQPLNPKGKACCECTES 365

RESULT 64
US-09-042-105-2
Sequence 2, Application US/09042105
Patent No. 6040157
GENERAL INFORMATION:
APPLICANT: HU, JING-SHAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: CAO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,105
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/207,550
FILING DATE: 8-MAR-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: TO BE ASSIGNED
FILING DATE: 24-DEC-1997

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ERIC K. STEFFE
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1000003/EKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-042-105-2

Query Match 19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYPDSLHACIPCOLRCSNTP--PLTCQRYCNAS 44
Db 327 QCGANREFDENTQCV-CKRTCPRNQPLNPKGKACCECTES 365

RESULT 65
US-09-042-105-18
Sequence 18, Application US/09042105
Patent No. 6040157
GENERAL INFORMATION:
APPLICANT: HU, JING-SHAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: CAO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,105
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/207,550
FILING DATE: 8-MAR-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,968
FILING DATE: 24-DEC-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ERIC K. STEFFE
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1000003/EKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids

TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-042-105-18

Query Match 19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYPDSLHACIPQCLRCSSNTP--PLTCORYCNAS 44
DB 327 QCGANREFDENTQCGV-CKRTCPRNQPLNPGKACACECTES 365

RESULT 66
US-08-795-430-8
Sequence 8, Application US/08795430
Patent No. 6130071
GENERAL INFORMATION:
APPLICANT: Aitalo, Kari
TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,430
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/00427
FILING DATE: 01-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/671,573
FILING DATE: 28-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/601,132
FILING DATE: 14-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,895
FILING DATE: 12-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/510,133
FILING DATE: 01-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,011
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28967/33691
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-795-430-8

Query Match 19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYPDSLHACIPQCLRCSSNTP--PLTCORYCNAS 44
DB 327 QCGANREFDENTQCGV-CKRTCPRNQPLNPGKACACECTES 365

RESULT 67
US-08-510-133A-35
Sequence 35, Application US/08510133A
Patent No. 6221839
GENERAL INFORMATION:
APPLICANT: Aitalo, Kari
Joukov, Vladimir
TITLE OF INVENTION: Receptor Ligand
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,133A
FILING DATE: 01-AUG-1995
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28113/32863
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 35:

US-08-510-133A-35

Query Match 19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYPDSLHACIPQCLRCSSNTP--PLTCORYCNAS 44
DB 327 QCGANREFDENTQCGV-CKRTCPRNQPLNPGKACACECTES 365

RESULT 68
US-09-355-700-8
Sequence 8, Application US/09355700
Patent No. 6361946
GENERAL INFORMATION:
APPLICANT: Ludwig Institute for Cancer Research
Helinski University Licensing
Aitalo, Kari (U.S. only)
Joukov, Vladimir (U.S. only)
TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
Protein and Gene, Mutants Thereof, and Uses Thereof

NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/355,700
FILING DATE: 05-NOV-1994
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/795,430
FILING DATE: 05-FEB-1997
APPLICATION NUMBER: PCT/FI96/00427
FILING DATE: 01-AUG-1996
APPLICATION NUMBER: 08/671,573
FILING DATE: 28-JUN-1996
APPLICATION NUMBER: 08/601,132
FILING DATE: 14-FEB-1996
APPLICATION NUMBER: 08/585,895
FILING DATE: 12-JAN-1996
APPLICATION NUMBER: 08/510,133
FILING DATE: 01-AUG-1995
APPLICATION NUMBER: 08/340,011
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gaas, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28967/34140
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-355-700-8

Query Match 19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

Qy 7 OCSQNEYPDLHACIPQQLRCSSNTP--PLTCORYCNAS 44
Db 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACCECTES 365

RESULT 69
US-09-355-700-58
Sequence 58, Application US/09355700
Patent No. 6361946
GENERAL INFORMATION:
APPLICANT: Ludwig Institute for Cancer Research
Heisinki University Licensing
Alitalo, Kari (U.S. only)
Joukov, Vladimir (U.S. only)
TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
Protein and Gene, Mutants Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/355,700
FILING DATE: 05-NOV-1994
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/795,430
FILING DATE: 05-FEB-1997
APPLICATION NUMBER: PCT/FI96/00427
FILING DATE: 01-AUG-1996
APPLICATION NUMBER: 08/671,573
FILING DATE: 28-JUN-1996
APPLICATION NUMBER: 08/601,132
FILING DATE: 14-FEB-1996
APPLICATION NUMBER: 08/585,895
FILING DATE: 12-JAN-1996
APPLICATION NUMBER: 08/510,133
FILING DATE: 01-AUG-1995
APPLICATION NUMBER: 08/340,011
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gaas, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28967/34140
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: other
LOCATION: 156
OTHER INFORMATION: /note="codon 156 can be anything other
than cysteine, or can be nothing"
SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-09-355-700-58

Query Match 19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

Qy 7 OCSQNEYPDLHACIPQQLRCSSNTP--PLTCORYCNAS 44
Db 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACCECTES 365

RESULT 70
US-08-601-132-33
Sequence 33, Application US/08601132
Patent No. 6403088
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
Joukov, Vladimir
TITLE OF INVENTION: Receptor Ligand
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago

```

; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/601,132
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28113/33118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEEX: 25-3856
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-601-132-33

Query Match      19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY      7  QCSQNEVFDLSLHACIPQCRCSNTP--PLTCQRYCNAS 44
DB      327  QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACACECTES 365

RESULT 71
US-08-706-054A-3
; Sequence 3, Application US/08706054A
; Patent No. 6451764
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; TITLE OF INVENTION: VEGF-Related Protein
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Minipatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/706,054A
; FILING DATE: 30-Aug-1996
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/003491
; FILING DATE: 08-Sep-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: P-40,378
; REFERENCE/DOCKET NUMBER: P0963R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/953-9881
; TELEEX: 910/371-7168
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; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 amino acids
; TYPE: Amino Acid
; TOPOLOGY: linear
; US-08-706-054A-3

Query Match      19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY      7  QCSQNEVFDLSLHACIPQCRCSNTP--PLTCQRYCNAS 44
DB      327  QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACACECTES 365

RESULT 72
US-09-313-299-3
; Sequence 3, Application US/09313299B
; Patent No. 6576608
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: VEGF-RELATED PROTEIN
; FILE REFERENCE: P0963R1D1
; CURRENT APPLICATION NUMBER: US/09/313,299B
; CURRENT FILING DATE: 1999-05-17
; EARLIER APPLICATION NUMBER: US 08/706,054
; EARLIER FILING DATE: 1996-08-30
; EARLIER APPLICATION NUMBER: US 60/003,491
; EARLIER FILING DATE: 1995-09-08
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 3
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: Human
; LOCATION: 1-419
; OTHER INFORMATION: Sequence source: VRP
; Patent No. 6576608
; US-09-313-299-3

Query Match      19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY      7  QCSQNEVFDLSLHACIPQCRCSNTP--PLTCQRYCNAS 44
DB      327  QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACACECTES 365

RESULT 73
US-08-465-968-2
; Sequence 2, Application US/08465968E
; Patent No. 6608182
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Vascular Endothelial Growth Factor 2
; FILE REFERENCE: P112P1
; CURRENT APPLICATION NUMBER: US/08/465,968E
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/207,550
; EARLIER FILING DATE: 1994-03-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-465-968-2
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Query Match 19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 OCSONEYFDSLHACIPCOLRCSSNTP--PLTCORYCNAS 44
DB 327 OCGANREFDENTCQCV-CKRTCPRNOPLNPGKACCECTES 365

RESULT 74
US-08-671-573B-33
Sequence 33, Application US/08671573B

PATENT INFORMATION:
PATENT NO. 6645933
APPLICANT: Altalo, Karl
APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Receptor Ligand
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/671,573B
FILING DATE: 28-JUN-1996
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/601,132
FILING DATE: 14-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,895
FILING DATE: 12-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/510,133
FILING DATE: 01-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gaas, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28967/33348
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-671-573B-33

Query Match 19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 OCSONEYFDSLHACIPCOLRCSSNTP--PLTCORYCNAS 44
DB 327 OCGANREFDENTCQCV-CKRTCPRNOPLNPGKACCECTES 365

RESULT 75
US-09-438-046-14
Sequence 14, Application US/09438046
Patent No. 6706687
GENERAL INFORMATION:

APPLICANT: ERIKSSON, Ulf
APPLICANT: AASE, Karin
APPLICANT: LEE, Xuri
APPLICANT: PONTN, Annica
APPLICANT: UTTELA, Marco
APPLICANT: ALITALO, Karl
APPLICANT: OESTMAN, Arne
APPLICANT: HELDIN, Carl-Henrik
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING
TITLE OF INVENTION: THEREFOR, AND USES THEREOF
FILE REFERENCE: Ulf Eriksson et al 1064-44833
CURRENT APPLICATION NUMBER: US/09/438,046
CURRENT FILING DATE: 1999-11-10
EARLIER APPLICATION NUMBER: 60/107,852
EARLIER FILING DATE: 1998-11-10
EARLIER APPLICATION NUMBER: 60/113,997
EARLIER FILING DATE: 1999-12-28
EARLIER APPLICATION NUMBER: 60/150,604
EARLIER FILING DATE: 1999-08-26
EARLIER APPLICATION NUMBER: 60/157,108
EARLIER FILING DATE: 1999-10-04
EARLIER APPLICATION NUMBER: 60/157,756
EARLIER FILING DATE: 1999-10-05
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens
US-09-438-046-14

Query Match 19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 OCSONEYFDSLHACIPCOLRCSSNTP--PLTCORYCNAS 44
DB 327 OCGANREFDENTCQCV-CKRTCPRNOPLNPGKACCECTES 365

RESULT 76
US-09-631-092B-33
Sequence 33, Application US/09631092B
Patent No. 6730658
GENERAL INFORMATION:
APPLICANT: Altalo et al.
FILE REFERENCE: 28967/33348A
CURRENT APPLICATION NUMBER: US/09/631,092B
CURRENT FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 08/671,573
PRIOR FILING DATE: 1996-06-28
PRIOR APPLICATION NUMBER: 08/601,132
PRIOR FILING DATE: 1996-02-14
PRIOR APPLICATION NUMBER: 08/585,895
PRIOR FILING DATE: 1996-01-12
PRIOR APPLICATION NUMBER: 08/510,133
PRIOR FILING DATE: 1995-08-01
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.2
SEQ ID NO 33
LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens
US-09-631-092B-33

Query Match 19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 OCSONEYFDSLHACIPCOLRCSSNTP--PLTCORYCNAS 44
DB 327 OCGANREFDENTCQCV-CKRTCPRNOPLNPGKACCECTES 365

RESULT 77
US-10-084-488-2
; Sequence 2, Application US/10084488
; Patent No. 6734285
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESSES:
; ADDRESS: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/084,488
; FILING DATE: 28-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/623,725
; FILING DATE: 07-Sep-2000
; APPLICATION NUMBER: US 09/042,105
; FILING DATE: 13-MAR-1998
; APPLICATION NUMBER: US 09/107,997
; FILING DATE: 30-JUN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: MICHELE M. WALES
; REGISTRATION NUMBER: 43,975
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301)309-8504
; TELEFAX: (301)309-8439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-084-488-2

Query Match 19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEVPSLHACIPQCLRCSSNTP--PLTCQRYCNAS 44
DB 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACECTES 365

RESULT 78
US-10-084-488-18
; Sequence 18, Application US/10084488
; Patent No. 6734285
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESSES:
; ADDRESS: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/084,488
; FILING DATE: 28-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/623,725
; FILING DATE: 07-Sep-2000
; APPLICATION NUMBER: US 09/042,105
; FILING DATE: 13-MAR-1998
; APPLICATION NUMBER: US 09/107,997
; FILING DATE: 30-JUN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: MICHELE M. WALES
; REGISTRATION NUMBER: 43,975
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301)309-8504
; TELEFAX: (301)309-8439
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-084-488-18

Query Match 19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEVPSLHACIPQCLRCSSNTP--PLTCQRYCNAS 44
DB 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACECTES 365

RESULT 79
US-09-375-248-4
; Sequence 4, Application US/09375248
; Patent No. 6764820
; GENERAL INFORMATION:
; APPLICANT: Bertelli, Robert E.
; APPLICANT: Altitalo, Kari
; APPLICANT: Rinegold, David N.
; APPLICANT: Karkkainen, Matika
; TITLE OF INVENTION: SCREENING AND THERAPY FOR LYMPHATIC DISORDERS INVOLVING
; FILE REFERENCE: 28967/35255A
; CURRENT APPLICATION NUMBER: US/09/375,248
; CURRENT FILING DATE: 1999-08-16
; EARLIER APPLICATION NUMBER: PCT/US99/06133
; EARLIER FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-375-248-4

Query Match 19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEVPSLHACIPQCLRCSSNTP--PLTCQRYCNAS 44
DB 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACECTES 365

```
RESULT 80
US-09-468-647A-108
; Sequence 108, Application US/09468647A
; Patent No. 6783953
; GENERAL INFORMATION:
; APPLICANT: Gordon, Robert D
; APPLICANT: Sprengel, Jorg J
; APPLICANT: Yon, Jeffery R
; APPLICANT: Dijkmans, Josiena J.H.
; APPLICANT: Gosiowska, Anna
; APPLICANT: Dhanaaraj, Srilevi N
; APPLICANT: Xu, Jean
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-X
; FILE REFERENCE: B0192,7001US00
; CURRENT APPLICATION NUMBER: US/09/468,647A
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: GB 9828377.3
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 60/124,967
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: US 60/164,131
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 108
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-468-647A-108

Query Match      19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

Qy      7 QCSQNEYPDSLHACIPQCLRCSSNTP--PLTCORYCNAS 44
Db      327 QCGANREFDENTCQCV-CRRTCPRNQPLNPGKACACECTES 365

RESULT 81
US-09-534-376A-8
; Sequence 8, Application US/09534376A
; Patent No. 6818220
; GENERAL INFORMATION:
; APPLICANT: Aitalo, Kari
; APPLICANT: Joukov, Vladimir
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR C (VEGF-C) PROTEIN
; FILE REFERENCE: 28967/34140A
; CURRENT APPLICATION NUMBER: US/09/534,376A
; CURRENT FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 09/355,700
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: PCT/US98/01973
; PRIOR FILING DATE: 1998-02-02
; PRIOR APPLICATION NUMBER: 08/795,430
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: PCT/FT96/00427
; PRIOR FILING DATE: 1996-08-01
; PRIOR APPLICATION NUMBER: 08/671,573
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 08/601,132
; PRIOR FILING DATE: 1996-02-14
; PRIOR APPLICATION NUMBER: 08/585,895
; PRIOR FILING DATE: 1996-01-12
; PRIOR APPLICATION NUMBER: 08/510,133
; PRIOR FILING DATE: 1995-08-01
; PRIOR APPLICATION NUMBER: 08/340,011
; PRIOR FILING DATE: 1994-11-14
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patentin Ver. 2.0
```

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; SEQ ID NO 8
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-376A-8

Query Match      19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

Qy      7 QCSQNEYPDSLHACIPQCLRCSSNTP--PLTCORYCNAS 44
Db      327 QCGANREFDENTCQCV-CRRTCPRNQPLNPGKACACECTES 365

RESULT 82
US-09-534-376A-58
; Sequence 58, Application US/09534376A
; Patent No. 6818220
; GENERAL INFORMATION:
; APPLICANT: Aitalo, Kari
; APPLICANT: Joukov, Vladimir
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR C (VEGF-C) PROTEIN
; FILE REFERENCE: 28967/34140A
; CURRENT APPLICATION NUMBER: US/09/534,376A
; CURRENT FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 09/355,700
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: PCT/US98/01973
; PRIOR FILING DATE: 1998-02-02
; PRIOR APPLICATION NUMBER: 08/795,430
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: PCT/FT96/00427
; PRIOR FILING DATE: 1996-08-01
; PRIOR APPLICATION NUMBER: 08/671,573
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 08/601,132
; PRIOR FILING DATE: 1996-02-14
; PRIOR APPLICATION NUMBER: 08/585,895
; PRIOR FILING DATE: 1996-01-12
; PRIOR APPLICATION NUMBER: 08/510,133
; PRIOR FILING DATE: 1995-08-01
; PRIOR APPLICATION NUMBER: 08/340,011
; PRIOR FILING DATE: 1994-11-14
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 58
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF-C delta Cys156 mutant
; OTHER INFORMATION: At position 156, "Xaa" can be anything other than cysteine or can
US-09-534-376A-58

Query Match      19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

Qy      7 QCSQNEYPDSLHACIPQCLRCSSNTP--PLTCORYCNAS 44
Db      327 QCGANREFDENTCQCV-CRRTCPRNQPLNPGKACACECTES 365

RESULT 83
US-09-169-079-21
; Sequence 21, Application US/09169079
; Patent No. 6824777
; GENERAL INFORMATION:
; APPLICANT: Aitalo, Kari
; APPLICANT: Kaipainen, Arja
```

```
; APPLICANT: Valicela, Reija
; APPLICANT: Jusella, Iolta
; TITLE OF INVENTION: Flt4 (VEGFR-3) as a Target for Tumor Imaging and Anti-Tumor Thera
; FILE REFERENCE: 28113/34891
; CURRENT APPLICATION NUMBER: US/09/169,079
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: 08/901,710
; EARLIER FILING DATE: 1997-07-28
; EARLIER APPLICATION NUMBER: 08/340,011
; EARLIER FILING DATE: 1994-11-14
; EARLIER APPLICATION NUMBER: 08/257,754
; EARLIER FILING DATE: 1994-07-09
; EARLIER APPLICATION NUMBER: 07/959,951
; EARLIER FILING DATE: 1992-10-09
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-169-079-21
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```
Query Match          19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred.No.1.4e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;
```

```
OY 7 QCSQNEYPDSLHACIPCOLRCSNTP--PLTCORYCNAS 44
DB 327 QCGANREFDENTCCCV-CKRTCPRNQPLNPGKCAECTES 365
```

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RESULT 84
US-09-214-982-29
; Sequence 29, Application US/09214982
; Patent No. 6828426
; GENERAL INFORMATION:
; APPLICANT: Hirata, Yuichi
; APPLICANT: Nezu, Junichi
; TITLE OF INVENTION: No. 6828426e1 VEGF-like Factor
; FILE REFERENCE: 50026/014001
; CURRENT APPLICATION NUMBER: US/09/214,982
; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 8-185216 Japan
; EARLIER FILING DATE: 1996-07-15
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-214-982-29
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```
Query Match          19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred.No.1.4e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;
```

```
OY 7 QCSQNEYPDSLHACIPCOLRCSNTP--PLTCORYCNAS 44
DB 327 QCGANREFDENTCCCV-CKRTCPRNQPLNPGKCAECTES 365
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RESULT 85
US-09-427-657-2
; Sequence 2, Application US/09427657
; Patent No. 6958147
; GENERAL INFORMATION:
; APPLICANT: Aitalo, Kari
; APPLICANT: Yl-Herttuala, Seppo
; APPLICANT: Hiltunen, Mikko O
; APPLICANT: Jeltsch, Markku M
; APPLICANT: Achen, Marc G
; TITLE OF INVENTION: Use of VEGF-C or VEGF-D Gene or Protein to Prevent Restenosis
; FILE REFERENCE: 28967/35601A
```

```
; CURRENT APPLICATION NUMBER: US/09/427,657
; CURRENT FILING DATE: 1999-10-26
; EARLIER APPLICATION NUMBER: US 60/105,587
; EARLIER FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-427-657-2
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Query Match          19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred.No.1.4e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;
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OY 7 QCSQNEYPDSLHACIPCOLRCSNTP--PLTCORYCNAS 44
DB 327 QCGANREFDENTCCCV-CKRTCPRNQPLNPGKCAECTES 365
```

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RESULT 86
US-09-795-006A-22
; Sequence 22, Application US/09795006A
; Patent No. 6965010
; GENERAL INFORMATION:
; APPLICANT: Aitalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; FILE REFERENCE: 28967/35977B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-795-006A-22
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Query Match          19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred.No.1.4e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;
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```
OY 7 QCSQNEYPDSLHACIPCOLRCSNTP--PLTCORYCNAS 44
DB 327 QCGANREFDENTCCCV-CKRTCPRNQPLNPGKCAECTES 365
```

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RESULT 87
US-08-743-868-2
; Sequence 2, Application US/08743868
; Patent No. 6994989
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D. et al.
; TITLE OF INVENTION: flk-1 Binding Protein
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,868
; FILING DATE: 05-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/554,374
; FILING DATE: 08-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2837
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-743-868-2

Query Match      19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

OY      7 OCSQNEVFDLSLHACIPCOLRGSSNTP--PLTCQRYCNAS 44
Db      327 QCGANREFDENTQCV-CKRTCPRNQPLNPGKCAECTES 365

RESULT 88
; US-09-499-468-2
; Sequence 2, Application US/09499468
; Patent No. 6995132
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig
; APPLICANT: et al,
; TITLE OF INVENTION: Vascular Endothelial Growth Factor 2
; FILE REFERENCE: PFI12U1
; CURRENT APPLICATION NUMBER: US/09/499,468
; CURRENT FILING DATE: 2000-02-07
; PRIOR APPLICATION NUMBER: 60/119,179
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 60/119,926
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: 60/137,796
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: 60/171,505
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 419
; TYPE: PRT
; ORGANISM: homo sapiens
;
US-09-499-468-2

Query Match      19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

OY      7 OCSQNEVFDLSLHACIPCOLRGSSNTP--PLTCQRYCNAS 44
Db      327 QCGANREFDENTQCV-CKRTCPRNQPLNPGKCAECTES 365

RESULT 89
; US-09-219-442-2
; Sequence 2, Application US/09219442
; Patent No. 6998366
; GENERAL INFORMATION:
;

```

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;
; APPLICANT: HU, JING-SHAN
; APPLICANT: ROSEN, CRAIG A.
; APPLICANT: CAO, LIANG
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/219,442
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/999,811
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,968
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MARKOWICZ, KAREN R.
; REGISTRATION NUMBER: 36,351
; REFERENCE/DOCKET NUMBER: 1488.1000004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2540
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-09-219-442-2

Query Match      19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

OY      7 OCSQNEVFDLSLHACIPCOLRGSSNTP--PLTCQRYCNAS 44
Db      327 QCGANREFDENTQCV-CKRTCPRNQPLNPGKCAECTES 365

RESULT 90
; US-09-765-534B-21
; Sequence 21, Application US/09765534B
; Patent No. 7034105
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Kaipainen, Arja
; APPLICANT: Valtola, Reija
; APPLICANT: Jussila, Iolita
; TITLE OF INVENTION: Flt4 (VEGFR-3) as a Target for Tumor Imaging and Anti-Tumor Therai
; FILE REFERENCE: PFI4 (VEGFR-3)
; CURRENT APPLICATION NUMBER: US/09/765,534B
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 08/901,710
; PRIOR FILING DATE: 1997-07-28
; PRIOR APPLICATION NUMBER: 08/340,011
; PRIOR FILING DATE: 1994-11-14
; PRIOR APPLICATION NUMBER: 08/257,754
; PRIOR FILING DATE: 1994-07-09
; PRIOR APPLICATION NUMBER: 07/959,951
; PRIOR FILING DATE: 1992-10-09
; NUMBER OF SEQ ID NOS: 22
;

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-765-534B-21

Query Match      19.3%; Score 54.5; DB 3; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYPDSLHACIPCOLRCSNTP--PLTCQRYCNAS 44
Db 327 QCGANREFDENTCQCV-CRRTCPRNQPLNPGKACCECTES 365

RESULT 91
PCT-US96-09001-2
; Sequence 2, Application PC/TUS9609001
; GENERAL INFORMATION:
; APPLICANT: HU, ET AL.
; TITLE OF INVENTION: Human Vascular Endothelial Growth Factor 2
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09001
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/465,968
; FILING DATE: 6 JUN 95
; APPLICATION NUMBER: 08/207,550
; FILING DATE: 8 MAR 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-288
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
PCT-US96-09001-2

Query Match      19.3%; Score 54.5; DB 5; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYPDSLHACIPCOLRCSNTP--PLTCQRYCNAS 44
Db 327 QCGANREFDENTCQCV-CRRTCPRNQPLNPGKACCECTES 365

RESULT 92
US-09-747-371-3
; Sequence 3, Application US/09747371
```

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; Patent No. 6750013
; GENERAL INFORMATION:
; APPLICANT: Gish, Kurt
; TITLE OF INVENTION: No. 6750013el Methods of Diagnosing Breast Cancer, Compositions, &
; TITLE OF INVENTION: Screening for Breast Cancer Modulators
; FILE REFERENCE: A-69028/DJB/JJD
; CURRENT APPLICATION NUMBER: US/09/747,371
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: PCT/ US/00/06952
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 997
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-747-371-3

Query Match      19.3%; Score 54.5; DB 2; Length 997;
Best Local Similarity 28.2%; Pred. No. 3.6e+02;
Matches 11; Conservative 4; Mismatches 11; Indels 13; Gaps 1;

QY 7 QCSQNEYPDSLHACIPCOL-----RCSNTP 32
Db 751 QCSFGHFYNTTTHRCIRCLGTYOPFEGKNNCVSCPGNT 789

RESULT 93
US-10-037-182-36
; Sequence 36, Application US/10037182
; Patent No. 6933273
; GENERAL INFORMATION:
; APPLICANT: Tytgvaason, Karl
; APPLICANT: Doi, Masayuki
; APPLICANT: Thyboll, Jill
; TITLE OF INVENTION: Recombinant Laminin 10
; FILE REFERENCE: 99-274-F
; CURRENT APPLICATION NUMBER: US/10/037,182
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,449
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/279,282
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 2743
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-037-182-36

Query Match      19.3%; Score 54.5; DB 2; Length 2743;
Best Local Similarity 26.7%; Pred. No. 1.1e+03;
Matches 16; Conservative 6; Mismatches 19; Indels 19; Gaps 3;

QY 7 QCSQNEYPD--SLHACIPCO-----LRCSNTPPLTCQRYCNASVTNS 48
Db 1844 ECAPEFYRDVKGCLFGRGCVPCQCGHSDRCLPGSGVCVDCQHNTEGACRER-CQAGFMSS 1902

RESULT 94
US-10-037-182-2
; Sequence 2, Application US/10037182
; Patent No. 6933273
; GENERAL INFORMATION:
; APPLICANT: Tytgvaason, Karl
; APPLICANT: Doi, Masayuki
; APPLICANT: Thyboll, Jill
; TITLE OF INVENTION: Recombinant Laminin 10
; FILE REFERENCE: 99-274-F
; CURRENT APPLICATION NUMBER: US/10/037,182
; CURRENT FILING DATE: 2001-12-21
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; PRIOR APPLICATION NUMBER: 60/257,449
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/279,282
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 3695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-037-182-2

Query Match
Best Local Similarity 19.3%; Score 54.5; DB 2; Length 3695;
                26.7%; Pred. No. 1.4e+03;
Matches 16; Conservative 6; Mismatches 19; Indels 19; Gaps 3;

QY 7 QCSQNYFP---SLHACIPCO-----LRCSSNTPPLTCORYCNASVTS 48
DB 1844 ECAPGFYRVKGLFGRVCVQCQCHGSHDRCLPGSGVCVDCQNTGEGHCR-CQAGFMSS 1902

RESULT 95
US-09-621-976-6330
; Sequence 6330, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6330
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6330

Query Match
Best Local Similarity 19.1%; Score 54; DB 2; Length 98;
                38.1%; Pred. No. 35;
Matches 8; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 21 CIPCOLRCSSNTPPLTCORYC 41
DB 58 CLPCPSQSPSSCPPOCTKPC 78

RESULT 96
US-09-471-276-1590
; Sequence 1590, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6822072
; FILE REFERENCE: GENSET.025CPI
; CURRENT APPLICATION NUMBER: US/09/471,276
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 09/057,719
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/069,047
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: PCT/IB99/00712
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 1590
; LENGTH: 98

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-471-276-1590

Query Match
Best Local Similarity 19.1%; Score 54; DB 2; Length 98;
                38.1%; Pred. No. 35;
Matches 8; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 21 CIPCOLRCSSNTPPLTCORYC 41
DB 58 CLPCPSQSPSSCPPOCTKPC 78

RESULT 97
US-09-544-618-12
; Sequence 12, Application US/09544618
; Patent No. 6503502
; GENERAL INFORMATION:
; APPLICANT: Teitelman, Adam
; APPLICANT: Amson, Robert
; APPLICANT: Cohen, Daniel
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, PROTEINS, DRUGS AND DIAGNOSTIC
; FILE REFERENCE: 065691-0139
; CURRENT APPLICATION NUMBER: US/09/544,618
; CURRENT FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 12
; LENGTH: 282
; TYPE: PRT
; ORGANISM: TSAP 3
US-09-544-618-12

Query Match
Best Local Similarity 19.1%; Score 54; DB 2; Length 282;
                34.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 3; Mismatches 16; Indels 14; Gaps 2;

QY 14 FDSLHACIPCO---LRCSSNTPPLTCORYCNA-----SVTNSV 49
DB 45 FDYVLPPIIQCOSGHLVCSNCRPKLTCPTCGPLGSINLMAMEKXANSV 94

RESULT 98
US-09-544-618-19
; Sequence 19, Application US/09544618
; Patent No. 6503502
; GENERAL INFORMATION:
; APPLICANT: Teitelman, Adam
; APPLICANT: Amson, Robert
; APPLICANT: Cohen, Daniel
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, PROTEINS, DRUGS AND DIAGNOSTIC
; FILE REFERENCE: 065691-0139
; CURRENT APPLICATION NUMBER: US/09/544,618
; CURRENT FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 19
; LENGTH: 282
; TYPE: PRT
; ORGANISM: MOUSE
US-09-544-618-19

Query Match
Best Local Similarity 19.1%; Score 54; DB 2; Length 282;
                34.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 3; Mismatches 16; Indels 14; Gaps 2;

QY 14 FDSLHACIPCO---LRCSSNTPPLTCORYCNA-----SVTNSV 49
DB 45 FDYVLPPIIQCOSGHLVCSNCRPKLTCPTCGPLGSINLMAMEKXANSV 94
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| 981 | 51 | 18.0 | 353 | 2 | Q90WMI_RANCA |
|------|----|------|-----|---|-------------------|
| 982 | 51 | 18.0 | 367 | 2 | Q17186_CAEEL |
| 983 | 51 | 18.0 | 376 | 1 | P45699_fusarim_ox |
| 984 | 51 | 18.0 | 389 | 2 | O6NUG6_BRARE |
| 985 | 51 | 18.0 | 392 | 2 | O23048_CAEEL |
| 986 | 51 | 18.0 | 416 | 2 | Q4WB88_ASFPF |
| 987 | 51 | 18.0 | 417 | 2 | Q6E4J7_PETMA |
| 988 | 51 | 18.0 | 425 | 2 | Q9NAK5_CAEEL |
| 989 | 51 | 18.0 | 447 | 2 | Q9MOTO_ARATH |
| 990 | 51 | 18.0 | 448 | 2 | O5EFZ7_CHICK |
| 991 | 51 | 18.0 | 453 | 2 | Q70R08_XENLA |
| 992 | 51 | 18.0 | 454 | 2 | Q762D1_MOUSE |
| 993 | 51 | 18.0 | 473 | 2 | Q8H1E1_ARATH |
| 994 | 51 | 18.0 | 473 | 2 | Q8YVY5_ARATH |
| 995 | 51 | 18.0 | 478 | 2 | Q4UUS5_THRAN |
| 996 | 51 | 18.0 | 484 | 2 | Q7UMZ5_RHOBA |
| 997 | 51 | 18.0 | 515 | 1 | MUTYH_MOUSE |
| 998 | 51 | 18.0 | 515 | 2 | Q3U0U6_MOUSE |
| 999 | 51 | 18.0 | 524 | 2 | Q3U1N8_MOUSE |
| 1000 | 51 | 18.0 | 527 | 2 | Q32PP5_BRARE |

ALIGNMENTS

RESULT 1
THR17 HUMAN
ID TNR17_HUMAN STANDARD; PRT: 184 AA.
AC Q02223;
DT 01-JUL-1993, integrated into UniProtKB/Swiss-Prot.
DT 01-JUL-1993, sequence version 1.
DE Tumor necrosis factor receptor superfamily member 17 (B-cell
DE maturation protein) (CD269 antigen).
GN Name=TNFRSF17; Synonyms=BCM, BCMA;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND CHROMOSOMAL TRANSLOCATION.
RC TISSUE=Lymph node, and Peripheral blood leukocyte;
RX MEDLINE=93010984; PubMed=1396583;
RA Laabli Y., Gras M.P., Carbonnel F., Brouet J.C., Berger R.,
RA Larsen C.-J., Tsapis A.;
RT "A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene
RT by a t(4;16)(q26;p13) translocation in a malignant T cell lymphoma.";
RL EMBL J. 113897-3904(1992).

RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94218235; PubMed=8165126;
RA Laabli Y., Gras M.P., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;
RT "The BCM gene, preferentially expressed during B lymphoid maturation,
RT is bidirectionally transcribed.";
RL Nucleic Acids Res. 22:1147-1154(1994).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=99425270; PubMed=10493829; DOI=10.1006/geno.1999.5927;
RA Lofthus B.J., Kim U.-J., Shedd V.P., Kalush F., Brandon L.,
RA Fuhrmann U., Mason T., Crosby M.L., Barnstead M., Cronin L.,
RA Deshastes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,
RA Eichler E.B., Harris P.C., Venter J.C., Adams M.D.;
RT "Genome duplications and other features in 12 Mb of DNA sequence from
RT human chromosome 16p and 16q.";
RL Genomics 60:295-308(1999).
RN [4]
RP NUCLEOTIDE SEQUENCE, AND VARIANT THR-153.
RX MEDLINE=21419161; PubMed=11528522; DOI=10.1038/sj/gene/6363770;
RA Kawasaki A., Tsuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.;
RT "Presence of four major haplotypes in human BCM gene: lack of
RT association with systemic lupus erythematosus and rheumatoid
RT arthritis.";

RL Genes Immun. 2:276-279(2001).
RN [5]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS VAL-54; VAL-65;
RP VAL-75; ASN-81 AND SER-165.
RA Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,
RA Nguyen C.P., Nguyen D.A., Foel C.L., Robertson P.D., Schackwitz W.S.,
RA Sherwood J.K., Sherwood A.M., Leithauser B.J., Nickerson D.A.;
RT "NIHES-SNPs, environmental genome project, NIHES ES15478, Department
RT of Genome Sciences, Seattle, WA (URL: <http://egp.gs.washington.edu>).";
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RN [6]
RP FUNCTION, AND INTERACTIONS WITH TRAF1 AND TRAF3.
RX MEDLINE=20363816; PubMed=10903733;
RA Hatzoglou A., Roussel J., Bourgeade M.-F., Rogier E., Madry C.,
RA Inoue J., Devergne O., Tsapis A.;
RT "TNF receptor family member BCMA (B cell maturation) associates with
RT TNF receptor-associated factor (TRAF) 1, TRAF2, and TRAF3 and
RT activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38 mitogen-
RT activated protein kinase.";
RL J. Immunol. 165:1322-1330(2000).
RN [7]
RP FUNCTION.
RX MEDLINE=20259066; PubMed=10801128; DOI=10.1038/35010115;
RA Gross J.A., Johnston J., Mudri S., Enselman R., Dillon S.R.,
RA Madden K., Xu W., Parrish-Novak J., Foster D., Lotton-Day C.,
RA Moore M., Littau A., Grossman A., Haugen H., Foley K., Blumberg H.,
RA Harrison K., Kindsvogel W., Clegg C.H.;
RT "TRAF1 and BCMA are receptors for a TNF homologue implicated in B-cell
RT autoimmune disease.";
RL Nature 404:995-999(2000).
RN [8]
RP FUNCTION, AND INTERACTIONS WITH APRIL AND BAFF.
RX MEDLINE=21170294; PubMed=10973284; DOI=10.1038/79802;
RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M.,
RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Sciolina M.,
RA Boyle W.J., Sarosi I., Hsu H., Senaldi G., Thellin L.E.;
RT "APRIL and TRAF1 and receptors BCMA and TRAF1: system for regulating
RT humoral immunity.";
RL Nat. Immunol. 1:252-256(2000).
RN [9]
RP INTERACTIONS WITH TRAF5 AND TRAF6.
RX MEDLINE=20381353; PubMed=10908663; DOI=10.1073/pnas.160213497;
RA Shu H.-B., Johnson H.;
RT B cell maturation protein is a receptor for the tumor necrosis factor
RT family member TRAF-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).
CC -!- FUNCTION: Receptor for TNFSF13B/BLyS/BAFF and TNFSF13/APRIL.
CC Promotes B-cell survival and plays a role in the regulation of
CC humoral immunity. Activates NF-kappa-B and JNK.
CC -!- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
CC -!- INTERACTION:
CC Q9Y275:TNFSF13B; NBEExp=1; InAct=EBI-519945; EBI-519169;
CC -!- SUBCELLULAR LOCATION: Type III membrane protein. Plasma membrane
CC and perinuclear Golgi-like structures.
CC -!- TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-
CC cells or monocytes.
CC -!- DISEASE: A chromosomal aberration involving TNFRSF17 is found in a
CC form of T-cell acute lymphoblastic leukemia (T-ALL). Translocation
CC t(4;16)(q26;p13) with IL2.
CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.
CC
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CC
DR EMBL, 214954; CAA78679.1; -; mRNA.
DR EMBL, 229575; CAA82691.1; -; mRNA.
DR EMBL, 229574; CAA82690.1; -; Genomic DNA.
DR EMBL, U95742; AA67251.1; -; Genomic DNA.
DR EMBL, AB052772; BAB60895.1; -; Genomic DNA.
DR EMBL, AY09112; AAR84240.1; -; Genomic DNA.
DR PIR, S43486; S43486.
DR PDB, 1XU2; X-ray; R/S/T=5-51.
DR

DR EMBL: AY684975; AAV92616.1; -; mRNA.
 DR GO: GO:0004872; F:receptor activity; IEA.
 KW Receptor.
 SQ SEQUENCE 135 AA, 14843 MW, FCD1DDBB1195989 CRC64;
 Query Match 86.6%; Score 245; DB 2; Length 135;
 Best Local Similarity 100.0%; Pred. No. 1.5e-22;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIMAGCSQNEYPDLHACTPCQRCSSNTPPLTCQYCN 43
 Db 1 MIMAGCSQNEYPDLHACTPCQRCSSNTPPLTCQYCN 43

RESULT 4
 TNRI7 MOUSE
 ID TNRI7 MOUSE STANDARD; PRT; 185 AA.
 AC O88472;
 DT 27-MAY-2002, integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1998, sequence version 1.
 DT 07-FEB-2006, entry version 34.
 DE Tumor necrosis factor receptor superfamily member 17 (B-cell
 maturation protein).
 DE Name=tnfrsf17; Synonyms=Bcm, Bcma;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 RX NUCLEOTIDE SEQUENCE (LRN) (ISOFORMS 1 AND 2).
 RC MEDLINE=99061155; PubMed=9846698; DOI=10.1093/intimm/10.11.1693;
 RA Madry C., Laabi Y., Callebaut I., Rousset J., Hatzoglou A.,
 RA Le Conat M., Morron J.P., Berger R., Tsapis A.;
 RT "The characterization of murine BCMA gene defines it as a new member
 of the tumor necrosis factor receptor superfamily";
 RT Int. Immunol. 10:1693-1702(1998).
 RL [2]
 RP NUCLEOTIDE SEQUENCE (LRN) (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=colon;
 RX PubMed=16141072; DOI=10.1126/science.1112014.
 RA Carrincci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
 RA Ambesi-Impomato A., Apweiler R., Atturliya R.N., Bailey T.L.,
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhury V., Christofels A., Clutterbuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
 RA Flecher C.F., Fukushima T., Furum M., Futaki S., Gariboldi M.,
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 RA Gusninch S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hill D., Hummichek L., Iacono M., Ikeo K., Iwama N., Ishikawa T.,
 RA Klat M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Koike S., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 RA Ljunf S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Marzuda H., Matsunawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Morasugi-Tibar S., Mulder N., Nakano N., Nakuchi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
 RA Petkovski N., Piazza S., Reid J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schonbach C., Sekiguchi K., Sempke C.A., Seno S., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugita K., Sultana R., Takenawa Y., Taki K.,
 RA Tamada K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yang K.,
 RA Yamamoto H., Zdobych E., Zhu S., Zimmer A., Hilde W., Bult C.,
 RA Grimmond S.M., Tesdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,

RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imanuma K., Itoh M., Kato T., Kawai H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Niimiya N.,
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome";
 RT Science 309:1559-1563 (2005).
 RL [3]
 RP NUCLEOTIDE SEQUENCE (LRN) (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=mammary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -I- FUNCTION: Receptor for TNFSF13B/BAF and TNFSF13/APRIL.
 CC Promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK (by similarity).
 CC -I- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (by
 CC similarity).
 CC -I- SUBCELLULAR LOCATION: Membrane; single-pass type III membrane
 CC protein (probable).
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=O88472-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=O88472-2; Sequence=VSP_006507;
 CC -I- TISSUE SPECIFICITY: Detected in spleen, thymus, bone marrow and
 CC heart, and at lower levels in kidney and lung.
 CC -I- SIMILARITY: Contains 1 TNFR-Cys repeat.
 CC -----
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 CC -----
 DR EMBL: AF061505; AAC23799.1; -; mRNA.
 DR EMBL: AK020247; BAB32038.1; -; mRNA.
 DR EMBL: BC027519; AAH27519.1; -; mRNA.
 DR HSSP: Q02223; 100D.
 DR Ensembl: ENSMUSG00000022496; Mus musculus.
 DR MGI: MGI:1343050; Tnfrsf17.
 DR GO: GO:0016021; C:integral to membrane; TAS.
 DR InterPro: IPR001368; TNFR_C6.
 DR PROSITE: PS00652; TNFR_NGFR_1; FALSE_NEG.
 DR PROSITE: PS50050; TNFR_NGFR_2; FALSE_NEG.
 KW Alternative splicing; Immune response; Membrane; Receptor;
 KW Signal-anchor; Transmembrane.
 FT CHAIN 1 185
 FT Tumor necrosis factor receptor
 FT superfamily member 17.
 FT /FTID=PRO_0000058936.
 FT Extracellular (Potential).
 FT Signal-anchor for type III membrane
 FT protein (Potential).
 FT Cytoplasmic (Potential).
 FT REPEAT 4 185
 FT TNFR-Cys.
 FT By similarity.
 FT DISUFID 5 18

FT DISULFID 21 32 By similarity.
 FT DISULFID 25 36 By similarity.
 FT VARSPPLIC 87 91 Missing (in isoform 2).
 FT /FTID=VSP_006507.
 SQ SEQUENCE 185 AA; 20442 MW; 8806352B4FD26A8E CRC64;

Query Match 64.0%; Score 181; DB 1; Length 185;
 Best Local Similarity 70.8%; Pred. No. 2.1e-14;
 Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 4 MAGGCSQNEYPFDSLHACIPQQLRCSSNTPPLTCQRYCNASTVNSVG 51
 Db 1 MAQGCSEYFDSLHACKRCHLRCSN--PAPCCPDPSPVTSVSKG 46

RESULT 5

QAS4Q3_TETNG PRELIMINARY; PRT; 184 AA.
 AC QAS4Q3;
 DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Chromosome 2 SCAP14738, whole genome shotgun sequence.
 GN ORFNames=GSTENG0024082001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OK NCBI_TaxID=99883;
 RN [1]

NUCLEOTIDE SEQUENCE.

RP Published=15496914; DOI=10.1038/nature03025;
 RA Jallion O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Coataz C., Bernot A.,
 RA Nicoud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
 RA Blemont C., Skalli Z., Catolico L., Poulain J., De Berardinis V.,
 RA Craud C., Duprat S., Brotier P., Coutanceau J.-P., Gouzy J.,
 RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.-N., Guiso R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Lander V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).
 RN [2]

NUCLEOTIDE SEQUENCE.

RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.

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 CC -----
 DR EMBL; CAAB01014738; CAG04379.1; -; Genomic DNA.
 SQ SEQUENCE 184 AA; 19133 MW; 3B21675E4FEB1BB7 CRC64;

Query Match 27.6%; Score 78; DB 2; Length 184;
 Best Local Similarity 30.4%; Pred. No. 0.15;
 Matches 14; Conservative 11; Mismatches 11; Indels 10; Gaps 1;

Qy 5 AAGCSQNEYPFDSLHACIPQQLRCSSNTPPLTCQRYCNASTVNSVG 50
 Db 91 AAGCSSEYFDSLHACKRCHLRCSN--PAPCCPDPSPVTSVSKG 126

RESULT 6
 Q9B107_ENTH1

ID Q9B107_ENTH1 PRELIMINARY; PRT; 718 AA.
 AC Q9B107;
 DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2001, sequence version 1.
 DT 07-FEB-2006, entry version 14.
 DE Putative cysteine surface protein (Fragment).
 GN Name=esp;
 OS Entamoeba histolytica.
 OC Eukaryota; Entamoebidae; Entamoeba.
 OK NCBI_TaxID=5759;

NUCLEOTIDE SEQUENCE.

RP MEDLINE=21428166; PubMed=11545438;
 RA Willhoelt U., Campos-Gongora E., Touzni S., Bruchhaus I., Tannich E.;
 RT "Introns of Entamoeba histolytica and Entamoeba dispar.";
 RL Probst 152:149-156(2001).
 CC -----

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DR EMBL; AJ409106; CAC34072.1; -; Genomic DNA.
 DR InterPro; IPR006212; Furin_repeat.

DR SMART; SM00261; FU; 1.
 FT NON_TER 718
 SQ SEQUENCE 718 AA; 80231 MW; FFF6362A49F2827A CRC64;

Query Match 25.8%; Score 73; DB 2; Length 718;
 Best Local Similarity 26.5%; Pred. No. 2.7;
 Matches 13; Conservative 7; Mismatches 29; Indels 0; Gaps 0;

Qy 3 QMAGCSQNEYPFDSLHACIPQQLRCSSNTPPLTCQRYCNASTVNSVG 51
 Db 136 ELGRCNDSDSYDSTTRTCQKCFNCELCTSTNCFKCSNKTILFESNG 184

RESULT 7

ID Q511P5_ENTH1 PRELIMINARY; PRT; 1113 AA.
 AC Q511P5;
 DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
 DT 07-JUN-2005, sequence version 1.
 DT 07-FEB-2006, entry version 8.
 DE Receptor protein kinase, putative.
 GN ORFNames=99.t00011;
 OS Entamoeba histolytica HM-1:IMSS.
 OC Eukaryota; Entamoebidae; Entamoeba.
 OK NCBI_TaxID=294381;
 RN [1]

NUCLEOTIDE SEQUENCE.

RP STRAIN=HM-1:IMSS;
 RC Published=15729342; DOI=10.1038/nature03291;
 RX Loftus B.J., Anderson I., Davies R., Almark U.C., Samuelson J.,
 RA Amado P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
 RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
 RA Hofer M., Bruchhaus I., Willhoelt U., Bhattacharya A.,
 RA Chillingworth T., Churcher C.M., Hance Z., Harris B., Harris D.,
 RA Jagels K., Moule S., Mungall K.L., Ormond D., Squares R.,
 RA Wang Z., Guillen N., Gluchrist C., Stroup S.E., Bhattacharya S.,
 RA Lohia A., Foster P.G., Sichert-Ponten T., Weber C., Singh U.,
 RA Mukherjee C., El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M.,
 RA Barrell B.G., Fraser C.M., Hall N.;
 RT "The genome of the protist parasite Entamoeba histolytica.";
 RL Nature 433:865-868(2005).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.

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 CC -----

DR EMBL; AAFB01000356; EAL47552.1; -; Genomic DNA.
 GO; GO:0005524; P:ATP binding; IEA.

```
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR006212; Furlin_repeat.
DR InterPro: IPR00719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR01245; Tyr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PP000001; Prot_kinase; 1.
DR SMART: SM00261; FU; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase; Receptor.
SQ SEQUENCE 1113 AA; 124275 MW; 8F6D9846EFCDD4D07 CRC64;

Query Match      25.8%; Score 73; DB 2; Length 1113;
Best Local Similarity 26.5%; Pred. No. 4.2;
Matches 13; Conservative 7; Mismatches 29; Indels 0; Gaps 0;

Cy 3 OMAGGCSQNEYFDSLHACIPQQLRCSSTPPLTQCRYNMASVTMSVVG 51
Db 125 ELGRCNDGSDYDSTRTTCQKFCNNECLCTSTNCFKCSNKTILTESNG 173
:::|||||:::|:::|

RESULT 8
088714_MOUSE PRELIMINARY; PRT; 499 AA.
ID 088714_MOUSE PRELIMINARY; PRT; 499 AA.
AC 088714;
DT 01-NOV-1998, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1998, sequence version 1.
DT 07-FEB-2006, entry version 26.
DE Gastric mucin-like protein (Fragment).
GN Name=Muc6; Synonyms=gastriic mucin-like;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Stomach;
RA Tomasetto C.; Masson R.; Wendling C.; Lefebvre O.; Chenard M.P.;
RA Rio M.C.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Stomach;
RA Tomasetto C.L.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
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-----
DR EMBL: AJ010752; CAA09343.1; -; mRNA.
DR HSSP: P56682; 1CCV.
DR Ensembl: ENSMUSG00000048191; Mus musculus.
DR MGI: MGI:263233; Muc6.
DR InterPro: IPR002919; Prot_Inh_CR_TTL.
DR InterPro: IPR001846; VWF_D.
DR Pfam: PF01826; TIL; 1.
DR Pfam: PF00094; VWD; 1.
DR SMART: SM00216; VWD; 1.
FT NON_TER 1
FT NON_TER 499
SQ SEQUENCE 499 AA; 54191 MW; 04F89E4F23EE61E CRC64;

Query Match      25.6%; Score 72.5; DB 2; Length 499;
Best Local Similarity 48.3%; Pred. No. 2.1;
Matches 14; Conservative 1; Mismatches 7; Indels 7; Gaps 1;

Cy 8 CSQNEYFDSLHACIPQQLRCSSTPPLT 36
Db 8 CSQNEYFDSLHACIPQQLRCSSTPPLT 36
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Db 430 CSQNEYFDSLHACIPQQLRCSSTPPLT 451
|||||||:::|:::|
|||:::|

RESULT 9
080218_MOUSE PRELIMINARY; PRT; 1674 AA.
ID 080218_MOUSE PRELIMINARY; PRT; 1674 AA.
AC 080218;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 15..
DE Secreted gel-forming mucin (Fragment).
GN Name=Muc6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RX PubMed=14984930; DOI=10.1016/j.bbaexp.2004.01.001;
RT "The mouse secreted gel-forming mucin gene cluster.";
RL Biochim. Biophys. Acta 1676:240-250(2004).
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DR EMBL: AJ511867; CAD54415.1; -; Genomic_DNA.
DR EMBL: AJ511868; CAD54415.1; JOINED; Genomic_DNA.
DR HSSP: Q46162; 1KJ0.
DR MGI: MGI:263233; Muc6.
DR InterPro: IPR002919; Prot_Inh_CR_TTL.
DR InterPro: IPR006552; VWC_out.
DR InterPro: IPR001846; VWF_D.
DR Pfam: PF01826; TIL; 2.
DR Pfam: PF00094; VWD; 3.
DR SMART: SM00216; VWD; 3.
FT NON_TER 1674
FT NON_TER 1674
SQ SEQUENCE 1674 AA; 181170 MW; 38C42CB004476309 CRC64;

Query Match      25.6%; Score 72.5; DB 2; Length 1674;
Best Local Similarity 48.3%; Pred. No. 7.5;
Matches 14; Conservative 1; Mismatches 7; Indels 7; Gaps 1;

Cy 8 CSQNEYFDSLHACIPQQLRCSSTPPLT 36
Db 1181 CSQNEYFDSLHACIPQQLRCSSTPPLT 1202
|||||||:::|:::|
|||:::|
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CC -----
DR EMBL, AY184388; AA047735.1; -, Genomic DNA.
DR EMBL, AY184385; AA047735.1; JOINED; Genomic DNA.
DR EMBL, AY184386; AA047735.1; JOINED; Genomic DNA.
DR EMBL, AY184387; AA047735.1; JOINED; Genomic DNA.
DR HSSP, O46162; 1k70.
DR MGI, MGI:2663233; Muc6.
DR InterPro, IPR006207; Cys_knot_C.
DR InterPro, IPR002919; Prot_inh_CR_TTL.
DR InterPro, IPR006552; VWF_out.
DR InterPro, IPR001846; VWF_D.
DR Pfam, PF01826; TIL; 2.
DR Pfam, PF00094; VMD; 3.
DR SMART, SM00216; VMD; 3.
DR PROSITE, PS01225; CTCK_2, 1.
SQ SEQUENCE 2850 AA; 300401 MW; 9CD95F0845C79C9D CRC64;

Query Match 25.6%; Score 72.5; DB 2; Length 2850;
Best Local Similarity 48.3%; Pred. No. 13;
Matches 14; Conservative 1; Mismatches 7; Indels 7; Gaps 1;

Qy 8 CSONEYFDSLHACIPQOLRCSSNTPPLT 36
Db 1222 CSONEYFDSHSEGTVCPC-----APPTT 1243

RESULT 11
OSSUB4_MOUSE
ID Q5SU84; PRELIMINARY; PRT; 74 AA.
AC Q5SU84;
DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.
DI 21-DEC-2004, sequence version 1.
DR 07-FEB-2006, entry version 6.
DE Tumor necrosis factor receptor superfamily, member 13b (Fragment).
GN Name=Trifsf13b; ORFNames=RP23-5512.2-002;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN NUCLEOTIDE SEQUENCE.
RA Holt K.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL, AL646093; CAI25894.1; -, Genomic DNA.
DR GO, GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 74
SQ SEQUENCE 74 AA; 8337 MW; DA8A3B06FE191A26 CRC64;

Query Match 25.3%; Score 71.5; DB 2; Length 74;
Best Local Similarity 35.3%; Pred. No. 0.37;
Matches 12; Conservative 8; Mismatches 13; Indels 1; Gaps 1;

Qy 8 CSONEYFDSLHACIPQOLRCSSNTPPLTCORYC 41
Db 6 CPKDYWDSRSKSCVSCALTCQSQR-GRCTDPC 38

RESULT 12
OSSUB3_MOUSE
ID Q5SU83; PRELIMINARY; PRT; 140 AA.
AC Q5SU83;
DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.
DI 21-DEC-2004, sequence version 1.
DR 07-FEB-2006, entry version 6.

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DE Tumor necrosis factor receptor superfamily, member 13b (Fragment).
GN Name=Trifsf13b; ORFNames=RP23-5512.2-003;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN NUCLEOTIDE SEQUENCE.
RA Holt K.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL, AL646093; CAI25895.1; -, Genomic DNA.
DR Ensembl, ENSMUSG00000010142; Mus musculus.
DR GO, GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 140
SQ SEQUENCE 140 AA; 15672 MW; 005D8CDF4E8E3D15 CRC64;

Query Match 25.3%; Score 71.5; DB 2; Length 140;
Best Local Similarity 35.3%; Pred. No. 0.73;
Matches 12; Conservative 8; Mismatches 13; Indels 1; Gaps 1;

Qy 8 CSONEYFDSLHACIPQOLRCSSNTPPLTCORYC 41
Db 6 CPKDYWDSRSKSCVSCALTCQSQR-GRCTDPC 38

RESULT 13
TR13B_MOUSE
ID TR13B_MOUSE; STANDARD; PRT; 249 AA.
AC Q9EN35; Q9DB23;
DT 27-MAY-2002, integrated into UniProtKB/Swiss-Prot.
DI 01-MAR-2001, sequence version 1.
DR 07-FEB-2006, entry version 28.
DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane
DE activator and CAML interactor).
GN Name=Trifsf13b; Synonyms=Taci;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN NUCLEOTIDE SEQUENCE [MRNA].
RA TISSUE=Spleen;
RC MEDLINE=21177254; PubMed=1081172; DOI=10.1038/76889;
RX van M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A., Dixit V.M.;
RT "Identification of a receptor for Blys demonstrates a crucial role in
RT humoral immunity.";
RL Nat. Immunol. 1:37-41 (2000).
RN (2)
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carinci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic M.J., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Williams L.G., Aldins V., Allen J.E.,
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Banerji M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutierbuch D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Furuki S., Gariboldi M.,
RA Georgii-Heminger P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Hummelbeck L., Iacono M., Ikey K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasaki Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,

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RA Kurochkin I V., Lazareu L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Medera M., Marchionni L.,
RA Maetuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Motetagni-Tabar S., Mulder N., Nakano N., Nakautchi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlandi V., Pand K.C., Pavan W.J., Pavasi G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Roer B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Sero S., Sessa L., Sheng Y.,
RA Shidara Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Spelling K., Stupka E., Sugtura K., Sultana R., Takemura Y., Taki K.,
RA Tammoja K., Tan S.-L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yaqi K.,
RA Yamamichi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Wahlstedt S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlstedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki T., Arakawa T.,
RA Iida Y., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Kono H., Nakano K., Niimomiya N.,
RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watabiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563 (2005).
RN [3]
RP FUNCTION.
RX MEDLINE=20341628; PubMed=1080535; DOI=10.1084/jem.192.1.137;
RA Xia X.-Z., Treanor V., Senaldi G., Khare S.D., Boone T., Kelley M.,
RA Thellil L.E., Colombero A., Solovay I., Lee F., McCabe S., Elliott R.,
RA Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J.,
RA Meng S.-Y., Boyle W.J., Hsu H.;
RT "TAC1 is a TRAF-interacting receptor for TLR1-1, a tumor necrosis
RT factor family member involved in B cell regulation.";
RL J. Exp. Med. 192:137-143 (2000).
RN [4]
RP FUNCTION.
RX MEDLINE=21322748; PubMed=11429548; DOI=10.1038/69782;
RA Wang H., Marsters S.A., Baker T., Chan B., Lee W.P., Fu L., Tumas D.,
RA Yan M., Dixit V.M., Ashkenazi A., Grewal I.S.;
RT "TAC1-ligand interactions are regulated for T cell activation and
RT collagen-induced arthritis in mice.";
RL Nat. Immunol. 2:632-637 (2001).
CC -I- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAPF/BLYS
CC that binds both ligands with similar high affinity. Mediates
CC calcineurin-dependent activation of NF-AT, as well as activation
CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
CC cell function and the regulation of humoral immunity (By
CC similarity).
CC -I- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
CC domain of CANNG with its C-terminus (By similarity).
CC -I- SUBCELLULAR LOCATION: Membrane; single-pass type III membrane
CC protein (Probable).
CC -I- SIMILARITY: Contains 2 TNFR-Cys repeats.
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CC
CC -----
CC EMBL, AF251673; AAG00081.1; -; mRNA.
CC EMBL, AK004668; BAB23457.1; -; mRNA.
CC Ensembl, ENSMUSG00000010142; Mus musculus.
CC MGI, MGI:1889411; Tnfrsf13b.
CC GO: GO:000897; C:external side of plasma membrane; IDA.
CC GO: GO:0005887; C:integral to plasma membrane; IDA.
CC GO: GO:0001782; P:B cell homeostasis; IMP.
CC GO: GO:0030889; P:negative regulation of B cell proliferation; IMP.
CC InterPro, IPR001368; TNFR_C.
CC PROSITE, PS00652; TNFR_NGFR_1; FALSE NEG.
CC PROSITE, PS50050; TNFR_NGFR_2; FALSE NEG.
CC Immune response; Membrane; Receptor; Repeat; Signal-anchor;
CC Transmembrane.
FT CHAIN 1 249 Tumor necrosis factor receptor
FT superfamily member 13b.
FT /FTID=PRO_0000058932.

| | | | | | | | | |
|--|--|---------|-----------|--|--|--|--|--|
| FT | TOPO_DOM | 1 | 128 | Extracellular (potential). | | | | |
| FT | TRANSMEM | 129 | 149 | Signal anchor for type III membrane protein (potential). | | | | |
| FT | TOPO_DOM | 150 | 249 | Cytoplasmic (potential). | | | | |
| FT | REPEAT | 5 | 38 | TNFR-Cys 1. | | | | |
| FT | REPEAT | 42 | 76 | TNFR-Cys 2. | | | | |
| FT | DISULFID | 6 | 19 | By similarity. | | | | |
| FT | DISULFID | 22 | 34 | By similarity. | | | | |
| FT | DISULFID | 26 | 38 | By similarity. | | | | |
| FT | DISULFID | 43 | 58 | By similarity. | | | | |
| FT | DISULFID | 61 | 72 | By similarity. | | | | |
| FT | DISULFID | 65 | 76 | By similarity. | | | | |
| FT | CONFLICT | 137 | 137 | 1 -> F (in Ref. 2). | | | | |
| SO | SEQUENCE | 249 AA; | 26947 MW; | CB2F2D61C2931D81 CRC64; | | | | |
| Query Match | | | | | | | | |
| Best Local Similarity 25.3%; Score 71.5; DB 1; Length 249; | | | | | | | | |
| Matches 12; Conservative 8; Mismatches 13; Indels 1; Gaps 1; | | | | | | | | |
| Oy | 8 CSQNEYFDSLHACIPCOLRCSSTPPLTCORC 41 | | | | | | | |
| Db | 6 CPKQGYWDSRRKSCVSCALTCGQRS-QRTCTDPC 38 | | | | | | | |
| RESULT 14 | | | | | | | | |
| 05SU82_MOUSE PRELIMINARY; PRT; 249 AA. | | | | | | | | |
| ID | 05SU82_MOUSE PRELIMINARY; PRT; 249 AA. | | | | | | | |
| AC | 05SU82; | | | | | | | |
| DT | 10-MAY-2005, integrated into UniProtKB/TrEMBL. | | | | | | | |
| DT | 10-MAY-2005, sequence version 1. | | | | | | | |
| DT | 07-FEB-2006, entry version 3. | | | | | | | |
| DE | Tumor necrosis factor receptor superfamily, member 13b. | | | | | | | |
| GN | Name=TNFRsf13b; ORFNames=RP23-5512.2-001; | | | | | | | |
| OS | Mus musculus (Mouse). | | | | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | | | | |
| OC | Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; | | | | | | | |
| OC | Muridea; Muridae; Murinae; Mus. | | | | | | | |
| OX | NCBI_TaxID=10090; | | | | | | | |
| RN | [1] | | | | | | | |
| RP | NCI BOTIDE SEQUENCE. | | | | | | | |
| RA | Holt K.; | | | | | | | |
| RL | Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases. | | | | | | | |
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| CC | Distributed under the Creative Commons Attribution-NonDerivs License | | | | | | | |
| CC | EMBL; AL646093; CAI25896.1; -, Genomic DNA. | | | | | | | |
| DR | Ensembl; ENSMUSG00000010142; Mus musculus. | | | | | | | |
| DR | GO; GO:0004872; F:receptor activity; IDA. | | | | | | | |
| KW | Receptor. | | | | | | | |
| SO | SEQUENCE 249 AA; 26947 MW; CB2F2D61C2931D81 CRC64; | | | | | | | |
| Query Match | | | | | | | | |
| Best Local Similarity 25.3%; Score 71.5; DB 2; Length 249; | | | | | | | | |
| Matches 12; Conservative 8; Mismatches 13; Indels 1; Gaps 1; | | | | | | | | |
| Oy | 8 CSQNEYFDSLHACIPCOLRCSSTPPLTCORC 41 | | | | | | | |
| Db | 6 CPKQGYWDSRRKSCVSCALTCGQRS-QRTCTDPC 38 | | | | | | | |
| RESULT 15 | | | | | | | | |
| ID | 05OPT4_ENTHI PRELIMINARY; PRT; 1150 AA. | | | | | | | |
| AC | 05OPT4; | | | | | | | |
| DT | 07-JUN-2005, integrated into UniProtKB/TrEMBL. | | | | | | | |
| DT | 07-JUN-2005, sequence version 1. | | | | | | | |
| DT | 07-FEB-2006, entry version 6. | | | | | | | |
| DE | Receptor protein kinase, putative. | | | | | | | |
| GN | ORFNames=359.t00009; | | | | | | | |
| OS | Entamoeba histolytica HM-1:IMSS. | | | | | | | |
| OC | Eukaryota; Entamoebidae; Entamoeba. | | | | | | | |
| OX | NCBI_TaxID=294381; | | | | | | | |

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RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=HM-1:IMSS;
RX      PubMed=15729342; DOI=10.1038/nature03291;
RA      Loftus B.J., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
RA      Amedeo P., Koncagila P., Bettman M., Hirt R.P., Mann B.J., Nozaki T.,
RA      Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leipzig M.,
RA      Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,
RA      Chillingworth T., Churcher C.M., Hance Z., Harris B., Harris D.,
RA      Jagals K., Moule S., Mungall K.L., Ormond D., Squares R.,
RA      Whitehead S., Quail M.A., Rabinowitsch E., Norbertczak H., Price C.,
RA      Wang Z., Gillen N., Gilchrist C., Strop S.E., Bhattacharya S.,
RA      Lohia A., Foster P.G., Sichteritz-Ponten T., Weber C., Singh U.,
RA      Mukherjee C., El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M.,
RA      Barrell B.G., Fraser C.M., Hall N.;
RT      "The genome of the protist parasite Entamoeba histolytica.";
RL      Nature 433:865-868(2005).
CC      -i- CAUTION: The sequence shown here is derived from an
CC      EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC      preliminary data.
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CC      -----
DR      EMBL; AAFB01000933; BAL3605.1; -; Genomic_DNA.
DR      GO; GO:0005524; P:ATP binding; IEA.
DR      GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR      GO; GO:0004713; P:protein-tyrosine kinase activity; IEA.
DR      GO; GO:0004872; P:receptor activity; IEA.
DR      GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR      InterPro; IPR006212; Furin repeat.
DR      InterPro; IPR008271; Ser Thr pkin AS.
DR      InterPro; IPR002290; Ser Thr pkinase.
DR      InterPro; IPR001245; Tyr_pkinase.
DR      Pfam; PF02420; AFP; 1.
DR      Pfam; PF00069; Pkinase; 1.
DR      PRINTS; PR00109; TYRKINASE.
DR      ProDom; PD000001; Prot_kinase; 1.
DR      SMART; SM00261; FU; 1.
DR      PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR      PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR      PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR      KEGG; K04499; Receptor.
SQ      SEQUENCE 1150 AA; 128939 MW; 0DBE7051D4B4E286 CRC64;

Query Match      25.1%; Score 71; DB 2; Length 1150;
Best Local Similarity 35.3%; Pred. No. 7.7;
Matches 12; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

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```

RA      Gromadka R., Noel B., Blanc I., Dessen P., Wincker P., Keller A.M.,
RA      Cohen J., Meyer E., Sperling L.;
RT      "High Coding Density on the Largest Parametium tetraurelia Somatic
RT      Chromosome.";
RL      Curr. Biol. 14:1397-1404(2004).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=stock d4-2;
RA      Nowak J.K., Migdalski A., Gromadka R., Zagulski M.;
RT      "Parametium megabase sequencing project.";
RL      Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
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CC      -----
DR      EMBL; CR548612; CAH03606.1; -; Genomic_DNA.
DR      InterPro; IPR006058; 2Fe2S_fd_BS.
DR      InterPro; IPR006210; EGF.
DR      InterPro; IPR013032; EGF_like_reg.
DR      InterPro; IPR006212; Furin_repeat.
DR      SMART; SM00181; EGF; 4.
DR      SMART; SM00261; FU; 1.
DR      PROSITE; PS00197; 2Fe2S_FER_1; UNKNOWN_1.
DR      PROSITE; PS01186; EGF_2; 12.
SQ      SEQUENCE 3005 AA; 343824 MW; D8CC6A247876A5A5 CRC64;

Query Match      25.1%; Score 71; DB 2; Length 3005;
Best Local Similarity 35.6%; Pred. No. 21;
Matches 16; Conservative 8; Mismatches 11; Indels 10; Gaps 3;

OY      1 M1QWAGOC-SONEYPDSLHACIPCOLRCSSNTPPLTCQ--RYC 41
DB      1177 I1KVGNGCCKDGYPSSSTNQCICQLDLC-----FTCGSSSKYC 1215

RESULT 17
PCSK5_MOUSE STANDARD; PRT; 1877 AA.
AC      Q04592; Q62040;
DT      01-FEB-1995, integrated into UniProtKB/Swiss-Prot.
DT      11-JAN-2001, sequence version 2.
DT      07-MAR-2006, entry version 59.
DE      Proprotein convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-)
DE      (Proteinase convertase PCS) (Subtilisin/kexin-like protease PCS) (PC6)
DE      (Subtilisin-like proprotein convertase 6) (SPC6).
GN      Name=PCSK5;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridae; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [MRNA] OF 330-1877 (ISOFORM PCSB).
RC      STRAIN=ICR; TISSUE=Intestine;
RX      MEDLINE=93327934; PubMed=8355106; DOI=10.1016/0014-5793(93)80163-O;
RA      Nakagawa T., Murakami K., Nakayama K.;
RT      "Identification of an isoform with an extremely large Cys-rich region
RT      of PC6, a Kex2-like processing endoprotease.";
RL      FEBS Lett. 327:165-171(1993).
RN      [2]
RP      NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM PCSA).
RC      TISSUE=Brain, and Intestine;
RX      MEDLINE=93224489; PubMed=8468318;
RA      Nakagawa T., Hosaka M., Torii S., Watanabe T., Murakami K.,
RA      Nakayama K.;
RT      "Identification and functional expression of a new member of the
RT      mammalian Kex2-like processing endoprotease family: its striking
RT      structural similarity to PACB4.";
RL      J. Biochem. 113:132-135(1993).
RN      [3]
RP      NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM PCSA).
RC      TISSUE=Adrenal cortex;
RX      MEDLINE=93342056; PubMed=8341687;

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FT SEQUENCE 1877 AA; 209289 MW; EC850E2DF20BA1C3 CRC64;
SQ
Query Match 24.9%; Score 70.5; DB 1; Length 1877;
Best Local Similarity 34.7%; Pred. No. 15;
Matches 17; Conservative 5; Mismatches 22; Indels 5; Gaps 1;

OY 7 QCSQNEYPDSLHACIPCOLRCSSNTP-----LTCQRYCNASVTSVK 50
DB 1480 ECAAVGYWBGSHRCPCCHKKRCRCGSPBEDQCYTCPRETFILNTTCVK 1528

RESULT 18
OYR6J7 GIALA PRELIMINARY; PRT; 1025 AA.
AC OYR6J7
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE GLP_170_141434_144511.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardia.
OX NCBI_TaxID=184922;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.,
RT "Draft sequence of the Giardia lamblia genome."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AACB01000001; BAA43000.1; -; Genomic_DNA.
DR HSSP; Q9S7B3; IEHD.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR002049; EGF_lamblin.
DR InterPro; IPR006212; Furin_repeat.
DR SMART; SM00261; FU; 2.
DR PROSITE; PS01248; EGF_IAM_1; UNKNOWN_1.
SQ SEQUENCE 1025 AA; 109045 MW; 36281DF3FE2DDB43 CRC64;

Query Match 24.7%; Score 70; DB 2; Length 1025;
Best Local Similarity 24.2%; Pred. No. 9.1;
Matches 15; Conservative 8; Mismatches 19; Indels 20; Gaps 2;

OY 4 MAGQCSQNEYPDSLHACIPCOLRCSS-----NTPLTCQRYCNASV 45
DB 75 ICSSCTDDYLDLSLFGCFSCHSSCTCGSPHFDCITCGVGLBESSPSACP--CDLQI 132

OY 46 TN 47
DB 133 TN 134

RESULT 19
OY99ND0 MOUSE PRELIMINARY; PRT; 5374 AA.
AC OY99ND0;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE ZAN (Zonadhesin).
GN Name=Zan;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
```

```
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/Sv;
RX MEDLINE=21139439; PubMed=11239002; DOI=10.1093/nar/29.6.1352;
RA Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,
RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
RA Miller W., Koop B.F.;
RT "Comparative analysis of the gene-dense ACHE/TFR2 region on human
RT chromosome 7q22 with the orthologous region on mouse chromosome 5."
RL Nucleic Acids Res. 29:1352-1365(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/Sv;
RA Cheung T.L., Wilson M.D., Koop B.F., Hardy D.M.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AF312033; AAK28824.1; -; Genomic_DNA.
DR EMBL; AY046056; AAL04416.1; -; Genomic_DNA.
DR HSSP; Q90248; IHX2.
DR Ensembl; ENSMUSG00000059973; Mus musculus.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007339; P:binding of sperm to zona pellucida; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR000742; EGF_3.
DR InterPro; IPR006209; EGF_1like.
DR InterPro; IPR013032; EGF_1like_reg.
DR InterPro; IPR003645; FOL_N.
DR InterPro; IPR000998; MAM.
DR InterPro; IPR002919; Prot_inh_CR_TIL.
DR InterPro; IPR003328; TILA_Cysrich.
DR InterPro; IPR006552; WVC_out.
DR InterPro; IPR001007; WVF_C.
DR InterPro; IPR001846; WVF_D.
DR Pfam; PF02363; C_triplex; 20.
DR Pfam; PF03128; CRXCXC; 11.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00629; MAM; 3.
DR Pfam; PF01826; TIL; 25.
DR Pfam; PF02345; TIL_assoc; 25.
DR Pfam; PF00094; VMD; 4.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00214; WVC; 18.
DR SMART; SM00215; WVC_out; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 18.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS00740; MAM_1; 1.
DR PROSITE; PS00060; MAM_2; 3.
SQ SEQUENCE 5374 AA; 579550 MW; 90D2D8CFE5DE24EB CRC64;

Query Match 24.6%; Score 69.5; DB 2; Length 5374;
Best Local Similarity 36.8%; Pred. No. 60;
Matches 14; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

OY 7 QCSQNEYPDSLHACIP--COLRCSSNTP--PLTCQRYC 41
DB 3297 QCPTNSQFTDCLPSCVPCSCNRCEVTSBPSPSCREGC 3334

RESULT 20
ZAN_MOUSE STANDARD; PRT; 5376 AA.
ID ZAN_MOUSE
AC O88799; O08647;
DT 27-APR-2001, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1998, sequence version 1.
DT 07-MAR-2006, entry version 50.
DE Zonadhesin precursor.
GN Name=Zan;
```


FT CARBOHYD 5136 5136 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 5252 5252 N-linked (GlcNAc...) (Potential).
FT DISULFID 5263 5274 By similarity.
FT DISULFID 5268 5283 By similarity.
FT DISULFID 5285 5294 By similarity.
SQ SEQUENCE 5376 AA; 579913 MW; 0E44DB77DF2A2620 CRC64;

Query Match 24.6%; Score 69.5; DB 1; Length 5376;
Best Local Similarity 36.8%; Pred. No. 60;
Matches 14; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

Qy 7 QCSQNEYPDSLHACIP-COLRCSNTP-PLTCQRYC 41
Db 3299 QCPNTOFTDCLPSCVPCSCNRCVTPSPVPSRCRG 3336

RESULT 21
Q3CXH7 ALTYAT PRELIMINARY; PRT; 544 AA.
AC Q3CXH7;
DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 22-NOV-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Electron-transferring-flavoprotein dehydrogenase (EC 1.5.5.1).
GN ORFNames=PatIDAF_0751;
OS Pseudomonas atlantica T6c.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Pseudomonadaceae; Pseudomonadaceae.
OX NCBI_TaxID=342610;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=T6c;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Campbell N., Lucas S., Lapidus A., Barry K., Dettler J.C., Glavina T.,
RA Hampton N., Istrati S., Plutnick S., Richardson P.;
RA "Sequencing of the draft genome and assembly of Pseudomonas atlantica T6c.";
RT Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=T6c;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RA "Annotation of the draft genome assembly of Pseudomonas atlantica T6c.";
RT Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.

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CC EMBL; AAKP0100001; EAO69851.1; Genomic DNA.
DR GO; GO:0004174; F-electron-transferring-flavoprotein dehydrog. .; IEA.
DR GO; GO:0016491; F-oxidoreductase activity; IEA.
DR GO; GO:0006118; P-electron transport; IEA.
DR GO; GO:0008152; P-metabolism; IEA.
DR GO; GO:0009228; P-thiamin biosynthesis; IEA.
KW Oxidoreductase.
SQ SEQUENCE 544 AA; 60059 MW; 5322D58507348A94 CRC64;

Query Match 24.4%; Score 69; DB 2; Length 544;
Best Local Similarity 28.6%; Pred. No. 63;
Matches 20; Conservative 6; Mismatches 18; Indels 26; Gaps 3;

Qy 2 LOMAGCCSNEY-----FDSLHACI-----PCQRCSSNTPPLT----- 36
Db 424 LKQAKCCQCRIDYPKYDVSFLKSSVFLSNTNHEEDPCCHKLKNTVPIVNLPLYDE 483
Qy 37 -CORYCNASV 45
Db 484 PAORICPAGV 493

RESULT 22
Q22378 CAEEL PRELIMINARY; PRT; 966 AA.
AC Q22378;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2001, sequence version 2.
DT 07-FEB-2006, entry version 37.
DE Hypothetical protein T10E10.4.
GN ORFNames=T10E10.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodietinae; Caenorhabditis.
OX NCBI_TaxID=6239;

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for investigating biology.";
RL Science 282:2012-2018(1998).

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CC EMBL; U39644; AAA80360.2; Genomic DNA.
DR PIR; T16840; T16840.
DR HSP; P10969; TWGT.
DR Intact; Q22378; -.
DR Ensemble; T10E10.4; Caenorhabditis elegans.
DR Wormbase; WBGenome0020421; T10E10.4.
DR GO; GO:0005576; C-cytoplasmic region; IEA.
DR GO; GO:0008061; P-chitin binding; IEA.
DR GO; GO:0006030; P-chitin metabolism; IEA.
DR InterPro; IPR006149; EB_region.
DR InterPro; IPR000794; Ketoacyl_synth.
DR InterPro; IPR002557; Pera_Chitin_bd.
DR InterPro; IPR003571; Snake_toxin.
DR InterPro; IPR006150; Worm_repeat_1.
DR Pfam; PF01607; CBM_14; 2.
DR Pfam; PF01683; EB; 1.
DR SMART; SM00289; WR1; 7.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
DR PROSITE; PS00272; SNAKE_TOXIN; UNKNOWN_1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 966 AA; 102461 MW; B565A3CDD25216D9 CRC64;

Query Match 24.2%; Score 68.5; DB 2; Length 966;
Best Local Similarity 36.2%; Pred. No. 13;
Matches 17; Conservative 10; Mismatches 15; Indels 5; Gaps 3;

Qy 7 QCSQNEYPDSLHACIPQRL-CSSNTPPLTCQRYCNASVTSYKG 51
Db 215 QCSQTFVNSDLNVCVPLAIONSCSSIQQPVCS--C-SQVSSCPG 258

RESULT 23
Q6W4X9 HUMAN PRELIMINARY; PRT; 1569 AA.
AC Q6W4X9;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Mucin glycoprotein (Fragment).
GN Name=MUC6;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Carnivora; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;

[1]
NM NUCLEOTIDE SEQUENCE.
RX PubMed=15081123; DOI=10.1016/j.ygeno.2003.11.003;
RA Rousseau K., Byrne C., Kim Y.S., Gum J.R., Swallow D.M.,
RA Toribara N.W.,
RT "The complete genomic organization of the human MUC6 and MUC2 mucin
RT genes".
RL Genomics 83:936-939 (2004).
CC -----
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CC -----
CC EMBL; AY312160; AA082434.1; -; mRNA.
DR HGNC; HGNC:7517; MUC6.
DR InterPro; IPR002919; Prot Inh_CR_TIL.
DR InterPro; IPR006552; Prot Out.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF01826; TIL; 2.
DR Pfam; PF00094; VWD; 3.
DR SMART; SM00216; VWD; 3.
DR NON TER 1569 1569
SQ SEQUENCE 1569 AA; 168066 MW; 6AEDEE143ECB855B CRC64;

Query Match 24.2%; Score 68.5; DB 2; Length 1569;
Best Local Similarity 45.2%; Pred. No. 22;
Matches 14; Conservative 2; Mismatches 8; Indels 7; Gaps 1;

QY 8 CSONEYPDSLHACIPCOLRGSSNTPPLTCQ 38
Db 1179 CSQDEYFDHBEQVCPDM-----PPTTPQ 1202
|||:|||||:|||||
RESULT 24
TR13B HUMAN STANDARD; PRT; 293 AA.
ID TR13B HUMAN
AC O14836; Q726F5; Integrated into UniProtKB/Swiss-Prot.
DT 01-JAN-2002, entry version 1.
DT 07-FEB-2006, entry version 45.
DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane
DE activator and CAML interactor) (CD267 antigen).
GN Name=TNFRSF13B; Synonyms=TACI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
CX NCBI_TaxID=9606;
NM NM NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RP TISSUE=B-cell;
RC MEDLINE=97458245; PubMed=9311921; DOI=10.1126/science.278.5335.138;
RA von Buehlow G.-U., Bram R.J.;
RT "NF-AT activation induced by a CAML-interacting member of the tumor
RT necrosis factor receptor superfamily.";
RL Science 278:138-141 (1997).
RN NM NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).
RA Zhou G., Ke R., Li H., Zheng G., Shen C., Lin L., Yang S.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN NM
RP FUNCTION.
RX MEDLINE=20519647; PubMed=10956646; DOI=10.1074/jbc.M005224200;
RA Wu Y., Bressette D., Carrell J.A., Kaufman T., Feng P., Taylor K.,
RA Gu Y., Cho Y.H., Garcia A.D., Gollatz E., Dimke D., Laflleur D.,
RA Mignone T.S., Nardelli B., Wei P., Ruben S.M., Ullrich S.J.,
RA Olsson H.S., Kanakaraj P., Moore P.A., Baker K.P.;
RT "Tumor necrosis factor (TNF) receptor superfamily member TACI is a
RT high affinity receptor for TNF family members APRIL and Blys.";
RL J. Biol. Chem. 275:35478-35485 (2000).
RN NM
RP FUNCTION.
RX MEDLINE=21170294; PubMed=10973384; DOI=10.1038/79802;
RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M.,

RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
RA Boyle W.J., Sarsel I., Hsu H., Senaldi G., Thell L.E.;
RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
RT humoral immunity".
RL Nat. Immunol. 1:252-256 (2000).
RN NM
RP INTERACTIONS WITH TRAF2 AND TRAF5.
RX MEDLINE=20341628; PubMed=10880535; DOI=10.1084/jem.192.1.137;
RA Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,
RA Thell L.E., Colombero A., Solovjev I., Lee F., McCabe S., Elliott R.,
RA Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J.,
RA Meng S.-Y., Boyle W.J., Hsu H.;
RT "TACI is a TRAF-interacting receptor for TALL-1, a tumor necrosis
RT factor family member involved in B cell regulation.";
RL J. Exp. Med. 192:137-143 (2000).
RN NM
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 68-109, AND STRUCTURE BY NMR
RP OF 68-109.
RX PubMed=15542592; DOI=10.1074/jbc.M411714200;
RA Hymowitz S.G., Patel D.R., Wallweber H.J., Runyon S., Yan M., Yin J.,
RA Shriver S.K., Gordon N.C., Pan B., Skelton N.J., Kelley R.F.,
RA Starovasnik M.A.;
RT "Structures of APRIL-receptor complexes: like BCMA, TACI employs only
RT a single cysteine-rich domain for high affinity ligand binding.";
RL J. Biol. Chem. 280:7218-7227 (2005).
RN NM
RP VARIANT CVID/IGAD2 ARG-104, AND VARIANTS CVID GLY-181 AND HIS-202.
RX PubMed=16007086; DOI=10.1038/ng1601;
RA Castigli E., Wilson S.A., Garibyan L., Rachid R., Bonilla F.,
RA Schneider L., Geha R.S.;
RT "TACI is mutant in common variable immunodeficiency and Iga
RT deficiency.";
RL Nat. Genet. 37:829-834 (2005).
RN NM
RP FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAPF/Blys
CC that binds both ligands with similar high affinity. Mediates
CC calcineurin-dependent activation of NF-AT, as well as activation
CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
CC cell function and the regulation of humoral immunity.
CC -1 SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
CC domain of CAMLG with its C-terminus.
CC -1 INTERACTION:
CC O75888:TNFSF13; NbExp=1; InChI=EBI-519160, EBI-519208;
CC O91275:TNFSF13B; NbExp=4; InChI=EBI-519160, EBI-519169;
CC -1 SUBCELLULAR LOCATION: Membrane; single-pass type III membrane
CC protein.
CC -1 ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O14836-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O14836-2; Sequence=VSP_013798;
CC -1 TISSUE SPECIFICITY: Highly expressed in spleen, thymus, small
CC intestine and peripheral blood leukocytes. Expressed in resting B-
CC cells and activated T-cells, but not in resting T-cells.
CC -1 DISEASE: Defects in TNFRSF13B are a cause of common variable
CC immunodeficiency (CVID) [MIM:240500]. CVID is characterized by a
CC deficiency in all immunoglobulin (Ig) isotypes. Individuals with
CC CVID suffer from recurrent sinopulmonary and gastrointestinal
CC infections and have an increased incidence of autoimmune disorders
CC and of lymphoid and nonlymphoid malignancies. There is evidence
CC for a global isotype switching defect in some individuals with
CC CVID. But CVID is a complex and heterogeneous disease in which
CC defects in B-cell survival, number of circulating CD27+ memory B
CC cells (including IgM+CD27+ B cells), B-cell activation after
CC antigen receptor cross-linking, T-cell signaling and cytokine
CC expression have been observed.
CC -1 DISEASE: Defects in TNFRSF13B are a cause of immunoglobulin A
CC deficiency 2 (IGAD2) [MIM:609529]. Selective deficiency of
CC immunoglobulin A (IgA) is the most common form of primary
CC immunodeficiency, with an incidence of approximately 1 in 600
CC individuals in the western world. Individuals with symptomatic
CC IGAD often have deficiency of IgG subclasses or decreased antibody
CC response to carbohydrate antigens such as pneumococcal

polysaccharide vaccine. Individuals with IGAD also suffer from recurrent sinuopulmonary and gastrointestinal infections and have an increased incidence of autoimmune disorders and of lymphoid and nonlymphoid malignancies. In vitro studies have suggested that some individuals with IGAD have impaired isotype class switching to IgA and others may have a post-switch defect. IGAD and CVID have been known to coexist in families. Some individuals initially present with IGAD1 and then develop CVID. These observations suggest that some cases of IGAD and CVID may have a common etiology.

 -1- SIMILARITY: Contains 2 TNFR-Cys repeats.

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 CC
 CC EMBL: AF023614; AAC51790.1; -; mRNA.
 CC EMBL: AY302137; AAP57629.1; -; mRNA.
 CC PDB: 1XU1; X-ray; R/S/T=68-109.
 CC PDB: 1XU1; NMR; A=68-109.
 CC DR Ensembl: ENSG00000108516; Homo sapiens.
 CC DR HGNC: HGNC:18153; TNFRSF13B.
 CC MIM: 240500; phenotype.
 CC MIM: 604907; gene.
 CC MIM: 609529; phenotype.
 CC DR GO: GO:0005887; C:integral to plasma membrane; TAS.
 CC DR GO: GO:0005515; F:protein binding; IPI.
 CC DR GO: GO:0004872; F:receptor activity; TAS.
 CC DR GO: GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
 CC DR InterPro: IPR001368; TNFR_C6.
 CC DR PROSITE: PS00652; TNFR_NGFR_1; 1.
 CC DR PROSITE: PS00650; TNFR_NGFR_2; FALSE NEG.
 CC DR 3D-structure; Alternative splicing; Disease mutation; Glycoprotein; Immune response; Membrane; Receptor; Repeat; Signal-anchor; Transmembrane.
 KM CHAIN 1 293
 FT
 FT
 FT TOPO_DOM 1 165
 FT TRASMEM 166 186
 FT
 FT TOPO_DOM 187 293
 FT REPEAT 33 67
 FT REPEAT 70 104
 FT CARBOHYD 128 128
 FT DISULFID 34 47
 FT DISULFID 50 62
 FT DISULFID 54 66
 FT DISULFID 71 86
 FT DISULFID 89 100
 FT DISULFID 93 104
 FT VARSPLIC 21 67
 FT
 FT
 FT VARIANT 104 104
 FT
 FT VARIANT 181 181
 FT
 FT VARIANT 202 202
 FT
 FT STRAND 66 66
 FT TURN 67 68
 FT HELIX 73 75
 FT TURN 76 76
 FT STRAND 77 80
 FT TURN 81 84
 FT STRAND 85 88
 FT HELIX 89 92
 FT TURN 93 94
 FT STRAND 95 95
 FT HELIX 98 104
 SO SEQUENCE 293 AA; 31816 MW; 411799F3DE17A5EB CRC64;

Query Match 23.9%; Score 67.5; DB 1; Length 293;
 Best Local Similarity 30.6%; Pred. No. 5;
 Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 8 CSQNEYPDSLHACIPQQLRGSSNTPPLTCQRYCNA 43
 DB 34 CPBEQYWDPLGTGTCMSCKTICNHOS-ORTCAFCRS 68

RESULT 25
 Q4ACX1_HUMAN PRELIMINARY; PRT; 293 AA.
 ID Q4ACX1;
 AC Q4ACX1;
 DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
 DT 13-SEP-2005, sequence version 1.
 DT 07-FEB-2006, entry version 2.
 DE TACI.
 GN Name=TACI;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN
 RP NUCLEOTIDE SEQUENCE.
 RA Kawasaki A., Tsuchiya N., Kusaoi M., Murakami Y., Fukazawa T.,
 RA Matsuta K., Hashimoto H., Tokunaga K.;
 RT "New polymorphisms of human BAF-R gene."
 RL Submitted (JUL-2005) to the EMBL/Genbank/DBD databases.
 RN
 RP NUCLEOTIDE SEQUENCE.
 RA Kawasaki A., Tsuchiya N., Kusaoi M., Murakami T., Fukazawa T.,
 RA Matsuta H., Hashimoto H., Tokunaga K.;
 RT "New polymorphisms of human TACI gene."
 RL Submitted (JUL-2005) to the EMBL/Genbank/DBD databases.
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 CC EMBL: AB222991; BAB1655.1; -; Genomic DNA.
 CC DR InterPro: IPR001368; TNFR_C6.
 CC DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN 1.
 CC DR PROSITE: PS00652; TNFR_NGFR_2; FALSE NEG.
 SO SEQUENCE 293 AA; 31816 MW; 411799F3DE17A5EB CRC64;

Query Match 23.9%; Score 67.5; DB 2; Length 293;
 Best Local Similarity 30.6%; Pred. No. 5;
 Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 8 CSQNEYPDSLHACIPQQLRGSSNTPPLTCQRYCNA 43
 DB 34 CPBEQYWDPLGTGTCMSCKTICNHOS-ORTCAFCRS 68

RESULT 26
 Q53F36_HUMAN PRELIMINARY; PRT; 293 AA.
 ID Q53F36;
 AC Q53F36;
 DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 24-MAY-2005, sequence version 1.
 DT 07-FEB-2006, entry version 4.
 DE Tumor necrosis factor receptor 13B variant (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Small intestine;
 RX MEDLINE=94171032; PubMed=8125298; DOI=10.1016/0378-1119(94)90802-8;
 RA Maruyama K., Sugano S.;
 RT "Oligo-capping: a simple method to replace the cap structure of eucaryotic mRNAs with oligoribonucleotides.";

RL Gene 138:171-174(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Small intestine;
RX MEDLINE=98038986; PubMed=9373149; DOI=10.1016/S0378-1119(97)00411-3;
RA Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano S.;
RT "Construction and characterization of a full length-enriched and a 5'-
RL end-enriched cDNA library.";
RN Gene 200:149-156(1997).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Small intestine;
RA Tokoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.;
RL Submitted (Apr-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL: AK223453; BAD97173.1; -; mRNA.
DR Ensembl: ENSG00000108516; Homo sapiens.
DR GO: GO:0004872; F:receptor activity; IEA.
DR InterPro: IPR001368; TFR G6.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
KM Receptor.
FT NON_TER
SQ SEQUENCE 293 AA; 31846 MW; D9EA2F28B3BFA66D CRC64;

Query Match 23.9%; Score 67.5; DB 2; Length 293;
Best Local Similarity 30.6%; Pred. No. 5;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

OY 8 CSQNEYFDSLHACIPQCRCSNTPPLTCQRYCNA 43
DB 34 CPBQYMDPLGTCTCMSCRTICNHQS-QRTCAFCSS 68

RESULT 27
O60WC9 CAEBR PRELIMINARY; PRT; 135 AA.
ID O60WC9 CAEBR
AC O60WC9;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Hypothetical protein CBG19174.
GN Name=CBG19174;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=AF16;
RX PubMed=14624247; DOI=10.1371/journal.pbio.0000045;
RA Stein L.D., Bao Z., Blaetler D., Blumenthal T., Brent M.R., Chen N.,
RA Chirwalla A., Clarke L., Clee C., Coghlan A., Coulson A.,
RA D'Eustachio P., Fitch D.H.A., Fulton L.A., Fulton R.E.,
RA Griffiths-Jones S., Harris T.W., Hillier L.W., Kamath R.,
RA Kuvshinov P.E., Mardis E.R., Marra E.R., Schein J.E., Soliman M.,
RA Smith J.C., Plumb R.W., Rogers J., Schen J.E., Soliman M.,
RA Speth J., Stajich J.E., Wei C., Willey D., Wilson R.K., Durbin R.,
RA Waterston R.H.;
RT "The genome sequence of *Caenorhabditis briggsae*: a platform for
RT comparative genomics.";
RL PLoS Biol. 1:166-192(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC EMBL: CAAC0100098; CAE72086.1; -; Genomic DNA.
DR InterPro: IPR013032; BGF_like_reg.

DR InterPro: IPR002919; Prot_Inh_CR_TIL.
DR Pfam: PF01826; TIL; 2.
DR PROSITE: PS01186; EGF 2; UNKNOWN 2.
KM Complete proteome; Hypothetical Protein.
SQ SEQUENCE 135 AA; 14981 MW; 74B210602AF39B6 CRC64;

Query Match 23.7%; Score 67; DB 2; Length 135;
Best Local Similarity 34.8%; Pred. No. 2.6;
Matches 16; Conservative 5; Mismatches 19; Indels 6; Gaps 2;

OY 7 QCSQNEYFDSLHACIP-QCRCSNTPPLTCQRYCNA SYNVKG 51
DB 79 KCPQNEQFRGGCTACEPYCE-----NPKPMACTQCTIINVCQCAKG 119

RESULT 28
O17496 ASCSU PRELIMINARY; PRT; 532 AA.
ID O17496 ASCSU
AC O17496;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1999, sequence version 2.
DT 21-FEB-2006, entry version 30.
DE Serotonin receptor.
DE Ascaris sum (Pig roundworm) (Ascaris lumbricoidea).
OS Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99339391; PubMed=10413046; DOI=10.1016/S0166-6851(99)00059-6;
RA Huang X., Duran E., Diaz F., Xiao H., Messer W.S., Jr., Komuniecki R.;
RT "Alternative-splicing of serotonin receptor isoforms in the pharynx
RT and muscle of the parasitic nematode, *Ascaris sum*.";
RL Mol. Biochem. Parasitol. 101:95-106(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22311325; PubMed=12423236;
RA Huang X., Xiao H., Rex E.B., Hobson R.J., Messer W.S.,
RA Komuniecki P.R., Komuniecki R.W.;
RT "Functional characterization of alternatively spliced 5-HT2 receptor
RT isoforms from the pharynx and muscle of the parasitic nematode,
RT *Ascaris sum*.";
RL J. Neurochem. 83:249-258(2002).
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -!- SUBCELLULAR LOCATION: Membrane (by similarity).
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CC -----
CC EMBL: AF005486; AAC78396.1; -; mRNA.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signaln. . .; IEA.
DR GO: GO:0007185; P:signal transduction; IEA.
DR InterPro: IPR00276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G-PROTEIN RECP_F1_1; 1.
DR PROSITE: PS00262; G-PROTEIN RECP_F1_2; 1.
KM G-protein coupled receptor; Membrane; Receptor; Transducer;
KW Transmembrane.
SQ SEQUENCE 532 AA; 60141 MW; 4D795D1C249D55F6 CRC64;

Query Match 23.7%; Score 67; DB 2; Length 532;
Best Local Similarity 23.8%; Pred. No. 11;
Matches 15; Conservative 14; Mismatches 14; Indels 20; Gaps 2;

OY 3 QMAGCCSNEYFDSLHACIPQ-----LRCSNTPPLTCQRYCNA SVTN 47
DB 434 KMGVCKRGEYWSN-----VSCRSRNEFVLTDRQLDNVKTTSERPLTCGKHCNSSSGN 488

QY 48 SVK 50
DB 489 SLQ 491

RESULT 29

054XL6_DICDI PRELIMINARY; PRT; 574 AA.
AC 054XL6;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 21-FEB-2006, entry version 11.
DE Hypothetical protein DDB0230012.
GN Name=DDB0230012; ORFNames=DDB0230012;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Eukaryota; Dictyosteliales; Dictyostelium.
OX NCBI_TaxId=4689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RX PubMed=15875012; DOI=10.1038/nature03481;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.A.,
RA Suckag R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E.J., Davis P.,
RA Kerhrou A., Nie X., Hall N., Anjard C., Hemphill L., Bacon N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.M.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D.M., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K.D., Quiles M., Madan Babu M., Salto T.,
RA Buchteser C., Wardrop A., Felder M., Thangavelu M., Johnson D.,
RA Knights A., Louised H., Mungall K.L., Oliver K., Price C.,
RA Quail M.A., Urushihara H., Hernandez J., Rabinowitsch E., Steffen D.,
RA Sanders M., Ma J., Kohara Y., Sharp S., Simmonds M.N., Spegler S.,
RA Tiver A., Sugano S., White B., Walker D., Woodward J.R., Winckler T.,
RA Tanaka Y., Shaulsky G., Schleicher M., Weinstock G.M., Rosenthal A.,
RA Cox E.C., Chisholm R.L., Gibbs R.A., Loomis W.F., Platzer M.,
RA Kay R.R., Williams J.G., Dear P.H., Noegel A.A., Barrell B.G.,
RA Kasper A.;
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 435:43-57(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
CC EMBL; AAF10100053; EMBL68033.1; -; Genomic DNA.
CC DR GO; GO:0005524; F:ATP binding; IEA.
CC DR GO; GO:000166; F:nucleotide binding; IEA.
CC DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
CC DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
CC DR GO; GO:0016740; F:transferase activity; IEA.
CC DR GO; GO:0004668; P:protein amino acid phosphorylation; IEA.
CC DR InterPro; IPR000719; Prot kinase.
CC DR InterPro; IPR002290; Ser Thr kinase.
CC DR InterPro; IPR001245; Tyr kinase.
CC DR Pfam; PF00069; Kinase; I.
CC DR PRINTS; PR00109; TYRKINASE.
CC DR PRODOM; PD000001; Prot kinase; 1.
CC DR SMART; SM00220; S_TKc; 1.
CC DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
CC DR ATP-binding; Hypothetical protein; Kinase; Nucleotide-binding;
CC KW Serine/threonine-protein kinase; Transferase;
CC SEQUENCE 574 AA; 64223 MW; 9D344378077A91C8 CRC64;

Query Match 23.7%; Score 67; DB 2; Length 574;
Best Local Similarity 35.7%; Pred. No. 12;
Matches 20; Conservative 6; Mismatches 16; Indels 14; Gaps 3;

QY 7 QCSQNEYPDS-LHACIPQOLR-----CSSNTP-----PLTCQRYCNASTVNS 48

DB 359 QAKNNYIVSHLHGLTPCEDRYRESMSPASSNTSPSSRPSSPHYHNGVNS 414

RESULT 30

Q4N599_THEPA PRELIMINARY; PRT; 1562 AA.
AC Q4N599;
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 02-AUG-2005, sequence version 1.
DT 21-FEB-2006, entry version 7.
DE ABC transporter, putative.
GN ORFNames=TP02_0391;
OS Theileria parva.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
OC Theileria.
OX NCBI_TaxId=5875;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga;
RX PubMed=15994558; DOI=10.1126/science.1110439;
RA Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,
RA Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shalom S.J., Weidman J.,
RA Jiang L., Lynn J., Weaver B., Shoabli A., Domingo A.R., Wasawo D.,
RA Crabtree J., Wortman J.R., Haas B., Angiolini S.V., Creasy T.H., Lu C.,
RA Suh B., Silva J.C., Utterback T.R., Feldblyum T.V., Pettea M.,
RA Allen J., Nieman M.C., Taracha E.L., Salzberg S.L., White O.R.,
RA Fitzhugh H.A., Morzaria S., Venter J.C., Fraser C.M., Nene V.;
RT "Genome Sequence of Theileria parva, a Bovine Pathogen That Transforms
RT Lymphocytes.";
RL Science 309:134-137(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga;
RA Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
RA Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
RA Ralph S.A., Mann D.J., Xiong Z., Shalom S.J., Weidman J., Jiang L.,
RA Lynn J., Weaver B., Shoabli A., Masawo D., Crabtree J., Wortman J.R.,
RA Haas B., Angiolini S., Creasy T.H., Lu C., Suh B., Silva J.C.,
RA Utterback T., Feldblyum T., Pettea M., Allen J., Taracha E.L.,
RA Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
RA Fraser C.M., Nene V.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC -!- SIMILARITY: Belongs to the ABC transporter family.
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CC -----
CC EMBL; AAKG01000002; EMBL32674.1; -; Genomic DNA.
CC DR GO; GO:0016021; C:integral to membrane; IEA.
CC DR GO; GO:0005524; F:ATP binding; IEA.
CC DR GO; GO:0016887; F:ATPase activity; IEA.
CC DR GO; GO:0046262; F:ATPase activity; IEA.
CC DR GO; GO:000166; F:nucleotide binding; IEA.
CC DR GO; GO:0006810; P:transporter; IEA.
CC DR InterPro; IPR003593; AAA_ATPase.
CC DR InterPro; IPR011527; ABC_TM_1.
CC DR InterPro; IPR003439; ABC_tranp_1like.
CC DR Pfam; PF00005; ABC_tran; 2.
CC DR SMART; SM00382; AAA; 2.
CC DR PROSITE; PS00929; ABC_TM1F; 1.
CC DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
CC DR PROSITE; PS00893; ABC_TRANSPORTER_2; 2.
CC DR ATP-binding; Membrane; Nucleotide-binding; Transport.
CC KW ATP-binding; Membrane; Nucleotide-binding; Transport.
CC SEQUENCE 1562 AA; 179264 MW; 44A17485D05BF8A0 CRC64;

Query Match 23.5%; Score 66.5; DB 2; Length 1562;
Best Local Similarity 30.9%; Pred. No. 39;
Matches 17; Conservative 12; Mismatches 9; Indels 17; Gaps 4;

QY 7 QCSQNEYPDS-LHACIPQOLR-----CSSNTP-----PLTCQRYCNASTVNS 48

```
OY 6 GQCSQNEVF-----DSLHACIPCOLRCSNTPLTLC--QRYCNASVT 46
Db 233 GLCTRRKRFNNVKGNSVNLVNCNSVHSCSP-ESKSEN--PLYCAPRRFONSDDIT 284

RESULT 31
O55NL5 CRYNE PRELIMINARY; PRT; 861 AA.
AC O55NL5-
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Hypothetical protein.
GN ORFNames=CNBH0730;
OS Cryptococcus neoformans var. neoformans B-3501A.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OC NCBI_TaxId=283643;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B-3501A;
RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
Wicks B.L., Fu J., Davis R.W.;
RT "Cryptococcus neoformans serotype D sequencing.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
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DR EMBL: AAEY01000041; EAL19380.1; -; Genomic DNA.
DR InterPro: IPR006210; EGF_3.
DR InterPro: IPR000742; EGF_3.
DR InterPro: IPR002049; EGF_laminin.
DR InterPro: IPR013032; EGF_like_reg.
DR InterPro: IPR006212; Furin_repeat.
DR Pfam: PF00008; EGF_1.
DR SMART: SM00181; EGF_3.
DR SMART: SM00261; FU; 2.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS50026; EGF_3; 1.
DR PROSITE: PS01248; EGF_LAM_1; UNKNOWN_1.
DR PROSITE: PS01248; EGF_LAM_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 861 AA; 93347 MW; 8745729FBD869366 CRC64;

Query Match 23.3%; Score 66; DB 2; Length 861;
Best Local Similarity 34.8%; Pred. No. 24;
Matches 16; Conservative 6; Mismatches 24; Indels 0; Gaps 0;

OY 6 GQCSQNEVFDSLHACIPCOLRCSNTPLTLCQRYCNASVTVSKG 51
Db 319 GTCSSGLVYDSTSTSCSPSCSPCTGTGTDCSCASPRVNLQG 364

RESULT 32
O26489 SPOFR PRELIMINARY; PRT; 1299 AA.
AC O26489;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 34.
DE Endoprotease FURIN.
GN Name=FURIN;
OS Spodoptera frugiperda (Fall armyworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Amphipyrinae; Spodoptera.
OC NCBI_TaxId=7108;
RN [1]
```

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RP NUCLEOTIDE SEQUENCE.
RC Tissue=sf9;
RA Cieplik M., Klenk H.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
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-----
DR EMBL: Z68888; CAA93116.1; -; mRNA.
DR PIR: T43251; T43251.
DR HSP; P23188; 1P87.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0008233; F:peptidase activity; IEA.
DR GO: GO:0004289; F:subtilase activity; IEA.
DR GO: GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO: GO:0006508; P:proteolysis; IEA.
DR GO: GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR InterPro: IPR006211; Furin-like.
DR InterPro: IPR006212; Furin_repeat.
DR InterPro: IPR002029; Pept_58_553.
DR InterPro: IPR002884; P:protonconvertsp.
DR Pfam: PF00757; Furin-like; 1.
DR Pfam: PF01483; P:proteolisin; 1.
DR Pfam: PF00082; Peptidase_S8; 1.
DR PRINTS: PR00723; SUBTILISIN.
DR SMART: SM00261; FU; 10.
DR PROSITE: PS00136; SUBTILASE_ASP; UNKNOWN_1.
DR PROSITE: PS00137; SUBTILASE_HIS; 1.
DR PROSITE: PS00138; SUBTILASE_SER; 1.
DR HYDROLASE; Protease; Serine protease.
SQ SEQUENCE 1299 AA; 142020 MW; 4C3799C7B8C572AB CRC64;

Query Match 23.1%; Score 65.5; DB 2; Length 1299;
Best Local Similarity 34.0%; Pred. No. 43;
Matches 18; Conservative 8; Mismatches 14; Indels 13; Gaps 4;

OY 8 GQNEVFPSLHACIPCOLRCS-----SNTPLTLCQRYCNAS---VTNSVKG 51
Db 1150 CSRPLRIRLNNQCPC---CSERGVTNTPPTDC-CHCNENGRCSINSVAG 1198

RESULT 33
O3K8P9 PSEPF PRELIMINARY; PRT; 554 AA.
AC O3K8P9;
ID O3K8P9 PSEPF
DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 08-NOV-2005, sequence version 1.
DE Electron transfer flavoprotein-ubiquinone oxidoreductase.
GN OrderedLocNames=Pfl 4118;
OS Pseudomonas fluorescens (strain PFO-1).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OC NCBI_TaxId=205922;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG US DOE Joint Genome Institute;
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler J.C., Glavina T.,
Hannon N., Istrati S., Pittlides S., Saunders E.H., Schmutz J.P.,
Larimer F., Land M., Kyriakides N., Anderson I., Richardson P.;
RT "Complete sequence of Pseudomonas fluorescens PFO-1."
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
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DR EMBL: CP000094; ABA75855.1; -; Genomic DNA.
DR GO: GO:0004174; F:electron-transferring-flavoprotein dehydrog. . .; IEA.
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
```

DR Interpro; IPR007859; ETEP.
 DR Interpro; IPR006076; Fad_oxred.
 DR Interpro; IPR00103; Pyridine_redox_2.
 DR Interpro; IPR003042; Rng_hydrolase.
 DR Pfam; PF01266; DAO_1.
 DR Pfam; PF05187; ETE_QO_1.
 DR PRINTS; PR00469; PNDRTASEII.
 DR PRINTS; PR00420; RNCNOMXGNASE.
 KW Complete proteome; Ubiquitome.
 SQ SEQUENCE 554 AA; 60840 MW; 333845A105D7744F CRC64;

Query Match 23.0%; Score 65; DB 2; Length 554;
 Best Local Similarity 28.6%; Pred. No. 20;
 Matches 20; Conservativity 7; Mismatches 17; Indels 26; Gaps 3;

OY 2 LOMAGGCSONEY-----FDLTHACT-----PCQLRCSSTPPLT----- 36
 DB 434 LKLAADCKRIDPKPDGKISFDKLSVFIISGTHNEEPOCHLKTPTTIPLSKNPLDYDE 493
 OY 37 -CORYCNASV 45
 DB 494 PAORYCPAGV 503

RESULT 34
 STAB2 HUMAN
 ID STAB2 HUMAN STANDARD; PRT; 2551 AA.
 AC 08MM05; 06ZMK2; 07ZSN9; 08IUG9; 08TES1; 09H7H7; 09NRY3;
 DT 19-JUL-2004, integrated into UniProtKB/Swiss-Prot.
 DT 19-JUL-2004, sequence version 2.
 DT 07-MAR-2006, entry version 34.
 DE Stabillin-2 precursor (FEEL-2 protein) (Fasciclin EGF-like laminin-type
 DE EGF-like and link domain-containing scavenger receptor 1) (FAS1 EGF-
 DE like and X-link domain-containing adhesion molecule 2) (Hyaluronan
 DE receptor for endocytosis) [contains: 190 kDa form stabillin-2 (190 kDa
 DE hyaluronan receptor for endocytosis)].
 GN Name=STAB2; Synonyms=FEEL2, FELU, FEK2, HARE;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RX MEDLINE=21818465; PubMed=11829752; DOI=10.1042/0264-6021.3620155;
 RA Politz O., Gratchev A., McCourt P.A.G., Schlichtzewska K., Guillot P.,
 RA Johansson S., Sviheng G., Franke P., Kamisch C., Kzyzhkovska J.,
 RA Longati P., Velten F.W., Johansson S., Goerd S.,
 RA "Stabillin-1 and -2 constitute a novel family of fasciclin-like
 RA hyaluronan receptor homologues.";
 RL Biochem. J. 362:155-164(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [MRNA], AND FUNCTION.
 RX MEDLINE=22206516; PubMed=12077138; DOI=10.1074/jbc.M204277200;
 RA Adachi H., Tsujimoto M.,
 RA "FEEL-1, a novel scavenger receptor with in vitro bacteria-binding and
 RA angiogenesis-modulating activities.";
 RL J. Biol. Chem. 277:34264-34270(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [MRNA], AND VARIANT PRO-510.
 RA Park S.-Y., Kim I.-S.,
 RA "FEK2, a novel cell adhesion molecule of Fas-1 superfamily mediates
 RA cell-cell interaction.";
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 35-2551.
 RC TISSUE=Spleen;
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,

RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Nimomiya K., Ishibashi T., Yamashita H., Murakami K., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hirooka S., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hottu T., Kusano J.,
 RA Kanehori K., Takahashi-Fuji A., Hara H., Tanase T.-O., Nomura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Musahino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshioka Y., Matsunawa H., Ichihara T., Shiohara T., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Teraishi Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hiro M., Omori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuno Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
 RA "Complete sequencing and characterization of 21,243 full-length human
 RA cDNAs.";
 RT Nat. Genet. 36:40-45(2004).
 RL [5]
 RN NUCLEOTIDE SEQUENCE [MRNA] OF 1136-2551, PROTEIN SEQUENCE OF
 RP 1136-1144; 1257-1269; 1597-1605; 1623-1645; 1655-1660; 1813-1817;
 RP 1834-1843; 1914-1918; 1953-1957; 2204-2217; 2211-2215 AND 2355-2367,
 RP AND TISSUE SPECIFICITY.
 RX MEDLINE=22588541; PubMed=12626425; DOI=10.1093/glycob/cwg029;
 RA Zhou B., McGary C.T., Weigel J.A., Saxena A., Weigel P.H.,
 RA "Purification and molecular identification of the human hyaluronan
 RA receptor for endocytosis.";
 RL Glycobiology 13:339-349(2003).
 RN [6]
 RP NUCLEOTIDE SEQUENCE [MRNA] OF 1599-2551.
 RA Tao Q., Zhang W., Cao X.,
 RT "Molecular cloning and characterization of human FEEL sharing homology
 RT with CD44.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Hyaluronan receptor that binds to and mediates
 CC endocytosis of hyaluronic acid. May serve to maintain tissue
 CC integrity by supporting extracellular matrix turnover or it may
 CC contribute to maintaining fluidity of bodily liquids by resorption
 CC of hyaluronan. Binds to both Gram-positive and Gram-negative
 CC bacteria and may play a role in defense against bacterial
 CC infection.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface.
 CC -!- TISSUE SPECIFICITY: Highly expressed in sinusoidal endothelial
 CC cells of liver, spleen and lymph nodes.
 CC -!- PTM: Prototypically processed to yield a 190 kDa protein.
 CC -!- SIMILARITY: Contains 17 EGF-like domains.
 CC -!- SIMILARITY: Contains 7 FAS1 domains.
 CC -!- SIMILARITY: Contains 2 laminin EGF-like domains.
 CC -!- SIMILARITY: Contains 1 link domain.
 CC -!- CAUTION: Ref.4 (BA884877) sequence differs from that shown due to
 CC a frameshift in position 1367.
 CC -!- CAUTION: Ref.4 (BAD18723) sequence differs from that shown due to
 CC frameshifts in positions 240, 253, 588 and 1586.
 CC Copied by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonCommercial License
 CC -----
 CC EMBL: AJ295695; CAC87105.1; -; mRNA.
 CC EMBL: AB052958; BAC15608.1; -; mRNA.
 CC EMBL: AV311388; AAP74958.1; -; mRNA.
 CC EMBL: AK024503; BAB15793.1; -; mRNA.
 CC EMBL: AK074051; BAB84877.1; ALT_FRAME; mRNA.
 CC EMBL: AK160380; BAD18723.1; ALT_FRAME; mRNA.
 CC EMBL: AY227444; AA039681.1; -; mRNA.
 CC EMBL: AF160476; AAF82398.1; ALT_INIT; mRNA.

DR HSGP; P16109; 1FSB.
 DR HGNC; HGNC:18629; STAB2.
 DR MIM; 608561; Gene.
 DR GO; GO:0009897; C:external side of plasma membrane; ISS.
 DR GO; GO:0005887; C:integral to plasma membrane; IDA.
 DR GO; GO:0008368; F:Gram-negative bacterial binding; IDA.
 DR GO; GO:0005540; F:hyaluronic acid binding; ISS.
 DR GO; GO:0005041; F:low-density lipoprotein receptor activity; IDA.
 DR GO; GO:0005515; F:protein binding; NAS.
 DR GO; GO:0005033; F:protein disulfide oxidoreductase activity; NAS.
 DR GO; GO:0005044; F:scavenger receptor activity; IDA.
 DR GO; GO:0001525; F:angiogenesis; NAS.
 DR GO; GO:0007155; P:cell adhesion; NAS.
 DR GO; GO:0042742; P:defense response to bacteria; IDA.
 DR GO; GO:0006898; P:receptor mediated endocytosis; TAS.
 DR InterPro; IPR00782; BIGH3_FAS1.
 DR InterPro; IPR006210; EGF.
 DR InterPro; IPR000742; EGF_3.
 DR InterPro; IPR006947; EGF_allilnase.
 DR InterPro; IPR01181; EGF_Ca_bd.
 DR InterPro; IPR01311; EGF_extracell.
 DR InterPro; IPR002049; EGF_laminin.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR013032; EGF_like_reg.
 DR InterPro; IPR000538; Link.
 DR InterPro; IPR000737; Prot_inh_squash.
 DR Pfam; PF009008; EGF_7.
 DR Pfam; PF04863; EGF_allilnase; 1.
 DR Pfam; PF02469; Fasciclin; 6.
 DR Pfam; PF00193; Xlink; 1.
 DR ProDom; PD000918; Link; 1.
 DR SMART; SM00181; EGF; 20.
 DR SMART; SM00554; FAS1; 7.
 DR SMART; SM00445; LINK; 1.
 DR PROSITE; PS00022; EGF_1; 7.
 DR PROSITE; PS01186; EGF_2; 16.
 DR PROSITE; PS00026; EGF_3; 21.
 DR PROSITE; PS01248; EGF_LAM_1; 2.
 DR PROSITE; PS00027; EGF_LAM_2; FALSE_NEG.
 DR PROSITE; PS00213; FAS1; 7.
 DR PROSITE; PS01241; LINK_1; 1.
 DR PROSITE; PS00963; LINK_2; 1.
 DR Direct protein sequencing; EGF-like domain; Endocytosis; Glycoprotein;
 KW Hyaluronic acid; laminin EGF-like domain; Membrane; Polymorphism;
 KW Proteoglycan; Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 19 Potential.
 FT CHAIN 20 2551 Sfablin-2.
 FT CHAIN 1136 2551 /FTID=PRO_0000007712.
 FT TOPO_DOM 20 2458 190 kDa form stabilin-2.
 FT TRANSMEM 2459 2479 /FTID=PRO_0000007713.
 FT TOPO_DOM 2480 2551 Extracellular (Potential).
 FT DOMAIN 108 148 Cytoplasmic (Potential).
 FT DOMAIN 156 193 EGF-like 1.
 FT DOMAIN 195 236 EGF-like 2.
 FT DOMAIN 237 276 EGF-like 3.
 FT DOMAIN 322 362 EGF-like 4.
 FT DOMAIN 371 505 EGF-like 5.
 FT DOMAIN 515 652 FAS1 1.
 FT DOMAIN 736 776 FAS1 2.
 FT DOMAIN 826 866 EGF-like 6.
 FT DOMAIN 867 909 EGF-like 7.
 FT DOMAIN 910 952 EGF-like 8.
 FT DOMAIN 953 992 EGF-like 9.
 FT DOMAIN 994 1127 EGF-like 10.
 FT DOMAIN 1137 1265 FAS1 3.
 FT DOMAIN 1343 1408 FAS1 4.
 FT DOMAIN 1432 1470 laminin EGF-like 1.
 FT DOMAIN 1471 1512 EGF-like 11.
 FT DOMAIN 1513 1554 EGF-like 12.
 FT DOMAIN 1555 EGF-like 13.
 FT DOMAIN 1594 EGF-like 14.

FT DOMAIN 1596 1724 FAS1 5.
 FT DOMAIN 1740 1881 FAS1 6.
 FT DOMAIN 1957 2022 laminin EGF-like 2.
 FT DOMAIN 2047 2081 EGF-like 15.
 FT DOMAIN 2082 2122 EGF-like 16.
 FT DOMAIN 2165 EGF-like 17.
 FT DOMAIN 2198 2291 Link.
 Query Match 23.0%; Score 65; DB 1; Length 2551;
 Best Local Similarity 30.0%; Pred. No. 1e+02;
 Matches 15; Conservative 4; Mismatches 9; Indels 22; Gaps 2;
 QY 18 LHACIPCOL-----RCSSNTPPLT-----CORYCNASV 45
 DB 674 LGTCVSCSLVWWSRCNPANSEPTALFTHRCVYSGRFGSLKSCARCYNATV 723
 RESULT 35
 Q5CZ68_HUMAN PRELIMINARY; PRT; 484 AA.
 AC Q5CZ68;
 DT 29-MAR-2005, integrated into UniProtKB/TrEMBL.
 DT 29-MAR-2005, sequence version 1.
 DT 07-FEB-2006, entry version 4.
 DE Hypothetical protein DKFZp686D20108 (Fragment).
 GN Name=DKFZp686D20108;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Fetal kidney;
 RG The German cDNA Consortium;
 RA Blocker H., Boeher M., Brandt P., Mewes H.W., Weil B., Amid C.,
 RA Sanger A., Fobo G., Han M., Wiemann S.;
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL; CR936873; CA159785.1; -.
 DR Ensembl; ENSG00000146197; Homo sapiens.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR011641; GCC2_GCC3.
 DR Pfam; PF00431; CUB; 1.
 DR Pfam; PF07699; GCC2_GCC3; 3.
 DR SMART; SM00042; CUB_1.
 DR PROSITE; PS01180; CUB; 1.
 KW Hypothetical protein.
 FT NON_TER 1
 FT SEQUENCE 484 AA; 53895 MW; 8895A63B9DB369C CRC64;
 Query Match 22.8%; Score 64.5; DB 2; Length 484;
 Best Local Similarity 30.8%; Pred. No. 20;
 Matches 12; Conservative 5; Mismatches 9; Indels 13; Gaps 1;
 QY 7 QCSQNEVPSLHACIPCOL-----RCSSNT 32
 DB 240 QCSQHYNTSIHRCIRCMGSIQDPFRQNCSCRCPNT 278
 RESULT 36
 Q8NAV8_HUMAN PRELIMINARY; PRT; 581 AA.
 AC Q8NAV8;
 DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2002, sequence version 1.
 DT 07-MAR-2006, entry version 17.
 DE CDNA FLJ34691 f1s, clone M85AN2000909, moderately similar to Homo
 DE sapiens CCGPI protein (CCGP1), mRNA.
 OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Makatsuta A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Ohtsushi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoki T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa K., Yamazaki M.,
RA Niimiya K., Ishihashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimura M., Watanabe M., Hirooka S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshioka Y., Matsunawa H., Ichihara T., Shibata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakabe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro S., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senda T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.
RT Nat. Genet. 36:40-45 (2004).
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CC -----
CC EMBL; AC092010; BAC03789.1; -, mRNA.
CC DR Ensembl; ENSG00000146197; Homo sapiens.
CC DR InterPro; IPR000859; CUB.
CC DR InterPro; IPR011641; GCC2_GCC3.
CC DR Pfam; PF00431; CUB; 1.
CC DR Pfam; PF07699; GCC2_GCC3; 3.
CC DR SMART; SM00042; CUB; 1.
CC DR PROSITE; PS01180; CUB; 1.
CC DR SEQUENCE 581 AA; 64343 MW; D17BC28CDA1E4EE1 CRC64;
SQ
Query Match 22.8%; Score 64.5; DB 2; Length 581;
Best Local Similarity 30.8%; Pred. No. 24;
Matches 12; Conservative 5; Mismatches 9; Indels 13; Gaps 1;
OY 7 QCSQNEYPFSLHACIPCO-----RCSSNT 32
DB 336 QCSQNEYPFSLHACIPCO-----RCSSNT 374

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RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HM-1:IMSS;
RX PubMed=15729342; DOI=10.1038/nature03291;
RA Loftus B.J., Anderson I., Davies R., Almark U.C., Samuelson J.,
RA Ahmed P., Konecigla P., Bettman M., Hitt R.P., Mann B.J., Nozaki T.,
RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leipe M.,
RA Hofer M., Bruchhaus I., Willhoft U., Bhattacharya A.,
RA Chillingworth T., Churcher C.M., Hance Z., Harris B., Harris D.,
RA Jagels K., Moule S., Mungall K.L., Ormond D., Squares R.,
RA Whitehead S., Quail M.A., Rabinowitch E., Norbertczak H., Price C.,
RA Wang Z., Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S.,
RA Lohia A., Foster P.G., Sichteritz-Ponten T., Weber C., Singh U.,
RA Mukherjee C., El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M.,
RA Barrett B.G., Fraser C.M., Hall N.;
RT The genome of the protist parasite Entamoeba histolytica.
RT Nature 433:865-868 (2005).
CC CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
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CC -----
CC EMBL; AAFB01001427; BAF42605.1; -, Genomic DNA.
CC DR GO; GO:0005524; F:ATP binding; IEA.
CC DR GO; GO:0000166; F:nucleotide binding; IEA.
CC DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
CC DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
CC DR GO; GO:0006468; F:protein kinase activity; IEA.
CC DR GO; GO:0016740; F:transferase activity; IEA.
CC DR InterPro; IPR006212; Protein amino acid phosphorylation; IEA.
CC DR InterPro; IPR000719; Prot. Kinase.
CC DR InterPro; IPR008271; Ser/Thr_pkin_AS.
CC DR InterPro; IPR002290; Ser/Thr_pkinase.
CC DR InterPro; IPR001245; Tyr_pkinase.
CC DR Pfam; PF00069; Pkinase; 1.
CC DR PRINTS; PR00109; TYRKINASE.
CC DR ProDom; PD000001; Prot_kinase; 1.
CC DR SMART; SM00261; FU; 1.
CC DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
CC DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC DR ATP-binding; Kinase; Nucleotide-binding;
CC Serine/threonine-protein kinase; Transferase.
CC FT NON_TER 1
CC SEQUENCE 799 AA; 91662 MW; D8BFE2F2E235989E CRC64;
SQ
Query Match 22.8%; Score 64.5; DB 2; Length 799;
Best Local Similarity 34.3%; Pred. No. 34;
Matches 12; Conservative 6; Mismatches 14; Indels 3; Gaps 1;
OY 7 QCSQNEYPFSLHACIPCO---LRSSNTPPULCQ 38
DB 136 RCQDNYYDKEQLQSCGSCSECTLCSNMDICFTCK 170

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RESULT 37
Q50LY7 ENTHI PRELIMINARY; PRT; 799 AA.
AC Q50LY7_
DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, sequence version 1.
DE 07-FEB-2006, entry version 6.
DE Protein kinase, putative (Fragment).
GN ORFNames=650.t00003;
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=294381;

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RESULT 38
Q50Y51 ENTHI PRELIMINARY; PRT; 802 AA.
AC Q50Y51_
DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 07-JUN-2005, sequence version 1.
DE 07-FEB-2006, entry version 4.
DE CXC-rich protein (Fragment).
GN ORFNames=141.t00017;
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=294381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HM-1:IMSS;

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RX PubMed:15729342; DOI=10.1038/nature03291;
RA Lottus B.J., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
RA Amedeo P., Roncesaglia P., Bertman M., Hirt R.P., Mann B.J., Nozaki T.,
RA Sub B., Pop M., Duchene M., Ackers J., Tannich E., Leipzig M.,
RA Hofer M., Bruchhaus I., Willhoest U., Bhattacharya A.,
RA Chillingworth T., Churcher C.M., Hance Z., Harris B., Harris D.,
RA Jagels K., Moule S., Mungall K.L., Ormond D., Squares R.,
RA Whitehead S., Quail M.A., Rabinowitsch E., Norbertczak H., Price C.,
RA Wang Z., Guillen N., Gluchrist C., Stroup S.E., Bhattacharya S.,
RA Lohia A., Foster P.G., Sichteritz-Ponten T., Weber C., Singh U.,
RA Mukherjee C., El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M.,
RA Barrell B.G., Fraser C.M., Hall N.; Entamoeba histolytica.;
RT "The genome of the protist parasite Entamoeba histolytica.";
RL Nature 433:865-868(2005).
CC -! EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC -----
DR EMBL: AAFB01000471; EAL46536.1; -: Genomic_DNA.
DR InterPro: IPR006212; Funtin_repeat.
DR SMART, SM00261; FU; 2.
DR NON_TER 1
FT SEQUENCE 802 AA; 90127 MW; 1425BP8514DED237 CRC64;

Query Match 22.8%; Score 64.5; DB 2; Length 802;
Best Local Similarity 34.3%; Pred. No. 34;
Matches 12; Conservative 6; Mismatches 14; Indels 3; Gaps 1;

OY 7 QCSQNEYPDSLHACIPCO--LRCSNTPPTTCQ 38
DB 653 RCQDNVYVDKELQSCVCGSCSECLTCSNKDICTCK 687

RESULT 39
ID Q5CZB3 HUMAN PRELIMINARY; PRT; 852 AA.
AC Q5CZB3;
DT 29-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 29-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Hypothetical protein DKFP686B1223 (Fragment).
GN Name=DKFP686B1223;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RP Tissue=Testis;
RC The German cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schnupp I., Wellenreuther R.,
RA Wees H.W., Weil B., Amd C., Osanger A., Fobbo G., Han M., Wiemann S.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL: CR936607; CA156752.1; -: mRNA.
DR Ensembl: ENSG00000146197; Homo sapiens.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR GO: GO:0004888; F:transmembrane receptor activity; IEA.
DR GO: GO:0007596; P:blood coagulation; IEA.
DR InterPro: IPR000152; Asx_hydroxyl_S.
DR InterPro: IPR000859; CUB.
DR InterPro: IPR006210; EGF_3.
DR InterPro: IPR000742; EGF_3.
DR InterPro: IPR001881; EGF_Ca_bd.
DR InterPro: IPR013091; EGF_Ca_bd_2.
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DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR013032; EGF_like_reg.
DR InterPro: IPR011641; GCC2_GCC3.
DR InterPro: IPR001491; Thrombomodulin.
DR Pfam: PF00431; CUB; 1.
DR Pfam: PF00008; EGF; 5.
DR Pfam: PF07645; EGF_CA; 2.
DR Pfam: PF07699; GCC2_GCC3; 3.
DR PRINTS: PR00907; THROMBOMODULIN.
DR SMART: SM00042; CUB; 1.
DR SMART: SM00181; EGF; 6.
DR SMART: SM00179; EGF_CA; 3.
DR PROSITE: PS00010; ASX_HYDROXYL; 3.
DR PROSITE: PS01186; CUB; 1.
DR PROSITE: PS01186; EGF_2; 4.
DR PROSITE: PS50026; EGF_3; 3.
DR PROSITE: PS01187; EGF_CA; 3.
KM EGF-like domain; Hypothetical protein.
FT NON_TER 1
FT SEQUENCE 852 AA; 93812 MW; 514918C0D126C7B2 CRC64;

Query Match 22.8%; Score 64.5; DB 2; Length 852;
Best Local Similarity 30.8%; Pred. No. 37;
Matches 12; Conservative 5; Mismatches 9; Indels 13; Gaps 1;

OY 7 QCSQNEYPDSLHACIPCOL-----RCSNTP 32
DB 607 QCSQHYNTSIRHCRCAMGSGYQDPFRQNCRCPCGNT 645

RESULT 40
ID Q8NAU9 HUMAN PRELIMINARY; PRT; 880 AA.
AC Q8NAU9;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-MAR-2006, entry version 19.
DE CDNA FLJ34743 f1s, clone MESAN2009019, moderately similar to CEGP1
DE protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RP PubMed:14702039; DOI=10.1038/ng1285;
RX Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obaishi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahori K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Niimiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoa S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanohori K., Takahashi-Fuji A., Hara H., Tanase T.-O., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Mizushino K., Yuki H., Oshino A., Sasaki N., Aotaka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Yeraehima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hiroo K., Omori Y., Okamoto S.,
RA Ohtani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsunura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki K.,
RA Togaishi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
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RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAUSBERG R.;
RA TISSUE=Pancreas;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL; BC052263; AAH52263.2; -; mRNA.
DR HSSP; P35555; 1EMN.
DR Ensemble; ENSG00000146197; Homo sapiens.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR00742; EGF_3.
DR InterPro; IPR001881; EGF_Ca_bd.
DR InterPro; IPR013091; EGF_Ca_bd_2.
DR InterPro; IPR006209; EGF_like_reg.
DR InterPro; IPR013032; EGF_like.
DR InterPro; IPR01641; GCC2_GCC3.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 6.
DR Pfam; PF07645; EGF_Ca; 4.
DR Pfam; PF07699; GCC2_GCC3; 3.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00181; EGF; 9.
DR SMART; SM00179; EGF_Ca; 6.
DR PROSITE; PS00010; ASX_HYDROXYL; 6.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS50026; EGF_3; 6.
DR PROSITE; PS01187; EGF_Ca; 6.
SQ SEQUENCE 992 AA; 109165 MW; 24093050738932E1 CRC64;

Query Match 22.8%; Score 64.5; DB 2; Length 992;
Best Local Similarity 30.8%; Pred. No. 43;
Matches 12; Conservative 5; Mismatches 9; Indels 13; Gaps 1;

QY 7 QCSQNEYFDSLILHACIPCOL-----RCSSNT 32
DB 747 QCSFGHYNTSIHRCIRCAMGSYOPDFRQNFCSRCPGNT 785

RESULT 43
Q81X30 HUMAN PRELIMINARY; PRT; 993 AA.
AC Q81X30;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE CUB and EGF containing protein (Signal peptide, CUB and EGF-like
DE domain containing protein 3 precursor) (OTTHUMP0000016250).
GN Name=SCUB3; Synonyms=CEGF3; ORFNames=RP3-329A5.4-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RX PubMed=15234972; DOI=10.1074/jbc.M405912200;

RA NUCLEOTIDE SEQUENCE.
RP Pfarr N., Bahr A., Cichutek A., Loebbert R., Zabel B.U., Schmidt E.R.,
RA Hankeln T., Winterpacht A.;
RA "Novel human gene family (CEGF) encoding mosaic proteins with EGF-
RT like, STR3 and a CUB module: cloning and expression analysis.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15234972; DOI=10.1074/jbc.M405912200;
```

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RA Wu B.T., Su Y.H., Teal M.T., Wasserman S.M., Topper J.N., Yang R.B.;
RT "A novel secreted, cell-surface glycoprotein containing multiple
RT epidermal growth factor-like repeats and one CUB domain is highly
RT expressed in primary osteoblasts and bones.";
RL J. Biol. Chem. 279:37485-37490(2004).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Williams S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AF452494; AAN76808.1; -; mRNA.
DR EMBL; AY639608; AAU08347.1; -; mRNA.
DR EMBL; 297832; CAI20187.1; -; Genomic_DNA.
DR HSSP; P35555; 1EMN.
DR Ensemble; ENSG00000146197; Homo sapiens.
DR HGNC; HGNC:13655; SCUB3.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR00742; EGF_3.
DR InterPro; IPR001881; EGF_Ca_bd.
DR InterPro; IPR013091; EGF_Ca_bd_2.
DR InterPro; IPR006209; EGF_like_reg.
DR InterPro; IPR013032; EGF_like.
DR InterPro; IPR01641; GCC2_GCC3.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 6.
DR Pfam; PF07645; EGF_Ca; 4.
DR Pfam; PF07699; GCC2_GCC3; 3.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00181; EGF; 9.
DR SMART; SM00179; EGF_Ca; 6.
DR PROSITE; PS00010; ASX_HYDROXYL; 6.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS50026; EGF_3; 6.
DR PROSITE; PS01187; EGF_Ca; 6.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 993 AA; 109282 MW; 19BBE0E5627EEAF4 CRC64;

Query Match 22.8%; Score 64.5; DB 2; Length 993;
Best Local Similarity 30.8%; Pred. No. 43;
Matches 12; Conservative 5; Mismatches 9; Indels 13; Gaps 1;

QY 7 QCSQNEYFDSLILHACIPCOL-----RCSSNT 32
DB 748 QCSFGHYNTSIHRCIRCAMGSYOPDFRQNFCSRCPGNT 786

RESULT 44
Q7QGV0 ANOGA PRELIMINARY; PRT; 1294 AA.
AC Q7QGV0;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 07-DEC-2004, sequence version 2.
DT 07-FEB-2006, entry version 13.
DE ENSANGP0000012534 (Fragment).
GN ORFNames=ENSANG0000010045;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;
OC Anophelinae; Anopheles.
NCBI_TaxID=180454;
RX PubMed=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation.";
```

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RN Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
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CC -----
CC EMBL; AAAB01008823; EAA05574.2; -; Genomic DNA.
CC
CC GO; GO:0016020; C:membrane; IEA.
CC GO; GO:0008565; F:protein transporter activity; IEA.
CC GO; GO:0006886; P:intracellular protein transport; IEA.
CC
CC InterPro; IPR006210; EGF.
CC InterPro; IPR002860; Glyco_hydro_BNR.
CC InterPro; IPR002172; LDL_rcpt_A.
CC InterPro; IPR000033; LDLR.
CC InterPro; IPR006581; VPS10.
CC Pfam; PF02012; BNR; 6.
CC Pfam; PF00057; Ldl_recept_a; 7.
CC Pfam; PF00058; Ldl_recept_b; 4.
CC PRINTS; PR00261; LDLRECEPTOR.
CC SMART; SM00181; EGF; 1.
CC SMART; SM00192; LDLa; 7.
CC SMART; SM00135; LY; 2.
CC SMART; SM00602; VPS10; 1.
CC PROSITE; PS01209; LDLRA_1; 5.
CC PROSITE; PS50068; LDLRA_2; 5.
CC PROSITE; PS51120; LDLRB; 4.
CC FT NON_TER 1 1
CC FT NON_TER 1294 1294
CC SEQUENCE 1294 AA; 146750 MW; 10C251750A3F0586 CRC64;

Query Match 22.8%; Score 64.5; DB 2; Length 1294;
Best Local Similarity 31.0%; Pred. No. 57;
Matches 13; Conservative 9; Mismatches 13; Indels 7; Gaps 1;

QY 7 GCGSQNEVFDLSLHACIPCOLRCS-----NTPPLTCQRC 41
DB 1130 ECKADEFCNVTNACLPQMRCTEXDCPDGSTPPRKDRTC 1171

RESULT 45
Q3AN9U5_THEPA PRELIMINARY; PRT; 1532 AA.
AC Q3AN9U5;
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 02-AUG-2005, sequence version 1.
DT 21-FEB-2006, entry version 7.
DE ABC transporter, putative.
GN ORFNames=TP01_0011;
OS Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
OC Theileria.
OX NCBI_TaxID=5875;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga;
RG Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,
RA Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,
RA Hall N., Ren O., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M.,
RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.,
RA Jiang L., Lynn J., Weaver B., Shoabli A., Domingo A.R., Masawo D.,
RA Cradree J., Wortman J.R., Haas B., Anginoli S.V., Creasy T.H., Lu C.,
RA Sub B., Silva J.C., Utterback T.R., Feldblyum T.V., Pertea M.,
RA Allen J., Nierman W.C., Taracha E.L., Salzberg S.L., White O.R.,
RA Fitzhugh H.A., Morzaria S., Venter J.C., Fraser C.M., Nene V.;
RT "Genome Sequence of Theileria parva, a Bovine Pathogen That Transforms
RT Lymphocytes.";
```

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RN Science 309:134-137 (2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga;
RG Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
RA Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M.,
RA Ren O., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
RA Ralph S.A., Mann D.J., Xiong Z., Shallom S.V., Weidman J., Jiang L.,
RA Lynn J., Weaver B., Shoabli A., Masawo D., Cradree J., Wortman J.R.,
RA Haas B., Anginoli S., Creasy T.H., Lu C., Sub B., Silva J.C.,
RA Utterback T., Feldblyum T., Pertea M., Allen J., Taracha E.L.,
RA Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
RA Fraser C.M., Nene V.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
CC EMBL; AAGK01000001; EAN33255.1; -; Genomic DNA.
CC
CC GO; GO:0016021; C:integral to membrane; IEA.
CC GO; GO:0005524; F:ATP binding; IEA.
CC GO; GO:0016887; F:ATPase activity; IEA.
CC GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. .; IEA.
CC GO; GO:0006810; P:transport; IEA.
CC InterPro; IPR003593; AAA_ATPase.
CC InterPro; IPR011527; ABC_TM_1.
CC InterPro; IPR003439; ABC_transp_like.
CC Pfam; PF00005; ABC_tran; 1.
CC PROSITE; PS50929; ABC_TM1F; 1.
CC PROSITE; PS50893; ABC_TRANSPORTER_2; 2.
CC KW Membrane; Transport.
CC SEQUENCE 1532 AA; 175403 MW; 33C652005EAD2774 CRC64;

Query Match 22.8%; Score 64.5; DB 2; Length 1532;
Best Local Similarity 32.7%; Pred. No. 68;
Matches 18; Conservative 7; Mismatches 13; Indels 17; Gaps 4;

QY 6 GCGSQNEVFDLSL-----LHACIPCOLRCSNTPPLTC--QRYCNASVT 46
DB 223 GNCYRKRRKFTNNINGNSLSVCGVHTHCSP--DSDCSRN--PLFCPRARKQNDIT 274

RESULT 46
Q3WG13_9ACTO PRELIMINARY; PRT; 192 AA.
AC Q3WG13;
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Hypothetical protein.
GN ORFNames=FraneanIDRAFT_6385;
OS Frankia sp. EAN1pec.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Frankineae; Frankiaceae; Frankia.
OX NCBI_TaxID=298653;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=EAN1pec.
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hamon N., Israni S., Plitnick S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Frankia sp. EAN1pec.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
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DR EMBL; AA101000007; EAM17768.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 192 AA; 20208 MW; 2BC6F837574F9D5C CRC64;

Query Match 22.6%; Score 64; DB 2; Length 192;
Best Local Similarity 39.0%; Pred. No. 8.8;
Matches 16; Conservative 4; Mismatches 13; Indels 8; Gaps 2;

OY 13 YFDSLHACIPQCRSSNTPELT---COR-----YCNAV 45
DB 48 HVDLFSHARSPEQLKSCGSPASADCRRAAGACGRNCRV 88

RESULT 47
O3GKS9_9GAMM PRELIMINARY; PRT; 210 AA.
AC O3GKS9;
DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Hypothetical protein.
GN ORFNames=PcrvODRAFT_0081;
OS Psychrobacter cryohalolentis K5.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Psychrobacter.
OX NCBI_TaxID=335284;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K5;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pittluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Psychrobacter
RT cryohalolentis K5.";
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K5;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Psychrobacter
RT cryohalolentis K5.";
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAJ01000044; EAO09707.1; -; Genomic_DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR000379; Ser esters.
DR InterPro; IPR008866; UPF0227.
DR Pfam; PF05728; UPF0227; 1.
KW Hydrolase; Hypothetical protein.
SQ SEQUENCE 210 AA; 23245 MW; 67558A60F75E9F9B CRC64;

Query Match 22.6%; Score 64; DB 2; Length 210;
Best Local Similarity 40.5%; Pred. No. 9.7;
Matches 15; Conservative 6; Mismatches 14; Indels 2; Gaps 1;
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RESULT 48
O729FO_DESVH PRELIMINARY; PRT; 494 AA.
AC O729FO;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Hydrogenase, iron-sulfur cluster-binding subunit, putative.
GN OrderedLocustNames=DVU2401; ORFNames=DVU 2401;
OS Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
OS 8303).
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
OC Desulfovibrionaceae; Desulfovibrio.
OX NCBI_TaxID=882;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15077118; DOI=10.1038/nbt959;
RA Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
RA Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,
RA Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
RA Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
RA Peterson J.D., Davidson T.M., Zafar N., Zhou L., Radune D.,
RA Dmitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
RA Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;
RT "The genome sequence of the anaerobic, sulfate-reducing bacterium
RT Desulfovibrio vulgaris Hildenborough."
RL Nat. Biotechnol. 22:554-559(2004).
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CC -----
DR EMBL; AE017285; AAS96874.1; -; Genomic_DNA.
DR TIGR; DVU2401; -
DR BioCyc; DVUL882; DVU2401-MONOMER; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0015948; P:methanogenesis; IEA.
DR InterPro; IPR001450; 4Fe4S_Fe_S_bd.
DR InterPro; IPR003813; FlpD.
DR InterPro; IPR012285; Fum_reductase_C.
DR InterPro; IPR006662; ThioRed.
DR Pfam; PF00037; Fer4; 1.
DR Pfam; PF02662; FlpD; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR PROSITE; PS00198; 4FE4S_FERRDOXIN; 2.
KW 4Fe-4S; Complete proteome; Electron transport; Iron; Iron-sulfur;
KW Metal-binding; Transport.
SQ SEQUENCE 494 AA; 54143 MW; 904B524BF3B118E CRC64;

Query Match 22.6%; Score 64; DB 2; Length 494;
Best Local Similarity 31.8%; Pred. No. 24;
Matches 14; Conservative 7; Mismatches 13; Indels 10; Gaps 1;

OY 2 LQWAGQCSQNEFYFSLHACIPQCRSSNTPELTQRYCNASV 45
DB 428 LHLAQRCTE-----CGECQACPVNIPLVALKQMKMRSV 461

RESULT 49
Q410Y5_GIBZE PRELIMINARY; PRT; 762 AA.
ID Q410Y5 GIBZE
AC Q410Y5;
DT 16-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Hypothetical protein.
GN ORFNames=FG09123.1;
OS Gibberella zeae (Fusarium graminearum).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
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OX NCB1_TaxID=5518;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=PH-1 / NRRL 31084.
RA Birren B.W., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Bouchgail H.M., Barua N., Bastien V., Bloom T., Boguslavskiy L.,
RA Bouthghalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collamore A., Cook A., Cooke P., Corum B., Dearrellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Eklins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D.,
RA Galagan J.E., Gaidyna S., Gierre S., Graham L., Grand-Pierre N.,
RA Hatz N., Hagopian D., Hago B., Hall J., Horton L., Hulme W.,
RA Karslav I., Jaffe C., Johnson R., Jones C., Kamal M., Kamat A.,
RA Killeen A., Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G.,
RA Lui A., Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J.,
RA Manning J., Matthews C., Mauceli E., McCarthy M., Meldrum J.,
RA Meneus L., Mihova T., Mienga V., Murphy T., Naylor J., Nguyen C.,
RA Nicol R., Nielsen C.B., Norbu C., O'Connor T., O'Donnell P.,
RA O'Neill D., Oliver J., Peterson K., Phunkhang P., Pierre N.,
RA Purcell S., Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C.,
RA Rogov P., Roman J., Schauer S., Schupack R., Seaman S., Severy P.,
RA Smitnov S., Smith C., Spencer B., Stange-Thomann N., Stojanovic N.,
RA Stubbs M., Talamas J., Tesfaye S., Theodore J., Topham K., Travets M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.S.;
RT "Fusarium graminearum genome sequence."
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
CC EMBL; AACW01000370; EAA78173.1; -; Genomic_DNA.
CC
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:00046872; F:metal ion binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR001138; Fungi_TFSCP_N.
DR Pfam; PF04082; Fungal_trans_1.
DR Pfam; PF00172; Zn_clus_1.
DR SMART; SM00066; GAL4; 1.
DR PROSITE; PS50048; ZN2_CY6_FUNGAL_2; 1.
KW Complete proteome; DNA-binding; Hypothetical protein; Metal-binding;
KW Nuclear protein; Transcription; Transcription regulation; Zinc.
SQ SEQUENCE 762 AA; 84756 MW; 55B25D037F21A35A CRC64;

Query Match 22.6%; Score 64; DB 2; Length 762;
Best Local Similarity 43.3%; Pred. No. 38;
Matches 13; Conservative 3; Mismatches 6; Indels 8; Gaps 2;

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RX PubMed=15875012; DOI=10.1038/nature03481;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.A., Xu Q.,
RA Sugang R., Bertman M., Song J., Olsen R., Szatranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivo F.,
RA Bankler A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E.J., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bacon N.,
RA Farbrother P., Desany B., Just E., Morio T., Post R., Churcher C.M.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D.M., Moutier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K.D., Quiles M., Madan Babu M., Saito T.,
RA Buchrieser C., Wardrop A., Felder M., Thangavelu M., Johnson D.,
RA Knights A., Louisedge H., Mungall K.L., Oliver K., Price C.,
RA Quail M.A., Unushihara H., Hernandez J., Rabinowitsch E., Steffen D.,
RA Sanders M., Ma J., Kohara Y., Sharp S., Simmonds M.N., Spiegler S.,
RA Tivey A., Sugano S., White B., Walker D., Woodward J.R., Winckler T.,
RA Tanaka Y., Shaulsky G., Schleicher M., Weinstein G.M., Rosenthal A.,
RA Cox E.C., Chisholm R.L., Gibbs R.A., Loomis W.F., Platzer M.,
RA Kay R.R., Williams J.G., Dear P.H., Noegel A.A., Barrett B.G.,
RA Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum."
RL Nature 435:43-57 (2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
CC EMBL; AAF101000151; EAL63792.1; -; Genomic_DNA.
CC
DR InterPro; IPR000024; Fz_domain.
DR PROSITE; PS50038; Fz_1.
KW Hypothetical protein.
SQ SEQUENCE 300 AA; 34483 MW; 9DB63B38B2007B61 CRC64;

Query Match 22.4%; Score 63.5; DB 2; Length 300;
Best Local Similarity 31.4%; Pred. No. 16;
Matches 16; Conservative 8; Mismatches 22; Indels 5; Gaps 2;

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OY 20 ACIPCO---LRCSNTPPLTCOR-----YC 41
DB 17 ACVPCQNSKKRCDSDSPCANCRRRDIPYC 46

RESULT 50
ID 054KFP9 D1CDI PRELIMINARY; PRT; 300 AA.
AC 054KFP9;
DT 24-MAY-2005; Integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005; sequence version 1.
DT 07-FEB-2006; entry version 4.
DE Hypothetical protein.
DE ORFNames=DD80219228;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCB1_TaxID=44689;
RN [1]

```

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RX PubMed=15875012; DOI=10.1038/nature03481;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.A., Xu Q.,
RA Sugang R., Bertman M., Song J., Olsen R., Szatranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivo F.,
RA Bankler A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E.J., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bacon N.,
RA Farbrother P., Desany B., Just E., Morio T., Post R., Churcher C.M.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D.M., Moutier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K.D., Quiles M., Madan Babu M., Saito T.,
RA Buchrieser C., Wardrop A., Felder M., Thangavelu M., Johnson D.,
RA Knights A., Louisedge H., Mungall K.L., Oliver K., Price C.,
RA Quail M.A., Unushihara H., Hernandez J., Rabinowitsch E., Steffen D.,
RA Sanders M., Ma J., Kohara Y., Sharp S., Simmonds M.N., Spiegler S.,
RA Tivey A., Sugano S., White B., Walker D., Woodward J.R., Winckler T.,
RA Tanaka Y., Shaulsky G., Schleicher M., Weinstein G.M., Rosenthal A.,
RA Cox E.C., Chisholm R.L., Gibbs R.A., Loomis W.F., Platzer M.,
RA Kay R.R., Williams J.G., Dear P.H., Noegel A.A., Barrett B.G.,
RA Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum."
RL Nature 435:43-57 (2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
CC EMBL; AAF101000151; EAL63792.1; -; Genomic_DNA.
CC
DR InterPro; IPR000024; Fz_domain.
DR PROSITE; PS50038; Fz_1.
KW Hypothetical protein.
SQ SEQUENCE 300 AA; 34483 MW; 9DB63B38B2007B61 CRC64;

RESULT 51
ID 09GQ45 G1ALA PRELIMINARY; PRT; 548 AA.
AC 09GQ45;
DT 01-MAR-2001; Integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001; sequence version 1.
DT 07-FEB-2006; entry version 21.
DE Variant-specific surface protein M21-1 (Fragment).
DE Name=M21-1;
OS Giardia lamblia (Giardia intestinalis).
OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.
OX NCB1_TaxID=5741;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Mansouri M., Ey P.L.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; AF298862; AAG37862.1; -; Genomic_DNA.
CC
DR HSSP; O16119; IEZG.
DR InterPro; IPR006058; 2Fe2S_fd_BS.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR006212; Furin_repeat.
DR InterPro; IPR002350; Prot_inh_kazal.
DR SMART; SM00181; BGF; 2.

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DR SMART; SM00261; FU; 2.
DR PROSITE; PS00197; 2FE2S_FER_1; UNKNOWN_1.
DR PROSITE; PS00282; KAZAL; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 548
SQ SEQUENCE 548 AA; 56557 MW; 578FE4FDA0A2CF0E CRC64;

Query Match 22.4%; Score 63.5; DB 2; Length 548;
Best Local Similarity 30.4%; Pred. No. 31;
Matches 17; Conservative 4; Mismatches 20; Indels 15; Gaps 2;

OY 5 AGCGSQNEYFDSLHACIPQQLRCSSNTPPLTQC-----RYCNASVTNSVK 50
DB 209 AGCCGCGTADPTTCCCKCKCGI-----TDCATCEVNATISQPCQCKTCSYSSNMWVK 259

RESULT 52
ID Q68FG9_MOUSE PRELIMINARY; PRT; 827 AA.
AC Q68FG9;
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2004, sequence version 1.
DE 07-FEB-2006, entry version 13.
DE Scube3 protein (Fragment).
GN Name=Scube3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Streusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Pange C.,
RA Raha S.S., Loujallan N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.T., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Director MGC Project;
RL Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; BC079849; AAH79849.1; -; mRNA.
CC Ensemble; ENSMUSG0000038677; Mus musculus.
CC MGI; MGI:3045253; Scube3.
CC GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR000742; EGF_3.
DR InterPro; IPR001881; EGF_Ca_bd.
DR InterPro; IPR013091; EGF_Ca_bd_2.

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DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR013032; EGF_like_reg.
DR InterPro; IPR011641; GCC2_GCC3.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 6.
DR Pfam; PF07645; EGF_CA; 3.
DR Pfam; PF07699; GCC2_GCC3; 2.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00181; EGF; 7.
DR SMART; SM00179; EGF_CA; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 5.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS01186; EGF_2; 6.
DR PROSITE; PS00026; EGF_3; 4.
DR PROSITE; PS01187; EGF_CA; 4.
DR EGF-like domain.
KW NON_TER 1
SQ SEQUENCE 827 AA; 90871 MW; DF6BB337B4CE91D CRC64;

Query Match 22.4%; Score 63.5; DB 2; Length 827;
Best Local Similarity 30.8%; Pred. No. 47;
Matches 12; Conservative 5; Mismatches 9; Indels 13; Gaps 1;

OY 7 QCSQNEYFDSLHACIPQQL-----RCSNT 32
DB 610 QCSQGHYYNTSIHRCIRCAVGSYQPDFRQNFCTRCPGNT 648

RESULT 53
ID Q66PY1_MOUSE PRELIMINARY; PRT; 993 AA.
AC Q66PY1;
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2004, sequence version 1.
DE 07-FEB-2006, entry version 9.
DE Signal peptide, CUB and EGF-like domain containing protein 3
DE precursor.
GN Name=Scube3; Synonyms=SCUB3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RX PubMed=15234972; DOI=10.1074/jbc.M405912200;
RA Wu B.T., Su Y.H., Tsai M.T., Wasserman S.M., Topper J.N., Yang R.B.,
RA "A novel secreted, cell-surface glycoprotein containing multiple
RT epidermal growth factor-like repeats and one CUB domain is highly
RT expressed in primary osteoblasts and bones.";
RL J. Biol. Chem. 279:37485-37490(2004).
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CC -----
CC EMBL; AY639609; AAU08348.1; -; mRNA.
CC Ensemble; ENSMUSG0000038677; Mus musculus.
CC MGI; MGI:3045253; Scube3.
CC GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR00742; EGF_3.
DR InterPro; IPR01881; EGF_Ca_bd.
DR InterPro; IPR013091; EGF_Ca_bd_2.
DR InterPro; IPR006209; EGF_like_reg.
DR InterPro; IPR013032; EGF_like_reg.
DR InterPro; IPR01641; GCC2_GCC3.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 6.
DR Pfam; PF07645; EGF_CA; 4.
DR Pfam; PF07699; GCC2_GCC3; 3.

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DR SMART; SM00042; CUB; 1.
 DR SMART; SM00181; EGF; 9.
 DR SMART; SM00179; EGF_CA; 6.
 DR PROSITE; PS00010; ASX_HYDROXYL; 6.
 DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS01186; EGF_2; 7.
 DR PROSITE; PS00026; EGF_3; 6.
 DR PROSITE; PS01187; EGF_CA; 6.
 KW SIGNAL.
 FT SIGNAL.
 SQ SEQUENCE 993 AA; 108984 MW; E43989ACACCC345F CRC64; Potential.

Query Match 22.4%; Score 63.5; DB 2; Length 993;
 Best Local Similarity 30.8%; Pred. No. 57;
 Matches 12; Conservative 5; Mismatches 9; Indels 13; Gaps 1;

Qy 7 QCSQNEFFSLHACFPCL-----RCSSNT 32
 Db 748 QCSQHYNTSIHRCICAVGSDYQDPDFRONFCTRCPGNT 786

RESULT 54
 Q4UE95_THEAN PRELIMINARY; PRT; 1563 AA.
 AC Q4UE95;
 DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2005, sequence version 1.
 DT 21-FEB-2006, entry version 8.
 DE (Subtelomeric) ABC-transporter family member, putative.
 OS ORNAMES=TA12925;
 OS Theileria annulata.
 OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
 OC Theileria.
 NCBI_Taxid=5874;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Ankara isolate clone C9;
 RX PubMed=15994597; DOI=10.1258/jrsm.98.7.320;
 RA Pain A., Renaud H., Berriman M., Murphy L., Yeats C.A., Weir W.,
 RA Kethornou A., Aslett M., Bishop R., Bouchier C., Cochet M.,
 RA Coulson R.M.R., Cronin A., de Villiers E.P., Fraser A., Foster N.,
 RA Gardner M., Goble A., Griffiths-Jones S., Harris D.E., Katzer F.,
 RA Larie N., Lord A., Maser P., McKellar S., Mooney P., Morton F.,
 RA Nene V., O'Neill S., Price C., Quail M.A., Rabinowitsch E.,
 RA Rawlings N.D., Rutter S., Saunders D., Seeger K., Shah T., Squares R.,
 RA Squares S., Tivey A., Walker A.R., Woodward J., Dobbelaere D.A.E.,
 RA Langsley G., Rajadream M.A., McKeever D., Shiels B., Tait A.,
 RA Bartell B., Hall N.;
 RT "Genome of the host-cell transforming parasite Theileria annulata
 compared with T. parva";
 RL Science 309:131-133(2005).
 CC -1- SIMILARITY: Belongs to the ABC transporter family.
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EMBL: CR940348; CA174594.1; -; Genomic DNA.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0016887; F:ATPase activity; IEA.
 DR GO: GO:0042626; F:ATPase activity, coupled to transmembrane m.; IEA.
 DR GO: GO:0000166; F:nucleotide binding; IEA.
 DR GO: GO:0006810; P:transport; IEA.
 DR InterPro: IPR003593; AAA ATPase.
 DR InterPro: IPR011527; ABC_TM_1.
 DR InterPro: IPR003439; ABC_transp_like.
 DR Pfam: PF00005; ABC_tran; 2.
 DR SMART; SM00382; AAA; 2.
 DR PROSITE; PS00929; ABC_TM1F; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
 DR PROSITE; PS00893; ABC_TRANSPORTER_2; 2.
 KW ATP-binding; Membrane; Nucleotide-binding; Transport.
 SQ SEQUENCE 1563 AA; 179754 MW; A6EB5972F6056CEE CRC64;

Query Match 22.4%; Score 63.5; DB 2; Length 1563;
 Best Local Similarity 30.9%; Pred. No. 92;
 Matches 17; Conservative 10; Mismatches 11; Indels 17; Gaps 4;

Qy 6 QCSQNEFF-----DSLHACFPCLRCSSNTPPLTC--QRCSNLSVT 46
 Db 233 GLCYRSPFFNVKGVANLVNVCNSVHSCSP--DSKCSN--PLCYCAPRRQNSDIT 284

RESULT 55
 Q3XSX7_MOUSE PRELIMINARY; PRT; 164 AA.
 AC Q3XSX7;
 DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
 DT 11-OCT-2005, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE Tfrsf13c protein (Activated spleen cDNA, RIKEN full-length enriched
 library, clone: F830206F13 product: tumor necrosis factor receptor
 superfamily, member 13c, full insert sequence).
 GN Name=Tfrsf13c;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=PCR rescued clones;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Scheffen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heshe F.,
 RA Datchenko L., Matusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uscud T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield V.S.N., Krzywinski M.I., Skalski U., Smalios D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=PCR rescued clones;
 RX NIH MGC Project;
 RL Submitted (Sep-2005) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=MOD; TISSUE=Activated spleen;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Methods Enzymol. 303:119-44(1999).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=MOD; TISSUE=Activated spleen;
 RX PubMed=1641072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
 RA Ambesi-Impombato A., Adeweller R., Acurallya R.N., Bailey T.L.,
 RA Baniel M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,

DB 21 OCNOTECFDPFLVNCVSCEL 40

RESULT 56

TRI3C_MOUSE STANDARD; PRT; 175 AA.

ID Q9DBD0; 27-MAY-2002, integrated into UniProtKB/Swiss-Prot.

DT 01-JUN-2001, sequence version 1.

DT 07-FEB-2006, entry version 30.

DE Tumor necrosis factor receptor superfamily member 13C (B cell-activating factor receptor) (BAFF receptor) (BAFF-R) (Blys receptor 3) (B-cell maturation defect).

DE (B-cell maturation defect).

GN Name=TNFRSF13C; Synonyms=BAFFr, Bcnd, Br3;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

OC NCBI_Taxid=10090;

OK (1)

NP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2).

RP STRAIN=BA16/C; Tissue=B-cell lymphoma;

RC MEDLINE=21442025; PubMed=11509692; DOI=10.1126/science.10611965;

RX Thompson J.S., Blixier S.A., Qian F., Vora K., Scott M.L., Cachero T.G., Hession C., Schneider P., Sizing I.D., Mullien C., Strauch K., Zafari M., Benjamin C.D., Tschopp J., Browning J.L., Ambrose C.;

RT "BAFF-R, a newly identified TNF receptor that specifically interacts with BAFF."

RT Science 293:2108-2111 (2001).

RL (12)

RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND DISEASE.

RC STRAIN=A/J;

RX MEDLINE=21475550; PubMed=11591325; DOI=10.1016/S0960-9822(01)00481-X;

RA Yan M., Brady J.R., Chan B., Lee W.P., Hsu B., Hartless S.M., Cancro M.P., Grewal I.S., Dixit V.M.;

RT "Identification of a novel receptor for B lymphocyte stimulator that is mutated in a mouse strain with severe B cell deficiency."

RT Curr. Biol. 11:1547-1552 (2001).

RL (3)

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).

RC STRAIN=C57BL/6J; Tissue=Small intestine;

RX PubMed=1611072; DOI=10.1126/science.1112014;

RA Carrincci P., Kasubawa T., Katayama S., Gough J., Fitch M.C., Maeda N., Oyama R., Ravasi T., Lemhard B., Wells C., Kodzius R., Shmorkawa K., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Aidinis V., Allen J.E., Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L., Banerji M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Chiu K.P., Choudhary V., Christofidels A., Clutterbuck D.R., Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G., Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M., Georgi-Jacob M., Gergely P., Gingeras T.R., Gojoboti T., Green R.E., Gustincich S., Hatters M., Hayashi Y., Hensch T.K., Hirokawa N., Hill D., Hummel L., Iacono M., Ikeo K., Iwano A., Ishikawa T., Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Kurochkin I.V., Lareu L.F., Lazarevic D., Lipovich L., Liu J., Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L., Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K., Motenagui-Tabar S., Mulder N., Nakano M., Nakachi H., Ng P., Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O., Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G., Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M., Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Schombach C., Sekiguchi K., Sempole C.A., Seno S., Sessa A., Sheng Y., Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Sperling S., Stupka E., Stupka K., Sultana R., Takenaka Y., Taki K., Tamada K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yang K., Yamashita H., Zdobych E., Zhu S., Zimmer A., Hide W., Bult C., Grimmond S.M., Teasdale R.D., Liu E.T., Bruste V., Quackenbush J.,

RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N., Nishio T., Okada M., Plesky C., Shibata K., Shiraki T., Suzuki S., Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J., Hayashizaki Y.;

RT "The transcriptional landscape of the mammalian genome.";

RT Science 309:1559-1563 (2005).

RL (4)

RP FUNCTION.

RX MEDLINE=21614654; PubMed=11747827; DOI=10.1016/S0960-9822(01)00598-X;

RA Hartless S.M., Lentz V.M., Sah A.P., Hsu B.L., Clise-Dwyer K., Hilbert D.M., Hayes C.E., Cancro M.P.;

RT "Competition for Blyt-mediated signaling through Bcnd/BR3 regulates peripheral B lymphocyte numbers."

RT Curr. Biol. 11:1986-1989 (2001).

RL (1)

CC FUNCTION: B-cell receptor specific for TNFSF13B/TALL1/BAFF/Blys.

CC Promotes the survival of mature B-cells and the B-cell response.

CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type III membrane protein (Probable).

CC -1- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=1;

CC IsoId=Q9DBD0-1; Sequence=Displayed;

CC Name=2;

CC IsoId=Q9DBD0-2; Sequence=VSP 006506;

CC -1- TISSUE SPECIFICITY: Highly expressed in spleen and testis;

CC detected at lower levels in lung and thymus.

CC -1- DISEASE: Defects in TNFRSF13C are a cause of severe B-cell deficiency. B-cell deficient strain A/WySn has a 4.7 kb insertion in the BAFFR gene leading to an altered C-terminus. The mutant RNA is not detectable. B-cell lymphoproliferation is normal, but the life span of peripheral B-cells is much reduced.

CC -1- SIMILARITY: Contains 1 TNFR-Cys repeat.

CC -----

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CC -----

DR EMBL: AF373847; AAK91827.1; -; mRNA.

DR EMBL: AK008142; BAB25490.1; -; mRNA.

DR HSPG: Q96R33; 100E.

DR WGI: WGI:1919299; TNFRSF13C.

DR GO: GO:0009897; C:external side of plasma membrane; IDA.

DR GO: GO:0016021; C:integral to membrane; TAS.

DR GO: GO:0031296; P:B cell costimulation; IDA.

DR GO: GO:0001782; P:B cell homeostasis; IMP.

DR GO: GO:0030890; P:positive regulation of B cell proliferation; IDA.

DR GO: GO:0045078; P:positive regulation of interleukin-gamma bio. .; IMP.

DR GO: GO:0042102; P:positive regulation of T cell proliferation; IDA.

DR GO: GO:0050776; P:regulation of immune response; IMP.

DR GO: GO:0031295; P:T cell costimulation; IDA.

DR InterPro: IPR001368; TNFR_C6.

DR PROSITE: PS00652; TNFR_NGFR_1; FALSE NEG.

DR PROSITE: PS00505; TNFR_NGFR_2; FALSE NEG.

KW Alternative splicing; Glycoprotein; Immune response; Membrane; Receptor; Signal-anchor; Transmembrane.

FT CHAIN 1 175

FT Tumor necrosis factor receptor superfamily member 13C.

FT /FTid=PRO_0000058934.

FT EXTRACELLULAR (Potential).

FT Signal-anchor for type III membrane protein (Potential).

FT Cytoplasmic (Potential).

FT TNFR-Cys (incomplete).

FT N-linked (GlcNAc...) (Potential).

FT By similarity.

FT Missing (in isoform 2).

FT /FTid=VSP_006506.

FT VARSPLIC 133 143

FT SEQUENCE 175 AA; 18798 MW; 28BC7C1A02F8B7EF CRC64;

Query Match 22.3%; Score 63; DB 1; Length 175;

Best Local Similarity 50.0%; Pred. No. 11;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 7 QCSQNEVFDLSLHACIPCOL 26
Db 21 QCNQTECFDPLVRNCVSCSEL 40

RESULT 57
Q3XS6_MOUSE PRELIMINARY; PRT; 175 AA.
AC Q3XS6;
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Tumor necrosis factor receptor superfamily, member 13C (BAF receptor).
GN Name=Trifsf13c;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=PCR rescued clones;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner C.M., Schuler G.D., Aleschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F., Diatchenko L., Marusina B., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C., Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosnak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W., Villalón D.K., Wuzny D.M., Sodergren E.U., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzywinski M.T., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=PCR rescued clones;
RG NIH MGC Project;
RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.
[3]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=A.S.W. and SuL/J; TISSUE=Spleen;
RA Libbey J.E., Peterson L.K., Tsunoda I., Fujinami R.S.; "Monoclonal MOG autoantibody from progressive EAE has the characteristics of a natural antibody.";
RT Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NonDerivs license
CC EMBL; BC104127; AA104128.1; -; mRNA.
DR EMBL; DQ294929; ABC24674.1; -; mRNA.
DR EMBL; DQ294928; ABC24673.1; -; mRNA.
DR MGI; MGI:1919299; Trifsf13c.
DR GO; GO:0009897; C:external side of plasma membrane; IDA.
DR GO; GO:0016021; C:integral to membrane; RCA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0031296; P:B cell costimulation; IDA.
DR GO; GO:0001782; P:B cell homeostasis; IMP.
DR GO; GO:0030890; P:positive regulation of B cell proliferation; IDA.

DR GO; GO:0045078; P:positive regulation of interferon-gamma bio. .; IMP.
DR GO; GO:0042102; P:positive regulation of T cell proliferation; IDA.
DR GO; GO:0050776; P:regulation of immune response; IMP.
DR GO; GO:0031295; P:T cell costimulation; IDA.
KM Receptor.
SQ SEQUENCE 175 AA; 18798 MW; 28BC7C1A02FB87EF CRC64;

Query Match 22.3%; Score 63; DB 2; Length 175;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 7 QCSQNEVFDLSLHACIPCOL 26
Db 21 QCNQTECFDPLVRNCVSCSEL 40

RESULT 58
Q8R4W8_MOUSE PRELIMINARY; PRT; 175 AA.
AC Q8R4W8;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE TRAF3 binding protein.
GN Name=Trifsf13c;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN NUCLEOTIDE SEQUENCE.
RP Mizuno K., Irie S., Sato T.-A.;
RA Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NonDerivs license
CC EMBL; AF350257; AAL63914.1; -; mRNA.
DR HSP; Q96R33; 100E.
DR Ensemble; ENSMUSG0000068105; Mus musculus.
DR MGI; MGI:1919299; Trifsf13c.
DR GO; GO:0009897; C:external side of plasma membrane; IDA.
DR GO; GO:0016021; C:integral to membrane; RCA.
DR GO; GO:0031296; P:B cell costimulation; IDA.
DR GO; GO:0001782; P:B cell homeostasis; IMP.
DR GO; GO:0030890; P:positive regulation of B cell proliferation; IDA.
DR GO; GO:0045078; P:positive regulation of interferon-gamma bio. .; IMP.
DR GO; GO:0042102; P:positive regulation of T cell proliferation; IDA.
DR GO; GO:0050776; P:regulation of immune response; IMP.
DR GO; GO:0031295; P:T cell costimulation; IDA.
SQ SEQUENCE 175 AA; 18846 MW; B64EFP4B52EE93B1 CRC64;

Query Match 22.3%; Score 63; DB 2; Length 175;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 7 QCSQNEVFDLSLHACIPCOL 26
Db 21 QCNQTECFDPLVRNCVSCSEL 40

RESULT 59
Q3U106_MOUSE PRELIMINARY; PRT; 200 AA.
AC Q3U106;
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Activated spleen cDNA, RIKEN full-length enriched library, clone:83001917 product:tumor necrosis factor receptor superfamily, member 13c, full insert sequence.
GN Name=Trifsf13c;

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Activated spleen;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Methods Enzymol. 303:19-44(1999).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Activated spleen;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Fritth M.C., Maeda N.,
 Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 Davis M.J., Wilmink L.G., Aidinis V., Allen J.E.,
 Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 Di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
 Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 Georgi-Jacob M., Gergely P., Gingeras T.R., Gojobori T., Green R.E.,
 Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 Hill D., Hummel L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 Liu S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 Matavuluri S., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 Motagui T., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 Ohtsuka Y., Orlowski V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
 Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
 Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 Sperling S., Stupka E., Sugtara K., Sultana R., Takenawa Y., Taki K.,
 Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yang K.,
 Yamashita H., Zdobych E., Zhu S., Zimmer A., Hide M., Bult C.,
 Glimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 Fuhueded C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Niimura N.,
 Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,
 Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Activated spleen;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RA Riken Genome Exploration Research Group, and Genome Science Group
 (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
 [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Activated spleen;
 RX MEDLINE=22354683; PubMed=1246851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 Okazaki Y., Otsu N., Saito R., Suzuki H., Yamana K., Kiyosawa H.,
 Yagi K., Tomaru Y., Hasegawa Y., Nogi A., Schonbach C., Gojobori T.,
 Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 Schiml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 Blake J.A., Brad D., Brusic V., Chochua C., Corbani L.E., Cousins S.,
 Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 Glimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 Maglott D.R., Maltais L., Marchionni L., McKenzie B., Miki H.,
 Nagashima T., Numata K., Okido T., Pavan W.J., Petrea G., Pesole G.,
 Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 Suterano R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 Wilmink L.G., Wyszewski-Boris A., Yanagisawa M., Yang I., Yang L.,
 Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Activated spleen;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
 Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 Kadota K., Matsuda H.A., Ashburner M., Batalov S., Caeavant T.,
 Fetschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 Schiml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
 Blake J., Bottelli D., Bojunga N., Carninci P., de Bonaldi M.F.,
 Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,
 Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilmink L.,
 Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Activated spleen;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Activated spleen;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 Kono H., Akiyama J., Nishi K., Kitsuwa T., Tashiro H., Itoh M.,
 Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
 Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Activated spleen;


```

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Cassavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan K.J., Malek J.A., Garcia A.M., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska M., Smolins D.E.,
RA Scherch A., Schein J.E., Jones S.U.M., Merra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: May be a germ cell-specific transcription factor that
CC plays important roles in spermatid differentiation and oocyte
CC development.
CC -1- SUBCELLULAR LOCATION: Nucleus (Potential).
CC -1- TISSUE SPECIFICITY: Exclusively expressed in testis and ovary.
CC localized to step 3-8 spermatids in testis and growing oocytes in
CC ovary.
CC -1- SIMILARITY: Contains 3 C2H2-type zinc fingers.
CC -----
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CC -----
DR EMBL: AF508984; AAN31656.1; -; mRNA.
DR EMBL: AK018361; BAB31177.1; -; mRNA.
DR EMBL: AK139827; BA24150.1; -; mRNA.
DR EMBL: BC064748; AA64748.1; -; mRNA.
DR Ensembl: ENSMUSG00000048626; Mus musculus.
DR MGI: MGI:2181068; Zfp393.
DR GO: GO:0007276; P:gametogenesis; IDA.
DR InterPro: IPR007087; ZnF_C2H2.
DR Pfam: PF00096; zf-C2H2; 3.
DR ProDom: PD000003; ZnF_C2H2; 2.
DR SMART: SM00355; ZnF_C2H2; 3.
DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE: PS00157; ZINC_FINGER_C2H2_2; 3.
KW DNA-binding; Metal-binding; Nuclear protein; Repeat; Transcription;
KW Transcription regulation; zinc; zinc-finger.
KM CHAIN 1 341
FT 1 341 /FTId=PRO_0000047556.
FT 2N_FING 256 280 C2H2-type 1.
FT 2N_FING 286 310 C2H2-type 2.
FT 2N_FING 316 338 C2H2-type 3.
FT 2N_FING 341 341 S -> G (in Ref. 3).
FT 2N_FING 341 341 L -> M (in Ref. 2; BAB31177).
FT 2N_FING 341 341 S -> G (in Ref. 3).
FT 2N_FING 341 341 L -> M (in Ref. 2; BAB31177).
SQ SEQUENCE 341 AA; 38076 MW; 03F400D4485DDB3A CRC64;

Query Match 22.3%; Score 63; DB 1; Length 341;
Best Local Similarity 28.2%; Pred. No. 22;
Matches 11; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

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DE Predicted protein.
GN ORFNames=A009001000683;
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eukaryotes; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxId=5062;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RIB 40;
RX PubMed=16372010; DOI=10.1038/nature04300;
RA Kusumoto K., Asai K., Sano M., Tanaka T., Kumagai T., Teraï G.,
RA Horiuchi H., Kitamoto K., Kobayashi T., Takeuchi M., Denning D.W.,
RA Galagan J.E., Nielsen W.C., Yu J., Archer D.B., Bennett J.W.,
RA Bhattacharya D., Cleveland T.E., Fedorova N.D., Gotch O., Horikawa H.,
RA Hosoyama A., Ichimomiya M., Igataishi R., Iwashita K., Juvadi P.R.,
RA Kato M., Kato Y., Kin T., Kokubun A., Maeda H., Maeyama N.,
RA Kato M., Kato Y., Kin T., Kokubun A., Maeda H., Maeyama N.,
RA Maruyama J., Nagasaki H., Nakajima T., Oda K., Okada K., Paulsen I.,
RA Sakamoto K., Sawano T., Takahashi M., Takase K., Terabayashi Y.,
RA Wortman J.R., Yamada O., Yamagata Y., Anzawa H., Hata Y., Koide Y.,
RA Komori T., Koyama Y., Minetoki T., Sunahara S., Tanaka A., Isono K.,
RA Kihara S., Ogasawara N., Kikuchi H.;
RT "Genome sequencing and analysis of Aspergillus oryzae."
RL Nature 438:1157-1161(2005).
CC -----
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CC -----
DR EMBL: AP007175; BAB65503.1; -; Genomic DNA.
DR EMBL: AP007175; BAB65503.1; -; Genomic DNA.
SQ SEQUENCE 345 AA; 38461 MW; 81A2549BFF02AD CRC64;

Query Match 22.3%; Score 63; DB 2; Length 345;
Best Local Similarity 34.9%; Pred. No. 22;
Matches 15; Conservative 11; Mismatches 15; Indels 2; Gaps 2;

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OY 1 MIMAGCCGQNEFYD-SLHACIPCOLRCSSNTPPLTCORYCN 42
DB 253 VIEILG-AGQDAFVSMHACAGKLCISVPEVHGYFPN 294

RESULT 63
O2WIG2 ASPOR PRELIMINARY; PRT; 442 AA.
ID O2WIG2 ASPOR PRELIMINARY; PRT; 345 AA.
AC O2WIG2;
RT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 3.
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 CC -----
 DR EMBL: AP007157; BAE58653.1; -; Genomic DNA.
 SO SEQUENCE 4427 AA; 49080 MW; 7877DD0025B08CA3 CRC64;
 Query Match 22.3%; Score 63; DB 2; Length 442;
 Best Local Similarity 39.0%; Pred. No. 28;
 Matches 16; Conservative 10; Mismatches 13; Indels 2; Gaps 2;
 Oy 1 MLOWAGCSQNEYPD-SILHACIPGOLRCSSNTPLTCGRY 40
 Db 349 ILEVVG-AGDEAFVSMHACKAGQLKCTIVPEVHGYF 388
 RESULT 64
 O3U022 MOUSE
 ID O3U022_MOUSE PRELIMINARY; PRT; 454 AA.
 AC O3U022;
 DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
 DT 11-OCT-2005, sequence version 1.
 DT 07-FEB-2006, entry version 5.
 DE 15 days embryo head cDNA, RIKEN full-length enriched library,
 DE clone: D93004D19; product: hypothetical Nectrin, C-terminal/laminin-type
 DE EGF-like domain/1IMP-like Ob-fold/EGF-like domain containing protein,
 DE full insert sequence.
 GN Name=Gm484;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RT "High-efficiency full-length cDNA cloning."
 RL Methods Enzymol. 303:19-44(1999).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Fritch M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Bremner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
 RA Ambesi-Impombato A., Apweiler R., Aurali R.N., Bailey T.L.,
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 RA Chu K.M., Dalla E., Daly M.P., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 RA Guentlich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hill D., Hummelbeck L., Iacono M., Ikeo K., Iwama A., Isikawa T.,
 RA Jaki M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Mortazavi A., Muller N., Nakano N., Nakaguchi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlandi V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
 RA Petrovski N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Roet B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schonbach C., Seligson K., Sempile C.A., Seno S., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Spelling S., Stupka E., Sugura K., Sultana R., Takemura Y., Taki K.,
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegener J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yang K.,
 RA Yamashita H., Zdobych E., Zhu S., Zimmer A., Hilde W., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,

RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Kono H., Nakano K., Nimomiya N.,
 RA Nishio T., Okada M., Plessey C., Shibata K., Shirai T., Suzuki S.,
 RA Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.,
 RT "The transcriptional landscape of the mammalian genome."
 RL Science 309:1559-1563(2005).
 [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the PANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome."
 RL Science 309:1564-1566(2005).
 [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nixaido I., Osato N., Saito R., Suzuki H., Yamamaki I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baladrelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schmitt L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Brad T., Brusic V., Chochia C., Corbani L.E., Cousins S.,
 RA Dalla E., Drigani T.A., Fletcher C.F., Forrest A., Fraser K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Guentlich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierzki R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Petrea G., Pesole G.,
 RA Petrovski N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita K.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imocani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino K., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Iwama M., Nishi K., Kiyosawa H., Kondo S., Yamamaki I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
 RA Kuehl P., Lewis S., Matsuo T., Nixaido I., Pesole G., Quackenbush J.,
 RA Schmitt L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baladrelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guentlich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombereis P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyoko-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).


```

RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
  Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
  prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
  Kono H., Akiyama Y., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
  Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
  Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
  Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
  Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J.,
  Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RA "RIKEN integrated sequence analysis (RISA) system-384-format
  sequencing pipeline with 384 multichannel sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
  Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
  Kawai J., Kojima M., Kono H., Murata M., Nakamura M., Niimomiya N.,
  Nishiyori H., Nomura K., Ohno M., Sakazume Y., Sano H., Sasaki D.,
  Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
  Muramatsu M., Hayashizaki Y.;
RA Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
EMBL AK142898; BAE2522.1; -; mRNA.
DR GO; GOI:005198; F:structural molecule activity; IEA.
DR InterPro; IPR002049; EGF_laminin.
DR InterPro; IPR013032; EGF_like_reg.
DR InterPro; IPR001134; Netrin_C.
DR Pfam; PF00053; laminin_BGF; 2.
DR Pfam; PF01759; NTR; 1.
DR SMART; SM00643; C345C; 1.
DR SMART; SM00180; EGF_lam; 2.
DR PROSITE; PS00022; EGF_1; UNKNOWN_2.
DR PROSITE; PS01248; EGF_LAM_1; 1.
DR PROSITE; PS00027; EGF_LAM_2; 2.
DR PROSITE; PS0189; NTR; 1.
KW Hypothetical protein.
SQ SEQUENCE 454 AA; 49238 MW; 24A0A9810BA5DF3 CRC64;
Query Match 22.3%; Score 63; DB 2; Length 454;
Best Local Similarity 29.9%; Pred. No. 29;
Matches 20; Conservative 6; Mismatches 19; Indels 22; Gaps 3;
QY 3 QMAGCSQNEYFDSL-LHAC-----IPCOLRCSNTPPLT-----CQRY 40
DB 242 QTSGGQSCKLTGTLTCNRCGPGYQOSRPRMFCQRIPEATITPATTPVASRSDPCCGG 301
QY 41 CNASVTN 47
DB 302 CNVSYS 308
RESULT 65
OSUSG7 HUMAN PRELIMINARY; PRT; 1560 AA.
ID OSUSG7 HUMAN PRELIMINARY; PRT; 1560 AA.
AC OSUSG7
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, sequence version 1.

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DT 07-FEB-2006, entry version 13.
DE Proprotein convertase subtilisin/kexin type 5 (Fragment).
GN Name=PCSK5; ORFNames=RP11-422N19.4-002;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Mashreghi-Mohammadi M.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Pelan S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Peck A.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
EMBL AL391868; CAI40809.1; JOINED; Genomic DNA.
DR EMBL; AL391868; CAI41234.1; -; Genomic DNA.
DR EMBL; AL391868; CAI41234.1; JOINED; Genomic DNA.
DR EMBL; AL589653; CAI41234.1; JOINED; Genomic DNA.
DR EMBL; AL589653; CAI40809.1; -; Genomic DNA.
DR EMBL; AL391868; CAI40809.1; JOINED; Genomic DNA.
DR EMBL; AL589653; CAI40675.1; JOINED; Genomic DNA.
DR EMBL; AL391868; CAI40675.1; JOINED; Genomic DNA.
DR EMBL; AL391868; CAI40675.1; -; Genomic DNA.
DR GO; GOI:0008233; F:peptidase activity; IEA.
DR GO; GO:004289; F:subtilase activity; IEA.
DR GO; GO:006508; F:proteolysis; IEA.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR006212; Furin_repeat.
DR InterPro; IPR002029; Pept_S8_S53.
DR InterPro; IPR002884; Protrcnconvertsp.
DR Pfam; PF02420; APP; 1.
DR Pfam; PF03860; DUF326; 2.
DR Pfam; PF01483; P_protein; 1.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Prodom; PD000717; Protrcnconvertsp; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00261; FU; 21.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Protease.
FT NON TER
SQ SEQUENCE 1560 AA; 173890 MW; 7211FBC127A8A08C CRC64;
Query Match 22.3%; Score 63; DB 2; Length 1560;
Best Local Similarity 32.6%; Pred. No. 11e+02;
Matches 14; Conservative 6; Mismatches 21; Indels 2; Gaps 1;
QY 7 QCSONEYFDSLHACIPCOLRCSNTPPLTCORYCNASTYNSV 49
DB 1154 KCSPEYWEDEAPGCKPCHVKCFHCGMPAEDG--QOTCMNSL 1194
RESULT 66
O4UHW4 THEAN
ID O4UHW4 THEAN PRELIMINARY; PRT; 974 AA.
AC O4UHW4
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE 1-phosphatidylinositol-4,5-bisphosphatephosphod ie sterase
DE (EC 3.1.4.11).
GN ORFNames=TA06965;
OS Theileria annulata.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;

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OC Theileria.
OX NCBI_TaxID=5874;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ankara isolate clone C9;
RX PubMed=1594597; DOI=10.1258/jism.98.7.320;
RA Pain A., Renaldi H., Berriman M., Murphy L., Yeats C.A., Weir W.,
RA Coulson R.M., Aslett S., Bishop R., Bouchier C., Cochet M.,
RA Coulson R.M., Cronin A., de Villiers E.P., Fraser A., Fosker N.,
RA Gardner M., Goble A., Griffiths-Jones S., Harris D.E., Katzer F.,
RA Latke N., Lord A., Maser P., McKellar S., Mooney P., Morton F.,
RA Nene V., O'Neill S., Price C., Quail M.A., Rabinowitz E.,
RA Rawlings N.D., Rutter S., Saunders D., Seeger K., Shah T., Squares R.,
RA Squares S., Tivey A., Walker A.R., Woodward J., Dobbelaere D.A.E.,
RA Langsley G., Rajandream M.A., McKeever D., Shields B., Tait A.,
RA Barrett B., Hall N.;
RT "Genome of the host-cell transforming parasite Theileria annulata
RT compared with T. parva.";
RL Science 309:131-133(2005).
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CC -----
CC EMBL, CR940347, CA173325.1; -, Genomic DNA.
DR GO; GO:0016787; F:hydrolyase activity; IEA.
DR GO; GO:0004433; F:phosphatidyl transferase activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006629; P:lipid metabolism; IEA.
DR InterPro; IPR000008; C2
DR InterPro; IPR011993; PH_type.
DR InterPro; IPR011192; PI_PLC.
DR InterPro; IPR000909; PI_PLC_X.
DR InterPro; IPR001711; PI_PLC_Y.
DR InterPro; IPR008162; Pyrophosphatase.
DR Pfam; PF00168; C2; 1
DR Pfam; PF00388; PI_PLC-X; 1.
DR Pfam; PF00387; PI_PLC-Y; 1.
DR PRINTS; PR00390; PHEPLIPASEC.
DR PRODOM; PD001202; PI_PLC_Y; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00148; PLCX; 1.
DR PROSITE; PS00004; C2_DOMAIN; 1.
DR PROSITE; PS00007; PI_PLC_X_DOMAIN; 1.
DR PROSITE; PS00008; PI_PLC_Y_DOMAIN; 1.
DR PROSITE; PS00387; PPASE; UNKNOWN_1.
KW Hydrolyase.
KW
SQ SEQUENCE 974 AA; 110874 MW; 0E4988BA23DBAE41 CRC64;

Query Match 22.1%; Score 62.5; DB 2; Length 974;
Best Local Similarity 29.2%; Pred. No. 75;
Matches 14; Conservative 9; Mismatches 24; Indels 1; Gaps 1;

QY 3 OMAGCGCNEVPSLLHACTPCQLRCSSNT-PPLTCQRCAVSNSV 49
DB 488 QIGGSASHSIAEALRGCRCLDCCQDGSSEPVLCIAWKCHITGV 535

RC Tissue=Testis;
RG The German cDNA consortium;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA) (ISOFORM 2), NUCLEOTIDE
RP SEQUENCE (LARGE SCALE MRNA) OF 2-995 (ISOFORM 1), AND VARIANT ILE-604.
RC TISSUE=Brain, and Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Narutina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stuppleon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighan S.J.,
RA Bosak S.A., McGwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Hellon E., Kettelman M., Madan A., Rodriguez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP VARIANT MKS3 PRO-376, AND TISSUE SPECIFICITY.
RX PubMed=16415887; DOI=10.1038/ng1713;
RA Smith U.M., Consuegra M., Tee L.J., McKee B.M., Maina E.N., Whelan S.,
RA Morgan N.V., Goranson E., Gissen P., Lillquist S., Aligians I.A.,
RA Ward C.J., Pasha S., Punyashetti R., Malik Sharif S., Bateman P.A.,
RA Bennett C.P., Woods C.G., McKown C., Bucourt M., Miller C.A., Cox P.,
RA Algezai L., Trembach R.C., Torres V.E., Attie-Bitach T., Kelly D.A.,
RA Maher R.R., Gattone V.H., Harris P.C., Johnson C.A.;
RT "The transmembrane protein meckelin (MKS3) is mutated in Meckel-Gruber
RT syndrome and the wpk rat.";
RL Nat. Genet. 38:191-196(2006).
CC -!- FUNCTION: May be related to the ciliary basal body.
CC -!- SUBCELLULAR LOCATION: Cell membrane; multi-pass membrane protein
CC (potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC Name=2;
CC IsoId=Q5HYA8-1; Sequence=Displayed;
CC IsoId=Q5HYA8-2; Sequence=VSP_017415, VSP_017416;
CC Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Widely expressed in adult and fetal tissues.
CC Expressed at higher level in spinal cord.
CC -!- DISEASE: Defects in TMEM67 are the cause of Meckel syndrome type 3
CC (MKS3) [MIM:607361]. MKS3 is an autosomal recessive disorder
CC characterized by a combination of renal cysts and variably
CC associated features including developmental anomalies of the
CC central nervous system (typically encephalocele), hepatic ductal
CC dysplasia and cysts, and polydactyly.
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CC -----
CC EMBL, BX648768; CA155999.1; -, mRNA.
DR EMBL; BC031220; AAH31220.1; -, mRNA.
DR EMBL; BC032835; AAH32835.1; ALT_INIT; mRNA.
DR EMBL; BC054338; AAH54338.1; ALT_INIT; mRNA.
DR Ensembl; ENSG00000154953; Homo sapiens.
DR HGNC; HGNC:28396; TMEM67.
DR MIM; 607361; phenotype.
DR InterPro; IPR000150; Hypoeth_cof.
DR Alternative splicing; Disease mutation; Membrane;
KW Polymorphism; Transmembrane.
FT CHAIN 1 995 Meckelin.


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FT TRANSMEM 9 29 /FTId=PRO_0000225689.
FT TRANSMEM 526 546 Potential.
FT TRANSMEM 570 590 Potential.
FT TRANSMEM 609 628 Potential.
FT TRANSMEM 689 709 Potential.
FT TRANSMEM 734 754 Potential.
FT TRANSMEM 939 959 Potential.
FT CARBOHYD 242 242 VER -> GKN (in isoform 2).
FT VARSPLIC 136 138 /FTId=VSP_017415.
FT VARSPLIC 139 995 Missing (in isoform 2).
FT VARSPLIC 376 376 /FTId=VSP_017416.
FT VARSPLIC 376 376 O -> P (in mks3).
FT VARSPLIC 604 604 /FTId=VAR_025474.
FT VARSPLIC 604 604 V -> I (in dbSNP:3134031).
FT VARSPLIC 604 604 /FTId=VAR_025475.
FT VARSPLIC 604 604 /FTId=VAR_025475.
SQ SEQUENCE 995 AA; 111731 MW; AEBD4A6B84F759A8 CRC64;

Query Match 22.1%; Score 62.5; DB 1; Length 995;
Best Local Similarity 21.4%; Pred. No. 77;
Matches 12; Conservative 10; Mismatches 15; Indels 19; Gaps 1;

OY 3 QNAGGCSQNEFPYSLHACIPC-----QURCSSNTPPLTCOR 39
DB 44 QQPEKCDNNQYFDISALSCVPCGANOROPAGRTSCVCLPGFQMTSNNGGPATICK 99

RESULT 68
ID 017969 CAEEL PRELIMINARY; PRT; 999 AA.
AC 017969; Q19998;
DT 01-NOV-1996; Integrated into UniProtKB/TrEMBL.
DT 01-MAY-1999; sequence version 2.
DT 07-FEB-2006; entry version 31.
DE Hypothetical protein.
GN ORFNames=F34D10.2;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology."
RL Science 282:2012-2018(1998).
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CC -----
EMBL: Z37139; CA85494.1; -, Genomic DNA.
EMBL: Z34799; CA85494.1; JOINED; Genomic DNA.
EMBL: Z34799; CA84320.1; -, Genomic DNA.
EMBL: Z37139; CA84320.1; JOINED; Genomic DNA.
DR PIR: T19275; T19275.
DR Ensembl: F34D10.2; Caenorhabditis elegans.
DR WormBase: WBGene00009372; F34D10.2.
DR WormBase: F34D10.2; CE01570.
DR GO: GO:0006270; P:DNA replication initiation; IEA.
DR GO: GO:0000074; P:regulation of progression through cell cycle; IEA.
DR InterPro: IPR003874; CDC45 like.
DR PANTHER: PTHR10507; CDC45 like; 4.
DR Pfam: PF02724; CDC45; 1.
DR Complete proteome: Hypothetical protein.
KW SEQUENCE 999 AA; 114888 MW; 8B46A4EB375357C9 CRC64;

Query Match 22.1%; Score 62.5; DB 2; Length 999;
Best Local Similarity 42.5%; Pred. No. 77;
Matches 17; Conservative 2; Mismatches 20; Indels 1; Gaps 1;
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OY 13 YEDSLHACIPCOL-RCSSTNTPPLTCORCNASVTNSVG 51
DB 516 YEDSLHACIPCOL-RCSSTNTPPLTCORCNASVTNSVG 555

RESULT 69
ID 051ED6 ENTHI PRELIMINARY; PRT; 1917 AA.
AC 051ED6;
DT 07-JUN-2005; Integrated into UniProtKB/TrEMBL.
DT 07-JUN-2005; sequence version 1.
DT 07-FEB-2006; entry version 8.
DE Protein kinase, putative.
GN ORFNames=10.t00040;
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=294381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HM-1:IMSS;
RX PubMed=15729342; DOI=10.1038/nature03291;
RA Loftus B.J., Anderson I., Davies R., Almark U.C., Samuelson J.,
RA Amodeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
RA Suh B., Pop M., Duchene M., Ackers J., Tannich B., Leipzig M.,
RA Hofer M., Bruchhaus I., Willhoest U., Bhattacharya A.,
RA Chillingworth T., Churche C.M., Hance Z., Harris B., Harris D.,
RA Jagels K., Moule S., Mungall K.L., Ormond D., Squares R.,
RA Whitehead S., Quail M.A., Rabinowitsch E., Norberts R., Price C.,
RA Wang Z., Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S.,
RA Lohia A., Foster P.G., Sitcheritz-Ponten F., Weber C., Singh U.,
RA Mukherjee C., El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M.,
RA Barrell B.G., Fraser C.M., Hall N.;
RT "The genome of the protist parasite Entamoeba histolytica."
RL Nature 433:865-868(2005).
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
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CC -----
EMBL: AAFB01000051; EAL5121.1; -, Genomic DNA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0004667; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO: GO:0004668; F:protein amino acid phosphorylation; IEA.
DR InterPro: IPR006210; EGF.
DR InterPro: IPR012286; Fc3 N_cyt.
DR InterPro: IPR006212; Furin repeat.
DR InterPro: IPR000719; Prot Kinase.
DR InterPro: IPR008271; Ser Thr_kin_AS.
DR InterPro: IPR002290; Ser Thr_kinase.
DR InterPro: IPR001368; TNFR_c6.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF02822; Anticstasin; 1.
DR Pfam: PF07699; GCC2 GCC3; 2.
DR Pfam: PF00069; PKinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: PD000001; Prot_Kinase; 1.
DR SMART: SM00181; EGF; 3.
DR SMART: SM00261; FU; 4.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS00108; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00109; PROTEIN KINASE ST; 1.
DR PROSITE: PS00050; TNFR_NGFR_2; 1.
KW SEQUENCE 1917 AA; 212684 MW; 4AD7144F6A3CF30D CRC64;

Query Match 22.1%; Score 62.5; DB 2; Length 1917;
Best Local Similarity 31.0%; Pred. No. 15e+02;
Matches 13; Conservative 7; Mismatches 21; Indels 1; Gaps 1;
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FT DOMAIN 983 1021 LDI-receptor class A 1.
FT DOMAIN 1022 1062 LDI-receptor class A 2.
FT DOMAIN 1063 1100 LDI-receptor class A 3.
FT DOMAIN 1103 1143 LDI-receptor class A 4.
FT DOMAIN 1143 1180 LDI-receptor class A 5.
FT DOMAIN 1180 1224 LDI-receptor class A 6.
FT DOMAIN 1230 1268 LDI-receptor class A 7.
FT DOMAIN 1273 1312 LDI-receptor class A 8.
FT DOMAIN 1324 1362 LDI-receptor class A 9.
FT DOMAIN 1376 1415 LDI-receptor class A 10.
FT DOMAIN 1419 1457 LDI-receptor class A 11.
FT DOMAIN 1462 1551 Fibrinectin type-III 1.
FT DOMAIN 1559 >1592 Fibrinectin type-III 2.
FT CARBOHYD 6 65 (Potential).
FT CARBOHYD 65 65 (Potential).
FT CARBOHYD 275 275 (Potential).
FT CARBOHYD 337 337 (Potential).
FT CARBOHYD 337 337 (Potential).
FT CARBOHYD 523 523 (Potential).
FT CARBOHYD 581 581 (Potential).
FT CARBOHYD 725 725 (Potential).
FT CARBOHYD 778 778 (Potential).
FT CARBOHYD 975 975 (Potential).
FT CARBOHYD 1098 1098 (Potential).
FT CARBOHYD 1152 1152 (Potential).
FT CARBOHYD 1366 1366 (Potential).
FT CARBOHYD 1454 1454 (Potential).
FT CARBOHYD 1514 1514 (Potential).
FT CARBOHYD 985 997 (Potential).
FT DISULFID 992 1010 By similarity.
FT DISULFID 1004 1019 By similarity.
FT DISULFID 1024 1038 By similarity.
FT DISULFID 1032 1051 By similarity.
FT DISULFID 1045 1060 By similarity.
FT DISULFID 1065 1077 By similarity.
FT DISULFID 1072 1090 By similarity.
FT DISULFID 1084 1099 By similarity.
FT DISULFID 1105 1117 By similarity.
FT DISULFID 1112 1130 By similarity.
FT DISULFID 1124 1141 By similarity.
FT DISULFID 1145 1155 By similarity.
FT DISULFID 1150 1168 By similarity.
FT DISULFID 1162 1222 By similarity.
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FT DISULFID 1190 1209 By similarity.
FT DISULFID 1232 1244 By similarity.
FT DISULFID 1239 1257 By similarity.
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FT DISULFID 1275 1288 By similarity.
FT DISULFID 1283 1301 By similarity.
FT DISULFID 1295 1310 By similarity.
FT DISULFID 1326 1338 By similarity.
FT DISULFID 1333 1351 By similarity.
FT DISULFID 1345 1360 By similarity.
FT DISULFID 1378 1391 By similarity.
FT DISULFID 1385 1404 By similarity.
FT DISULFID 1398 1413 By similarity.
FT DISULFID 1421 1433 By similarity.
FT DISULFID 1427 1446 By similarity.
FT DISULFID 1440 1455 By similarity.
FT NON_TER 1 1
FT NON_TER 1592 1592
SQ SEQUENCE 1592 AA; 178411 MW; 24EDAA5BA231B203 CRC64;

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Query Match 21.9%; Score 62; DB 1; Length 1592;
 Best Local Similarity 33.3%; Pred. No. 1.4e+02;
 Matches 15; Conservative 6; Mismatches 18; Indels 6; Gaps 2;

QY 6 GCSQNEYFDSLHACIP-----CQLR--CSSNTPPTLCORYCNAS 44
 Db 1376 GRCSTRFECCQAHKICPMWKRCDGRDRCDGDRSICPTHSLS 1420

RESULT 72

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Q6BG85 PARTE
ID Q6BG85 PARTE PRELIMINARY; PRT; 3622 AA.
AC Q6BG85;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DE 07-FEB-2006, entry version 8.
DE Extracellular matrix-like protein, putative.
GN ORFNames=PTMB_137c;
OS Paramesicium tetraurelia.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Periculida;
OC Paramesicidae; Paramesicium.
OX NCBI_TaxId=5886;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Stock d4-2;
RX PubMed=15296759; DOI=10.1016/j.cub.2004.07.029;
RA Zagulski M., Nowak J.K., Le Mouel A., Nowacki M., Migdalski A.,
RA Gromadka R., Noel B., Blanc I., Dessen P., Wincker P., Keller A.M.,
RA Cohen U., Meyer E., Sperling L.;
RT "High Coding Density on the Largest Paramesicium tetraurelia Somatic
RT Chromosome."
RL Curr. Biol. 14:1397-1404(2004).
RL [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Stock d4-2;
RA Nowak J.K., Migdalski A., Gromadka R., Zagulski M.,
RT "Paramesicium megabase sequencing project."
RT Submitted (Jul-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; CR548612; CAH0335.1; -; Genomic DNA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001450; 4Fe4S_Fe_S_bd.
DR InterPro; IPR013320; ConA_like_subgrp.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR013111; EGF extracell.
DR InterPro; IPR006212; EGF-like_reg.
DR InterPro; IPR001368; TNER_c6.
DR PRINTS; PR00353; 4FE4SFROXIN.
DR SMART; SM00181; EGF 4.
DR SMART; SM00261; FU; 10.
DR PROSITE; PS01186; EGF 2; UNKNOWN 2.
DR PROSITE; PS00652; TNER_NGFR_1; UNKNOWN 1.
SQ SEQUENCE 3622 AA; 418776 MW; F042B2B5C3BB8BD0 CRC64;

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Query Match 21.9%; Score 62; DB 2; Length 3622;
 Best Local Similarity 29.3%; Pred. No. 3.4e+02;
 Matches 12; Conservative 6; Mismatches 15; Indels 8; Gaps 2;

QY 7 GCSQNEYFDSLHACIPQRCSSNTPPTLCORYCNASVTN 47
 Db 2224 QCDHQYQDK--NGCLPCSIKCGNG-----CYTYGNMNCIN 2256

RESULT 73
 ID GASAJ_ARATH STANDARD; PRT; 99 AA.
 AC P46687;
 DT 01-NOV-1995, integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1995, sequence version 1.
 DT 07-MAR-2006, entry version 38.
 DE Gibberellin-regulated protein 3 precursor.
 GN Name=GASAJ; OrderedLocustNames=At4g09600; ORFNames=TT25P22.40;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxId=3702;

RA NUCLEOTIDE SEQUENCE.
 RP STRAIN=cv. Columbia; Tissue=seed;
 RC MEDLINE=95248483; PubMed=772751;
 RA Herzog M., Dorne A.-M., Grellet F.;
 RT "GASA, a gibberellin-regulated gene family from Arabidopsis thaliana
 RL Plant Mol. Biol. 27:743-752(1995).
 [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083488; PubMed=10617198; DOI=10.1038/47134;
 RA Mayer K.F.X., Schnell C., Wandt R., Murphy G., Volckaert G.,
 RA Pohl T., Duesterhoef A., Stiekema W., Entian K.-D., Terry N.,
 RA Harris B., Ansoer W., Brandt P., Griwell L.A., Rieger M.,
 RA Weichselgartner M., de Simone V., Obermaier B., Mahe R., Mueller M.,
 RA Kreis M., Delseny M., Pisdemenech P., Watson M., Schmidheini T.,
 RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
 RA Vos P., Hohnel J., Zimmermann W., Wedler H., Ridley P.,
 RA Langham S.-A., McCullagh B., Billam L., Roben J.,
 RA Van der Schueren J., Grymoprez B., Chuang Y.-J., Vandebussche F.,
 RA Breken M., Weltjens I., Voet M., Baetiaens I., Aert R., Defoor E.,
 RA Weitzengerger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
 RA Holzner E., Brandt A., Peters S., van Staveren M., Dirxse W.,
 RA Woolfman P., Klein Lankhorst R., Rose M., Hauf J., Koester P.,
 RA Bernels S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
 RA De Keyser A., Buyschaert C., Gielen J., Villarreal R., De Clercq R.,
 RA Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,
 RA Clark L., Dosselt J., Hall S., Kay M., Lennard N., Mcay K., Mayes R.,
 RA Petrelet A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
 RA Borikova D., Bloecher H., Scharte M., Grimm M., Loehner T.-H.,
 RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fairman B., Granderath K., Dauner D., Herzl A.,
 RA Neumann S., Argifolou A., Vitale D., Liguori R., Piravandi E.,
 RA Masenat O., Ouglet F., Clabaud G., Muendlein A., Felber R.,
 RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
 RA Ghibdon F., Cooke R., Berger C., Montfort A., Casachertta E.,
 RA Hejnen L., Weber N., Vandenbol M., Bagues M., Terol J., Torres A.,
 RA Perez-Perez A., Furnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
 RA Hejnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielek C.,
 RA Fishman P., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
 RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
 RA Parnell L., Dedha N., Gnoj L., Schutz K., Huang E., Spiegel L.,
 RA Sekon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
 RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
 RA Lacroille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
 RA Mux P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
 RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W.,
 RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
 RA Du H., Ali J., Berghoff A., Jones K., Dione K., Cotton M., Joshu C.,
 RA Antonou B., Zidanic M., Strong C., Sun H., Lamar B., Jordan C.,
 RA Ma P., Zhong J., Preston R., Vill D., Shepher M., Matero A., Shah R.,
 RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Tili S.,
 RA Granat S., Shohdy N., Hasegawa A., Hameed A., Iodhi M., Johnson A.,
 RA Chen E., Maria M.A., Martensen R., McCombe W.R.;
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
 RL thaliana.";
 RL Nature 402:769-777(1999).
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=cv. Columbia;
 RX MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1088305;
 RA Yamada K., Lim J., Dale J.M., Chen H., Shim P., Palm C.J.,
 RA Chantwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
 RA Karlin-Neumann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
 RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
 RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansaty Y.,
 RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
 RA Chao Q., Choy N., Enju A., Goldsmith A.D., Guiraj M., Hansen N.F.,
 RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
 RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
 RA Kamuya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
 RA Satou M., Tame R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,

RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
 RT "Empirical analysis of transcriptional activity in the Arabidopsis
 RL genome.";
 RL Science 302:842-846(2003).
 CC -!- FUNCTION: Involved in late stages of seed maturation, or in early
 CC steps of germination.
 CC -!- SUBCELLULAR LOCATION: Secreted protein.
 CC -!- TISSUE SPECIFICITY: Siliques and dry seeds.
 CC -!- PTM: Six disulfide bonds may be present.
 CC -!- SIMILARITY: Belongs to the GAST1 family.
 CC
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 CC Distributed under the Creative Commons Attribution-NonDerivs license
 CC
 DR EMBL: U11764; AAB0308.1; -; mRNA.
 DR EMBL: AL161515; CAB78083.1; -; Genomic DNA.
 DR EMBL: AL161831; CAB82127.1; -; Genomic DNA.
 DR EMBL: AY052302; AAK96495.1; -; mRNA.
 DR PIR: S60231; S60231.
 DR GenomeReviews; CT486007_GR; AT4G09600.
 DR TAIR: At4G09600; -.
 DR LinkHub: P46687; -.
 DR InterPro: IPR003854; GASA.
 DR Pfam: PF02704; GASA; 1.
 DR Signal.
 FT SIGNAL 1 18 Potential.
 FT CHAIN 19 99 Gibberellin-regulated protein 3.
 FT FTID=PRO_0000021324.
 SQ SEQUENCE 99 AA; 10705 MW; 84549B74B08A47FA CRC64;
 Query Match 21.7%; Score 61.5; DB 1; Length 99;
 Best Local Similarity 35.6%; Pred. No. 9;
 Matches 16; Conservative 7; Mismatches 17; Indels 5; Gaps 2;
 QY 6 GCGGCGNEFDSLTHACTPQGLRCSSNPPLFCQRY----CNASVT 46
 DB 47 GRCSSKRPNUCLPRACNSCYRCNC-VPGTAGNHHLCPCTASIT 90
 RESULT 74
 ID Q85Z58 DROME PRELIMINARY; PRT; 353 AA.
 AC Q85Z58;
 DT 01-UN-2002, integrated into UniProtKB/TrEMBL.
 DT 01-UN-2002, sequence version 1.
 DT 07-FEB-2006, entry version 11.
 DE RE16222D.
 DE ORFNames=CG7348;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Berkley.
 RC Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Doresett V., Dresnek D., Farfan D., Fisse E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Ceñikler S.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
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 CC
 DR EMBL: AY071103; AAL8725.1; -; mRNA.
 DR FlyBase: FBgn0036940; CG7348.
 DR GO: GO:0005576; C:extracellular region; IEA.
 DR GO: GO:0008061; F:chitin binding; IEA.
 DR GO: GO:0006030; P:chitin metabolism; IEA.
 DR InterPro: IPR002557; Pfam: Chitin_bd.

```

DR Pfam; PF01607; CBM_14; 4.
DR SMART; SM00494; ChtBD2; 3.
DR PROSITE; PS50940; CHIT_BIND_II; 4.
SQ SEQUENCE 353 AA; 39713 MW; F5AB27B9ACFF9921 CRC64;

Query Match 21.7%; Score 61.5; DB 2; Length 353;
Best Local Similarity 28.1%; Pred. No. 34;
Matches 16; Conservative 8; Mismatches 20; Indels 13; Gaps 3;

QY 7 OCSQNEYPDSLHACIPCOL-----RCSSNTP-----PLTCGRY--CNASTVNSVX 50
DB 118 KCSVGNYPDPARRACLPVAISAHQSCVLPDPNATLANPSDCEYFRCHSGCAELVQ 174

RESULT 75
O9VW81 DROME PRELIMINARY; PRT; 353 AA.
ID O9VW81 DROME PRELIMINARY; PRT; 353 AA.
AC O9VW81;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DE 07-FEB-2006, entry version 23.
DE CG7348-PA.
CN ORFNames=CG7348, Dmel_CG7348;
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amaralides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mills G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Buck J., Brockstein P., Brodtier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Deodhon K., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durkin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalili B., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasro P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Moadary C., Morris J., Moshireli A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Pui V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.F., Smith T.,
RA Spier E., Spirding A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"the genome sequence of Drosophila melanogaster.";
Science 287:2185-2195 (2000).
[2]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,

```

DE Hypothetical protein CBG08690.
GN Name=CBG08690;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
CC Rhabditidae; Peloderinae; Caenorhabditis.
LN NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=AF16;
RX PubMed=14624247; DOI=10.1371/journal.pbio.0000045;
RA Stein L.D., Bao Z., Blasiar D., Blumenthal T., Brent M.R., Chen N.,
RA Chinwalla A., Clarke L., Clee C., Coghlan A., Coulson A.,
RA D'Eustachio P., Fitch D.H.A., Fulton L.A., Fulton R.E.,
RA Griffiths-Jones S., Harris T.W., Hillier L.W., Kamath R.,
RA Kuwabara P.E., Mardis E.R., Marra M.A., Miner T.L., Mink P.,
RA Mullikin J.C., Plumb R.W., Rogers J., Schein J.E., Solomon M.,
RA Speth J., Stajich J.E., Wei C., Wiley D., Wilson R.K., Durbin R.,
RA Waterston R.H.;
RT "The genome sequence of *Caenorhabditis briggsae*: a platform for
RT comparative genomics."
RL PLOS Biol. 1:166-192(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; CAAC0100037; CAB64085.1; -; Genomic_DNA.
DR InterPro; IPR009475; DUF1096.
DR InterPro; IPR00341; DUF139_Cys_rich.
DR Pfam; PF02363; C_triplex; 10.
DR Pfam; PF06493; DUF1096; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 432 AA; 46913 MW; CIDBA1E739E95F6 CRC64;

Query Match 21.7%; Score 61.5; DB 2; Length 432;
Best Local Similarity 31.9%; Pred. No. 42;
Matches 15; Conservative 4; Mismatches 15; Indels 13; Gaps 2;

Qy 3 QMAGGCGSNEYFDSLHACIPQLRCSNTPTTCORYCNASVTSV 48
Db 361 QCAAGCGS-----CQAGCVCQQQDPACQCAACGSSCSNS 395

RESULT 77
Q22423 CAEBL PRELIMINARY; PRT; 483 AA.
AC Q22423;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 2.
DT 21-FEB-2006, entry version 42.
DE Hypothetical protein.
GN ORFNames=T12A7.2;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
CC Rhabditidae; Peloderinae; Caenorhabditis.
LN NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode *C. elegans*: a platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
CC -----
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CC -----
DR EMBL; Z73911; CAA98142.2; -; Genomic_DNA.
DR PIR; G88846; G88846.
DR PIR; T24856; T24856.

DR HSSP; P00750; ITPG.
DR Ensemble; T12A7.2; Caenorhabditis elegans.
DR WormBase; WBGene00011723; T12A7.2.
DR WormRep; T12A7.2; CE23979.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR00742; EGF_3.
DR InterPro; IPR013032; EGF_like_reg.
DR SMART; SM00181; EGF; 1.
DR PROSITE; PS00022; EGF_1; 3.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 1.
KW Cell adhesion; Complete proteome; EGF-like domain;
KW Hypothetical protein; Membrane.
SQ SEQUENCE 483 AA; 54281 MW; 4B2B7AB14BE0890E CRC64;

Query Match 21.7%; Score 61.5; DB 2; Length 483;
Best Local Similarity 31.8%; Pred. No. 48;
Matches 14; Conservative 5; Mismatches 20; Indels 5; Gaps 1;

Qy 8 CSONEYFDSLHACIPQLRCSNTPTTCORYCNASVTSV 51
Db 108 CMNDGYFNHTLGRGV-----CTSNWGEHCIFRNSGVNKTSG 146

RESULT 78
Q5UOL4 MIMIV PRELIMINARY; PRT; 491 AA.
ID Q5UOL4 MIMIV
AC Q5UOL4;
DT 07-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 07-DEC-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Hypothetical protein.
GN ORFNames=MIMI_L417;
OS Mimivirus.
OC Viruses; dsDNA viruses, no RNA stage; Mimivirus.
LN NCBI_TaxID=212035;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Rowbotham-Bradford;
RX MEDLINE=22550848; PubMed=12663918; DOI=10.1126/science.1081867;
RA La Scola B., Audic S., Robert C., Abergel C., Renesto P., Ogata H.,
RA Drancourt M., Birtles R., Claverie J.M., Raoult D.;
RT "A giant virus in amoebae."
RL Science 299:2033-2033(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Rowbotham-Bradford;
RX PubMed=15486256; DOI=10.1126/science.1101485;
RA Raoult D., Audic S., Robert C., Abergel C., Renesto P., Ogata H.,
RA La Scola B., Susan M., Claverie J.-M.;
RT "The 1.2-megabase genome sequence of Mimivirus."
RL Science 306:1344-1350(2004).
CC -----
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CC -----
DR EMBL; AY653733; AAV50686.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 491 AA; 56133 MW; A3E1516CA622D31F CRC64;

Query Match 21.7%; Score 61.5; DB 2; Length 491;
Best Local Similarity 31.4%; Pred. No. 49;
Matches 16; Conservative 9; Mismatches 21; Indels 5; Gaps 2;

Qy 2 LQMGCGSNEYFDSLHACIPQ---LRCSNTPTTCORYCNASVTSV 49
Db 77 IKMTGQ--TQETLDLVKAVIRSNIIILSCNNNISQALCONFYGLSTSL 125

RESULT 79
Q5VTR9 DROME PRELIMINARY; PRT; 798 AA.
ID Q5VTR9 DROME

AC Q9VTR9; 01-MAY-2000, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-2000, sequence version 1.
 DT 07-FEB-2006, entry version 27.
 DE CG17824.PA.
 GN ORFNames=CG17824, Dmel_CG17824;
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertan B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunker B.C., Dunn P.,
 RA Durkin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacible J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reibert K., Remington K., Saunders R.D.C., Scheeler F., Shen T.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spredling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitskas R., Tecior C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan W., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celinker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacible J.M., Park S., Pfeiffer B.D., Richards S., Soddegren E.J.,
 RA Svitskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
 melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svitskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celinker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 a genomic perspective.";
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).

RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Miara S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Bernan B.P.,
 RA Bertencourt B.R., Celinker S.E., de Grey A.D.N.-J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RG Berkeley *Drosophila* Genome Project;
 RA Celinker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
 RA Hoskins R., Stapleton M., Pacible J., Park S., Svitskas R., Smith E.,
 RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RG Flybase;
 RL Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.
 CC -1- INTERACTION:
 Q9VW72:CG10154; NBExp=1; Intact=EBI-155190, EBI-166182;
 Q9VW8:CG15032; NBExp=1; Intact=EBI-155190, EBI-172473;
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 EMBL: AE003543; AAF49977.1; -; Genomic_DNA.
 DR Flybase: FBgn0036234; CG17824.
 DR GO: GO:000515; F:protein binding; IPT.
 DR InterPro: IPR02557; Pfam: Pfam01607; CSM_14; 12.
 DR Pfam: PF01607; CSM_14; 12.
 DR SMART: SM00494; CHTBD2_7.
 DR PROSITE: PS00940; CHTT BIND II; 12.
 SQ SEQUENCE 798 AA, 88442 MW, 19579816980DF483 CRC64;
 Query Match 21.7%; Score 61.5; DB 2; Length 798;
 Best Local Similarity 35.5%; Pred. No. 8;
 Matches 11; Conservative 9; Mismatches 10; Indels 1; Gaps 1;
 QY 3 QMAGCQSNVEYFDLILHAC-IPQIARCSNT 32
 DB 758 QIDGCAQGEFNRRLNCEVDALQCKSDT 788
 RESULT 80
 Q3UTW2_MOUSE PRELIMINARY; PRT; 186 AA.
 ID Q3UTW2;
 AC Q3UTW2;
 DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
 DT 11-OCT-2005, sequence version 1.
 DT 07-FEB-2006, entry version 5.
 DE Adult male aorta and vein cDNA. RIKEN full-length enriched library,
 DE clone: A530084C06 product: hypothetical Arginine-rich region profile
 DE containing protein, full insert sequence.
 GN Name=Foxq1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6876(99)03004-9;
 RA Carinci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";

Methods Enzymol. 303:19-44(1999).

[2]

NUCLEOTIDE SEQUENCE.

RX STRAIN=C57BL/6J; TISSUE=Aorta and vein;
DOI=10.1126/science.1112014;
PubMed=16141072;

RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Bremner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilmung L.G., Aldins V., Allen J.E., Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L., Banerji M., Baxter L., Beisler K.W., Bersano T., Bonio H., Chalk A.M., Chin K.P., Chowdhury V., Christoffels A., Clutcher D.K., Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G., Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M., Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E., Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N., Hill D., Hummelink L., Iacono M., Ikeo K., Ikoma A., Ishikawa T., Jack M., Kanapin A., Katoh M., Kawasawa Y., Kelso A., Kitamura H., Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Kurochkin I.V., Laeaue L.F., Lazarevic D., Lipovich L., Liu J., Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L., Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K., Motegual-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P., Okazaki Y., Orlowski V., Pang K.C., Pavan W.J., Pavoni G., Pesole G., Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M., Rosset B., Rubin Y., Salzberg S.L., Sandelin A., Schneider C., Schombach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y., Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Sperling S., Stump C.E., Sugita K., Sultana R., Takehana Y., Taki K., Tammoja K., Tan S.H., Tang S., Taylor M.S., Tegner U., Teichmann S.A., Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yeig K., Yamamoto S.M., Yeates R.D., Zhu E.T., Brusic A., Hide W., Bult C., Grimmond S.M., Tesdale R.D., Liu E.T., Bruscia V., Quackenbush J., Wahlestedt C., Mattick J.S., Hume D.A., Kai C.,asaki D., Tomaru Y., Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Kawahara T., Kohjima M., Kondou S., Konno H., Nakano K., Niimura N., Nishino T., Okada M., Plešny C., Shibata K., Shiraki T., Suzuki S., Tagami M., Waki K., Watanabe A., Okumura-Oho Y., Suzuki H., Kawai J., Hayashizaki Y.;

RT "The transcriptional landscape of the mammalian genome.";
Science 309:1559-1563(2005).

RN [3]

NUCLEOTIDE SEQUENCE.

RX STRAIN=C57BL/6J; TISSUE=Aorta and vein;
PubMed=16141073; DOI=10.1126/science.1112009;
RIKEN Genome Exploration Research Group, and Genome Science Group

RG (Genome Network Core Team) and the RANOM Consortium;

RT "Antisense Transcription in the Mammalian Transcriptome.";
Science 309:1564-1566(2005).

RN [4]

NUCLEOTIDE SEQUENCE.

RX STRAIN=C57BL/6J; TISSUE=Aorta and vein;
MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Mikado I., Osato N., Saito R., Suzuki H., Yanahara I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kannadin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Bruce V., Choithia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grilmond S., Gustincich S., Hirokawa N., Jackson I.U., Jarvis E.D., Kanai A., Kawaji H., Kawasaki Y., Kedzierzki R.M., King B.L., Kangaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Malais L., Marchionni L., McKenzie L., Miki H., Nagashina T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sultana R., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takemura Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilmung L.G., Wyshnaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirokawa K., Kishikawa T., Komoto H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki K., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;

RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).

RL [5]

NUCLEOTIDE SEQUENCE.

RX STRAIN=C57BL/6J; TISSUE=Aorta and vein;
MEDLINE=21085560; PubMed=11217851; DOI=10.1038/35055500;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Komoto H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Scuderi P., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barab G., Blake J., Bedford D., Bojunga N., Carninci P., de Bona M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofman M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima Y., Mazzarelli J., Monbaets P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaka H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilmung L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai J., Kohzuki S., Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).

RL [6]

NUCLEOTIDE SEQUENCE.

RX STRAIN=C57BL/6J; TISSUE=Aorta and vein;
MEDLINE=204939374; PubMed=11042159; DOI=10.1101/gr.145100;

RA Carninci P., Shibata Y., Hayatsu N., Sugihara Y., Shibata K., Itoh M., Komoto H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).

RL [7]

NUCLEOTIDE SEQUENCE.

RX STRAIN=C57BL/6J; TISSUE=Aorta and vein;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoke S., Sasaki N., Carninci P., Komoto H., Akiyama Y., Nishi K., Kitunari T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishie T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuzawa S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multiplexed sequencer.";
Genome Res. 10:1757-1771(2000).

RL [8]

NUCLEOTIDE SEQUENCE.

RX STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S., Kawai J., Kojima M., Komoto H., Murata M., Nakamura M., Niimura N., Nishiyori H., Nomura K., Ono M., Sakazume N., Sano H., Saeki D., Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watabiki A., Muramatsu M., Hayashizaki Y.;

RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.

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DR EMBL: AK139028; BAE23868.1; -; mRNA.
DR MGI: MGI:1298228; Foxq1.
DR GO: GO:0031069; P.hair follicle morphogenesis; IMP.
KW Hypochemical protein.
SQ SEQUENCE 186 AA; 21105 MW; CBFEDB01FDC4181C CRC64;

Query Match
Best Local Similarity 21.6%; Score 61; DB 2; Length 186;
Matches 16; Conservative 11; Mismatches 11; Indels 22; Gaps 3;

QY 2 LOMAGCCSQNEVFDSLHHCIPQLACS-----SNTPPLTCQRYC--MASVTMSVVG 51
DB 87 VEMARCC-----CRPPDRCPCPCRGRLVRGRTPIPSICRWKCFQGTVPFLRG 134

RESULT 81
O32LX4 HUMAN PRELIMINARY; PRT; 247 AA.
AC O32LX4;
DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 06-DEC-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE TNFRSF13B protein.
GN Name=TNFRSF13B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stadelman M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mollath S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Maria M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RG NIH MGC Project;
RL Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs license
CC EMBL: BC109392; AAI09393.1; -; mRNA.
DR EMBL: BC109392; AAI09393.1; -; mRNA.
SQ SEQUENCE 247 AA; 26664 MW; 850R1F4C2578B8E6 CRC64;

Query Match
Best Local Similarity 21.6%; Score 61; DB 2; Length 247;
Matches 12; Conservative 7; Mismatches 19; Indels 2; Gaps 1;

QY 10 QNEVFDLSLHACIPQLRCSSNTPPLTCQRYCASVTNSV 49
DB 29 QGKPYDHLARDTSCASICGQH--PQGCAYFCENKLRISV 66

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RESULT 82
Q9WEJ8_9HIV1 PRELIMINARY; PRT; 263 AA.
AC Q9WEJ8;
DT 01-NOV-1999, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1999, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99214314; PubMed=10196271;
RA Bagaricelli P., Mazza F., Menzo S., Montironi M., Butini L.,
RA Clementi M.;
RT "Host-specific modulation of the selective constraints driving human
RT immunodeficiency virus type 1 env gene evolution."
RL J. Virol. 73:3764-3777(1999).
CC
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CC Distributed under the Creative Commons Attribution-NonDerivs license
CC EMBL: AF105857; AAD27431.1; -; Genomic_RNA.
DR HSP; P19549; IMBO.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 263 AA; 29480 MW; C62BBB189C7BC96 CRC64;

Query Match
Best Local Similarity 21.9%; Score 61; DB 2; Length 263;
Matches 14; Conservative 13; Mismatches 15; Indels 22; Gaps 2;

QY 8 CSQNEVFDLSLH-----ACIPQLRCSSN-----TPPLTCQRYCASV 45
DB 132 CNSTLPDFTSMWNGSNNTGNDITLLPDKRIINMKGKAMVTPISQIRCSN 191

QY 46 TNSV 49
DB 192 TGLI 195

RESULT 83
Q4RNR8_TETNG PRELIMINARY; PRT; 354 AA.
AC Q4RNR8;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Chromosome 2 SCAP15010, whole genome shotgun sequence. (Fragment).
GN ORFNames=GSTENG00031440001.
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99863;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496914; DOI=10.1038/nature03025;
RA Jallion O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bounneau L., Fischer C., Ozout-Costaz C., Bernot A.,
RA Nicard S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Caetelli V., Katinka M., Vacherie B.,

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RA Bieumont C., Skalli Z., Catcolico L., Poulain J., De Bernardinis V.,
RA Ciraud C., Duprat S., Brottier P., Contanceau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volf J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Lander V., Schachter V., Queller F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RL
RP NUCLEOTIDE SEQUENCE.
RG Genoscope, Whitehead Institute Centre for Genome Research,
RL Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivs license
CC -----
DR EMBL: CAE0101501.0; CAG09964.1; -: Genomic DNA.
DR GO: GO:0003676; F:nucleic acid binding; IEA.
DR GO: GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro: IPR001427; Rnasea.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 354 AA; 39608 MW; CEBB4C670F2BDC03 CRC64;

Query Match 21.6%; Score 61; DB 2; Length 354;
Best Local Similarity 30.6%; Pred. No. 40;
Matches 15; Conservative 7; Mismatches 21; Indels 6; Gaps 2;

3 OMAGGCSNVEYFDSLHACIPQGRCSNTPPLTCQRCNASTNSVKG 51
Db 279 QPCGCLNRKGEVRDALDPEWRC---PP-CRGICNCSFCARDG 321

RESULT 84
Q4ZLE4_PSEU2
ID Q4ZLE4_PSEU2 PRELIMINARY; PRT; 815 AA.
AC Q4ZLE4_PSEU2
DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 07-JUN-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Hypothetical protein.
GN OrderedLocNames=Psyr 5001;
OC Pseudomonas syringae p₁ syringae (strain B728a).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=205918;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=16043691; DOI=10.1073/pnas.0504930102;
RA Fell H., Feil W.S., Chain P., Larimer F., Dibartolo G., Copeland A.,
RA Lygidis A., Trong S., Nolan M., Goldstein E., Thiel J., Malfatti S.,
RA Loper J.E., Lapidus A., Dettler J.C., Land M., Richardson P.M.,
RA Kyripides N.C., Ivanova N., Lindow S.E.;
RT "Comparison of the complete genome sequences of Pseudomonas syringae
RT pv. syringae B728a and pv. tomato DC3000.";
RL Proc. Natl. Acad. Sci. U.S.A. 102:11064-11069(2005).
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CC -----
DR EMBL: CP0000075; AAY40028.1; -: Genomic DNA.
DR GO: GO:0016772; F:transferase activity, transferring phosphor. .; IEA.
DR GO: GO:0016310; F:phosphorylation; IEA.
DR InterPro: IPR008279; PEP mobile.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 815 AA; 90782 MW; 8A638679CAFA477D6 CRC64;

Query Match 21.6%; Score 61; DB 2; Length 815;

Best Local Similarity 30.4%; Pred. No. 96;
Matches 17; Conservative 9; Mismatches 22; Indels 8; Gaps 2;

4 MAGGCSNVEYFDSLHACIPQGRCSNTPPLTCQ---RYCNASTNSVKG 51
Db 10 LAGNGSSAEMWDALPHRQGHVPLELPGFNGNPQPCEDLASVADLLATVKG 65

RESULT 85
Q2M0X9_DROPS
ID Q2M0X9_DROPS PRELIMINARY; PRT; 279 AA.
AC Q2M0X9;
DT 21-FEB-2006, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, sequence version 1.
DT 21-FEB-2006, entry version 1.
DE GA20283-PA (Fragment)
GN Name=Dpse\GA20283; ORFNames=Dpse_GA20283;
OS Drosophila pseudoobscura (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7237;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=MV2-25;
RX PubMed=15632085; DOI=10.1101/gr.3059305;
RA Richards S., Liu Y., Bettencourt B.R., Hradecky P., Letovsky S.,
RA Nielsen R., Thornton K., Hubisz M.J., Chen R., Meisel R.P.,
RA Couronne O., Hua S., Smith M.A., Zhang P., Liu J., Bussemann H.J.,
RA van Batenburg M.F., Howells S.L., Scherer S.E., Sodergren E.,
RA Matthews B.B., Crosby M.A., Schroeder A.J., Ortiz-Barrientos D.,
RA Rives C.M., Metzker M.L., Munzy D.M., Scott G., Steffen D.,
RA Wheeler D.A., Worley K.C., Havlak P., Durbin K.J., Egan A., Gill R.,
RA Hume J., Morgan M.B., Miner G., Hamilton C., Huang Y., Waldron L.,
RA Verduzco D., Clerc-Blankenburg K.P., Dubchak I., Noor M.A.F.,
RA Anderson W., White K.P., Clark A.G., Schaeffer S.W., Gelbart W.,
RA Weinstock G.M., Gibbs R.A.;
RT "Comparative genome sequencing of Drosophila pseudoobscura:
RT chromosomal, gene, and cis-element evolution.";
RL Genome Res. 15:1-18(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=MV2-25;
RG FlyBase;
RL Submitted (JUN-2005) to the EMBL/Genbank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=MV2-25;
RG Human Genome Sequencing Center;
RA Richards S., Liu Y., Bettencourt B.R., Hradecky P., Letovsky S.,
RA Chen R., Smith M.A., Howells S.L., Scherer S.E., Sodergren E.,
RA Rives C.M., Metzker M.L., Munzy D.M., Wheeler D.A., Worley K.C.,
RA Havlak P., Durbin K.J., Egan A., Gill R., Hume J., Morgan M.B.,
RA Huang Y., Waldron L., Verduzco D., Blankenburg K.P., Adams C.,
RA Allen C., Allen H., Anyalebechi V., Asomugha C., Bellard T.,
RA Buchner E., Biswal K., Blair J., Blomstrom D., Burrell K.,
RA Chander V., Cawthon K., Carter K., Cavazos I., Ceasar H., Chacko J.,
RA Chavez D., Chu J., Cockrell R., Cox C., Coyte M., Davila M., Davis C.,
RA Davy-Carroll L., De A., Delgado O., Denison S., Deramo C., Dinh H.,
RA Eaves K., Escotto M., Eugene C., Falls T., Fernandez S., Flagg N.,
RA Forbes L., Garner T., Garza M., Ghose S., Grady M., Hamilton C.,
RA Hernandez J., Hines S., Hognes M., Hollins B., Idlebird D., Imo K.,
RA Jimenez A., Johnson B., Jolivet A., Kelly S., King L., Klsano P.,
RA Kovar C., Lebow H., Lee K., Legall F., Lewis L., Li Z., London P.,
RA Lopez J., Lozano R., Malloy K., Martinez E., Mercader C., Mier G.,
RA Mijla E., Moore S., Nanavati A., Ngo R., Nguyen N., Nwackemehe O.,
RA Okunnu G., Parks K., Pasternak S., Patel B., Paul H., Payne C.,
RA Poindexter A., Primus E., Pu L.-L., Puazo M., Quitor J., Rabata D.,
RA Reigh R., Ruiz S., Sanders W., Sisson I., Sorelle R., Taylor C.,
RA Taylor T., Thomas N., Trejos Z., Usmani K., Vera V., Villasana D.,
RA Wang S., Warren J., Warren R., White F., Wleczek R., Wright R.,
RA Noor M.A.F., Schaeffer S.W., Gelbart W., Weinstock G.M., Gibbs R.A.,
RA Weinstock G., Gibbs R.;

Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.

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DR EMBL: CH379069; EAL30797.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 279
SQ SEQUENCE 279 AA; 30682 MW; 1CAC8116E04E7100 CRC64;

Query Match 21.4%; Score 60.5; DB 2; Length 279;
Best Local Similarity 33.3%; Pred. No. 36;
Matches 15; Conservative 4; Mismatches 15; Indels 11; Gaps 2;

QY 7 CSONEYFDSLHACIPCOL-----PLTCORY 40
DB 116 RCVSGSYFDSGRACLPVALTAHQSCCLPDHATVENPSDCETY 160

RESULT 86
061818 CAEBR PRELIMINARY; PRT; 339 AA.
AC 061818
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 21-FEB-2006, entry version 16.
DE Hypothetical protein CBG06165 (Fragment).
GN Name=CBG06165;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_Taxid=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=AF16;
RX PubMed=14624247; DOI=10.1371/journal.pbio.0000045;
RA Steen L.D., Bao Z., Blasitar D., Blumenthal T., Brent M.R., Chen N.,
RA Chivallia A., Clarke L., Clee C., Coghlan A., Coulson A.,
RA D'Eustachio P., Fitch D.H.A., Fulton L.A., Fulton R.E.,
RA Griffiths-Jones S., Harris T.W., Hillier L.W., Kamath R.,
RA Kumbhara P.E., Mardis E.R., Marra M.A., Miner T.L., Minx P.,
RA Mullikin J.C., Plumb R.W., Rogers J., Schein J.E., Schumann M.,
RA Spielh J., Stajich J.E., Wei C., Willey D., Wilson R.K., Durbin R.,
RA Waterston R.H.;
RT "The genome sequence of *Caenorhabditis briggsae*: a platform for
RT comparative genomics.";
RT PLoS Biol. 1:166-192(2003).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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DR EMBL: CAACO100028; CAE62124.1; -; Genomic_DNA.
DR InterPro: IPR006210; EGF.
DR InterPro: IPR000742; EGF 3.
DR InterPro: IPR013032; EGF_like_reg.
DR SMART: SM00181; EGF; 1.
DR PROSITE: PS00022; EGF_1; 3.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS50026; EGF_3; 1.
KW Complete proteome; EGF-like domain; Hypothetical protein.
FT NON_TER 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 37704 MW; 2469B38E5B95B43 CRC64;

Query Match 21.4%; Score 60.5; DB 2; Length 339;
Best Local Similarity 31.8%; Pred. No. 44;
Matches 14; Conservative 5; Mismatches 20; Indels 5; Gaps 1;

QY 8 CSONEYFDSLHACIPCOLRCSSNTPLTCORYCQNASVNSVVG 51
DB 108 CNDGTFNFTLGRCV-----CTSNWGEHCIFRCNSGVNKTSG 146

RESULT 87
06DEJ5 BRARE
AC 06DEJ5
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Zgc:101066.
GN ORFNames=zgc:101066;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_Taxid=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Singapore local strain; TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange S.J.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mallya S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Munz D.M., Sodergren E.U., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield V.S.N., Krzywinski M.T., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Singapore local strain; TISSUE=Embryo;
RA Director MGC Project;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.

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DR EMBL: BC077118; AAH77118.1; -; mRNA.
DR Ensembl: ENSDARG0000015747; Danio rerio.
DR ZFIN: ZDB-GENE-040801-91; Zgc:101066.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:001674; F:Ligase activity; IEA.
DR GO: GO:000166; F:Nucleotide binding; IEA.
DR GO: GO:0004812; F:tRNA ligase activity; IEA.
DR GO: GO:0006412; P:protein biosynthesis; IEA.
DR InterPro: IPR012947; tRNA_SAD.
DR Pfam: PF07973; tRNA_SAD; 1.
KW ATP-binding; Aminoacyl-tRNA synthetase; Ligase; Nucleotide-binding;
KW Protein biosynthesis.
SQ SEQUENCE 412 AA; 45517 MW; 4321F90E712F3200 CRC64;

Query Match 21.4%; Score 60.5; DB 2; Length 412;
Best Local Similarity 38.7%; Pred. No. 54;
Matches 12; Conservative 8; Mismatches 8; Indels 3; Gaps 1;

QY 4 MAGCSQNEY---FDSLHACIPCOLRCSSN 31
DB 1 MAFQCCORDCYMDFDSQCVSVCPALFKLENN 31

RESULT 88

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O50M54_ENTHI PRELIMINARY; PRT; 710 AA.
ID O50M54_ENTHI
AC O50M54;
DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 07-JUN-2005, sequence version 1.
DE CXc-rich protein.
GN ORFNames=594.t00001;
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
CX NCBI_TaxId=294381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HM-1:IMSS;
RX PubMed=15729342; DOI=10.1038/nature03291;
RA Amedeo P., Roncaglia P., Berrian M., Hirt R.P., Mann B.U., Nozaki T.,
RA Sun B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
RA Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,
RA Jagels K., Moule S., Mungall K.L., Ormond D., Squares R.,
RA Chillingworth T., Churcher C.M., Hance Z., Harris B., Harris D.,
RA Whitehead S., Quail M.A., Rabbinowitsch E., Norbertczak H., Price C.,
RA Lohia A., Foster P.G., Sichert-Ponten T., Weber C., Singh U.,
RA Mukherjee C., El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M.,
RA Barrett B.G., Fraser C.M., Hall N.;
RT "The genome of the protist parasite Entamoeba histolytica."
RL Nature 433:865-868(2005).
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAFB01001350; EAL42672.1; -; Genomic_DNA.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR006212; Furin_repeat.
DR InterPro; IPR002350; Prot_inh_Kazal.
DR SMART; SM00181; EGF; 3.
DR SMART; SM00261; FU; 1.
DR PROSITE; PS00282; KAZAL; UNKNOWN_1.
SQ SEQUENCE 710 AA; 78593 MW; 3F87CD72831B4B69 CRC64;

Query Match 21.4%; Score 60.5; DB 2; Length 710;
Best Local Similarity 28.6%; Pred. No. 95;
Matches 12; Conservative 6; Mismatches 23; Indels 1; Gaps 1;

OY 7 OCSONEYFDSLHACIPQLRCSSNTPPTTCORYCNASTVNS 48
DB 624 RCDSGYLTDL-MCDPCIENCECQCNPTTCOKSSGYILNN 664

RESULT 89
O51CE3_ENTHI PRELIMINARY; PRT; 1083 AA.
ID O51CE3_ENTHI
AC O51CE3;
DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 07-JUN-2005, sequence version 1.
DE CXc-rich protein.
GN ORFNames=20.t00061;
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
CX NCBI_TaxId=294381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HM-1:IMSS;
RX PubMed=15729342; DOI=10.1038/nature03291;
RA Amedeo P., Roncaglia P., Berrian M., Hirt R.P., Mann B.U., Nozaki T.,
RA Sun B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
RA Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,
RA Jagels K., Moule S., Mungall K.L., Ormond D., Squares R.,
RA Chillingworth T., Churcher C.M., Hance Z., Harris B., Harris D.,
RA Whitehead S., Quail M.A., Rabbinowitsch E., Norbertczak H., Price C.,
RA Lohia A., Foster P.G., Sichert-Ponten T., Weber C., Singh U.,
RA Mukherjee C., El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M.,
RA Barrett B.G., Fraser C.M., Hall N.;
RT "The genome of the protist parasite Entamoeba histolytica."
RL Nature 433:865-868(2005).
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
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CC -----
DR EMBL; AAFB01000754; EAL44430.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.

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RA Chillingworth T., Churcher C.M., Hance Z., Harris B., Harris D.,
RA Jagels K., Moule S., Mungall K.L., Ormond D., Squares R.,
RA Whitehead S., Quail M.A., Rabbinowitsch E., Norbertczak H., Price C.,
RA Wang Z., Guillen N., Gilchrist C., Strop S.E., Bhattacharya S.,
RA Lohia A., Foster P.G., Sichert-Ponten T., Weber C., Singh U.,
RA Mukherjee C., El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M.,
RA Barrett B.G., Fraser C.M., Hall N.;
RT "The genome of the protist parasite Entamoeba histolytica."
RL Nature 433:865-868(2005).
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAFB01000094; EAL50563.1; -; Genomic_DNA.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR006212; Furin_repeat.
DR InterPro; IPR002350; Prot_inh_Kazal.
DR Pfam; PF02420; AFP; 2.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00261; FU; 3.
DR PROSITE; PS00282; KAZAL; UNKNOWN_1.
SQ SEQUENCE 1083 AA; 119576 MW; 058CE4C31B43489C CRC64;

Query Match 21.4%; Score 60.5; DB 2; Length 1083;
Best Local Similarity 28.6%; Pred. No. 1.5e+02;
Matches 12; Conservative 6; Mismatches 23; Indels 1; Gaps 1;

OY 7 OCSONEYFDSLHACIPQLRCSSNTPPTTCORYCNASTVNS 48
DB 997 RCDSGYLTDL-MCDPCIENCECQCNPTTCOKSSGYILNN 1037

RESULT 90
O50S60_ENTHI PRELIMINARY; PRT; 1100 AA.
ID O50S60_ENTHI
AC O50S60;
DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 07-JUN-2005, sequence version 1.
DE Receptor protein kinase.
DE 07-FEB-2006, entry version 6.
GN ORFNames=268.t00007;
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
CX NCBI_TaxId=294381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HM-1:IMSS;
RX PubMed=15729342; DOI=10.1038/nature03291;
RA Amedeo P., Roncaglia P., Berrian M., Hirt R.P., Mann B.U., Nozaki T.,
RA Sun B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
RA Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,
RA Chillingworth T., Churcher C.M., Hance Z., Harris B., Harris D.,
RA Jagels K., Moule S., Mungall K.L., Ormond D., Squares R.,
RA Whitehead S., Quail M.A., Rabbinowitsch E., Norbertczak H., Price C.,
RA Wang Z., Guillen N., Gilchrist C., Strop S.E., Bhattacharya S.,
RA Lohia A., Foster P.G., Sichert-Ponten T., Weber C., Singh U.,
RA Mukherjee C., El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M.,
RA Barrett B.G., Fraser C.M., Hall N.;
RT "The genome of the protist parasite Entamoeba histolytica."
RL Nature 433:865-868(2005).
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAFB01000754; EAL44430.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.

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DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR006210; EGF.
 DR InterPro: IPR006212; Furin_repeat.
 DR InterPro: IPR000719; Prot_Kinase.
 DR InterPro: IPR008271; Ser_thr_pkin_AS.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; Pkinase_1.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Prot_Kinase; 1.
 DR SMART: SM00261; FU; 3.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR Kinase; Receptor.
 SQ SEQUENCE 1100 AA; 122965 MW; DCAC28AE874A07BD CRC64;

Query Match 21.4%; Score 60.5; DB 2; Length 1100;
 Best Local Similarity 30.0%; Pred. No. 1.5e+02;
 Matches 12; Conservative 5; Mismatches 22; Indels 1; Gaps 1;

OY 3 QMAGCQNEYPDSLHACIPCOLRCSSNTPPLTCQRYCN 42
 DB 130 EACGRCPAGKGFIDQNKVCTECMCALCTDQYNCYQ-CN 168

RESULT 91
 Q6B534_WHEAT PRELIMINARY; PRT; 1155 AA.
 AC Q6B534;
 DT 13-SEP-2004, integrated into UniProtKB/TrEMBL.
 DT 13-SEP-2004, sequence version 1.
 DT 07-FEB-2006, entry version 7.
 DE Gigantea 3.
 GN Name=TAG13;
 OS Triticum aestivum (wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep clade;
 OC Poideae; Triticeae; Triticum.
 OC NCBI_TaxID=4565;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Zhao X., Zhang X.;
 RT "Rhythmic expression of wheat TAG1 genes introduced by photoperiod and
 RT ectopic expression of Tag1 promoting flowering in transgenic
 RT Arabidopsis";
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
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 CC EMBL: AY679115; AAT79487.1; -; mRNA.
 DR Gramene; Q6B534; -;
 DR SEQUENCE 1155 AA; 126088 MW; 9D6BF52D8B36DA11 CRC64;

Query Match 21.4%; Score 60.5; DB 2; Length 1155;
 Best Local Similarity 35.1%; Pred. No. 1.6e+02;
 Matches 13; Conservative 8; Mismatches 15; Indels 1; Gaps 1;

OY 14 PDSLHACIPCOLRCSSNTPPLTCQRYCNASVTSVK 50
 DB 633 PDSYVLAHV-CALSCLELQFPLICKSATNSNVKDSIK 668

RESULT 92
 Q717V9_WHEAT PRELIMINARY; PRT; 1155 AA.
 AC Q717V9;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.

DT 07-FEB-2006, entry version 7.
 DE Gigantea.
 GN Name=TAG11;
 OS Triticum aestivum (wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep clade;
 OC Poideae; Triticeae; Triticum.
 OC NCBI_TaxID=4565;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=16028116; DOI=10.1007/s11103-005-4162-2;
 RA Zhao X.Y., Liu W.S., Li J.R., Guan C.M., Zhang X.S.;
 RT "The wheat Tag11, involved in photoperiodic flowering, encodes an
 RT Arabidopsis GI ortholog";
 RL Plant Mol. Biol. 58:53-64(2005).
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 CC EMBL: AF543844; AAQ11738.1; -; mRNA.
 DR Gramene; Q717V9; -;
 DR SEQUENCE 1155 AA; 125966 MW; 6D8597F27D6DE2B2 CRC64;

Query Match 21.4%; Score 60.5; DB 2; Length 1155;
 Best Local Similarity 35.1%; Pred. No. 1.6e+02;
 Matches 13; Conservative 8; Mismatches 15; Indels 1; Gaps 1;

OY 14 PDSLHACIPCOLRCSSNTPPLTCQRYCNASVTSVK 50
 DB 633 PDSYVLAHV-CALSCLELQFPLICKSATNSNVKDSIK 668

RESULT 93
 Q4UFT2_THEAN PRELIMINARY; PRT; 1516 AA.
 AC Q4UFT2;
 DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2005, sequence version 1.
 DT 21-FEB-2006, entry version 8.
 DE (Subtelomeric) ABC-transporter protein family member, putative.
 GN ORFNames=TA16015;
 OS Theileria annulata.
 OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
 OC Theileria.
 OC NCBI_TaxID=5874;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Ankara isolate clone C9;
 RX PubMed=15943597; DOI=10.1258/jism.98.7.320;
 RA Pain A., Renauld H., Berriman M., Murphy L., Yeats C.A., Weir W.,
 RA Keshornou A., Aslett M., Bishop R., Bouchier C., Cochet M.,
 RA Coulson R.M.R., Cronin A., de Villiers E.P., Fraser A., Foster N.,
 RA Gardner M., Goble A., Griffiths-Jones S., Harris D.E., Katzer F.,
 RA Larte N., Lord A., Maser P., McKellar S., Mooney P., Morton F.,
 RA Nene V., O'Neill S., Price C., Quail M.A., Rabbhnowitch E.,
 RA Rawlings N.D., Rutter S., Saunders D., Seeger K., Shah T., Squares R.,
 RA Squares S., Tivey A., Walker A.R., Woodward J., Dobbelaere D.A.E.,
 RA Langsley G., Rajandream M.A., McKeever D., Shields B., Tait A.,
 RA Barrell B., Hall N.;
 RT "Genome of the host-cell transforming parasite Theileria annulata
 RT compared with T. parva";
 RL Science 309:131-133(2005).
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 CC EMBL: CR940348; CAI74034.1; -; Genomic_DNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0016887; F:ATPase activity; IEA.
 DR GO; GO:0046265; F:ATPase activity, coupled to transmembrane m. .; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro: IPR003593; AAA_ATPase.

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DR InterPro; IPR011527; ABC_TM1.1.
DR InterPro; IPR003439; ABC_transp_like.
DR Pfam; PF00005; ABC_tran; 1.
DR PROSITE; PS50929; ABC_TM1F; 1.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 2.
DR Membrane; Transport.
SQ SEQUENCE 1516 AA; 174536 MW; AAE1191E45953CB1 CRC64;

Query Match      21.4%; Score 60.5; DB 2; Length 1516;
Best Local Similarity 37.8%; Pred. No. 2.1e+02;
Matches 14; Conservative 9; Mismatches 9; Indels 5; Gaps 3;

OY 15 DSLHACIPQCLRCSSNTPLTC--QRYCNASVTNV 49
Db 244 NSVLHSCSP-ESNCSKN--PLFCPPARYQNKDINSNI 277

RESULT 94
ID Q4NOVO_THEPA PRELIMINARY; PRT; 1529 AA.
AC Q4NOVO;
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 02-AUG-2005, sequence version 1.
DI 21-FEB-2006, entry version 7.
DE ABC transporter, putative.
OS ORNames=IP03_0007;
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
OC Theileria.
OX NCBI_Taxid=5875;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga;
RX PubMed=15994558; DOI=10.1126/science.1110439;
RA Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,
RA Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M.,
RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.,
RA Jiang L., Lynn J., Weaver B., Shoabli A., Domingo A.R., Masawo D.,
RA Crabtree J., Wortman J.R., Haas B., Anguilo S.V., Creasy T.H., Lu C.,
RA Suh B., Silva J.C., Uteback T.R., Feldlyum T.V., Perteau M.,
RA Allen J., Niemman W.C., Taracha E.L., Salzberg S.L., White O.R.,
RA Fitchugh H.A., Morzaria S., Venter J.C., Fraser C.M., Nene V.;
RT "Genome Sequence of Theileria parva, a Bovine Pathogen That Transforms
RT Lymphocytes."
RL Science 309:134-137(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga;
RA Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
RA Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
RA Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiang L.,
RA Lynn J., Weaver B., Shoabli A., Masawo D., Crabtree J., Wortman J.R.,
RA Haas B., Anguilo S., Creasy T.H., Lu C., Suh B., Silva J.C.,
RA Uteback T., Feldlyum T., Perteau M., Allen J., Taracha E.L.,
RA Salzberg S.L., White O., Fitchugh H.A., Morzaria S., Venter J.C.,
RA Fraser C.M., Nene V.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAGK01000005; EAN30743.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016887; F:ATPase activity; IEA.
DR GO; GO:0042626; F:ATPase activity; coupled to transmembrane m. . .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011527; ABC_TM1.1.
DR InterPro; IPR003439; ABC_transp_like.
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DR Pfam; PF00005; ABC_tran; 1.
DR PROSITE; PS50929; ABC_TM1F; 1.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 2.
DR Membrane; Transport.
SQ SEQUENCE 1529 AA; 176490 MW; FD0330BE6CF6C52A CRC64;

Query Match      21.4%; Score 60.5; DB 2; Length 1529;
Best Local Similarity 27.3%; Pred. No. 2.1e+02;
Matches 15; Conservative 11; Mismatches 12; Indels 17; Gaps 4;

OY 6 GQCGQNEFYFDL-----LHACIPQCLRCSSNTPLTC--QRYCNASVT 46
Db 223 GMCYRRKHFFNNINSNLSVCNVLHFCPLP-DSCSQSN--PMFCPPARFQNKDIT 274

RESULT 95
ID Q4N3N8_THEPA PRELIMINARY; PRT; 1545 AA.
AC Q4N3N8;
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 02-AUG-2005, sequence version 1.
DI 21-FEB-2006, entry version 7.
DE ABC transporter, putative.
OS ORNames=IP02_0951;
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
OC Theileria.
OX NCBI_Taxid=5875;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga;
RX PubMed=15994558; DOI=10.1126/science.1110439;
RA Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,
RA Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M.,
RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.,
RA Jiang L., Lynn J., Weaver B., Shoabli A., Domingo A.R., Masawo D.,
RA Crabtree J., Wortman J.R., Haas B., Anguilo S.V., Creasy T.H., Lu C.,
RA Suh B., Silva J.C., Uteback T.R., Feldlyum T.V., Perteau M.,
RA Allen J., Niemman W.C., Taracha E.L., Salzberg S.L., White O.R.,
RA Fitchugh H.A., Morzaria S., Venter J.C., Fraser C.M., Nene V.;
RT "Genome Sequence of Theileria parva, a Bovine Pathogen That Transforms
RT Lymphocytes."
RL Science 309:134-137(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga;
RA Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
RA Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
RA Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiang L.,
RA Lynn J., Weaver B., Shoabli A., Masawo D., Crabtree J., Wortman J.R.,
RA Haas B., Anguilo S., Creasy T.H., Lu C., Suh B., Silva J.C.,
RA Uteback T., Feldlyum T., Perteau M., Allen J., Taracha E.L.,
RA Salzberg S.L., White O., Fitchugh H.A., Morzaria S., Venter J.C.,
RA Fraser C.M., Nene V.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAGK01000002; EAN33235.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016887; F:ATPase activity; IEA.
DR GO; GO:0042626; F:ATPase activity; coupled to transmembrane m. . .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011527; ABC_TM1.1.
DR InterPro; IPR003439; ABC_transp_like.
DR Pfam; PF00005; ABC_tran; 1.
DR PROSITE; PS50929; ABC_TM1F; 1.
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DR PROSITE; PS0893; ABC_TRANSPORTER_2; 2.
KW Membrane; Transport.
SQ SEQUENCE 1545 AA; 177739 MW; 3A37B004165A9063 CRC64;
Query Match 21.4%; Score 60.5; DB 2; Length 1545;
Best Local Similarity 27.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 11; Mismatches 12; Indels 17; Gaps 4;
OY 6 GOCSONEYFDSL-----LHACIPQQLRCSSNTPPLTC--QRYCNASVT 46
DB 224 GNCYRKHKHNNNGNSLSVCNNVLTCLP-DSECCQN--PMCCPARRFQNDIT 275
RESULT 96
EGF13 RAT STANDARD; PRT; 1574 AA.
AC 088281;
DT 13-APR-2004, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1998, sequence version 1.
DT 07-MAR-2006, entry version 36.
DE EGF-like domain-containing protein 3 precursor (Multiple EGF-like
DE domain protein 3) (Multiple epidermal growth factor-like domains 6).
GN Name=EGF13; Synonyms=Megf6;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], AND TISSUE SPECIFICITY.
RC STRAIN=Dprague-Dawley; TISSUE=Brain;
RA MEDLINE:98360089; PubMed:9693030; DOI=10.1006/geno.1998.5341;
RA Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.;
RT Identification of high-molecular-weight proteins with multiple EGF-
RT like motifs by motif-trap screening";
RL Genomes 51:27-34(1998).
CC -1- TISSUE SPECIFICITY: Expressed in lung.
CC -1- SIMILARITY: Contains 32 EGF-like domains.
CC -1- SIMILARITY: Contains 1 EMI domain.
CC -----
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CC -----
DR EMBL; AB011532; BAA32462.1; -; mRNA.
DR PIR; T13954; T13954.
DR HSSP; P00736; IAP0.
DR Ensembl; ENSRNOG0000000156; Rattus norvegicus.
DR RGD; 621188; EGF13.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR000742; EGF_3.
DR InterPro; IPR001881; EGF_Ca_bd.
DR InterPro; IPR013091; EGF_Ca_bd.2.
DR InterPro; IPR013111; EGF_extract1.
DR InterPro; IPR002049; EGF_lamlnn.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR013032; EGF_like_reg.
DR InterPro; IPR011489; EMI.
DR Pfam; PF00008; EGF_4.
DR Pfam; PF07974; EGF_2; 8.
DR Pfam; PF07645; EGF_CA; 3.
DR Pfam; PF07546; EMI; 1.
DR Pfam; PF00053; Lamlnn EGF; 8.
DR PRINTS; P00011; EGF_LAMININ.
DR SMART; SM00181; EGF; 28.
DR SMART; SM00179; EGF_CA; 4.
DR SMART; SM00180; EGF_Lam; 11.
DR PROSITE; PS00010; ASX_HYDROXYL; 5.
DR PROSITE; PS00022; EGF_1; 23.
DR PROSITE; PS01186; EGF_2; 23.
DR PROSITE; PS50026; EGF_3; 21.
DR PROSITE; PS01187; EGF_CA; 5.
DR PROSITE; PS1041; EMI; 1.

KW EGF-like domain; Repeat; Signal.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 1574 EGF-like domain-containing protein 3.
FT EMI /FTid=PRO_0000007525.
FT 122 EGF-like 1; calcium-binding (Potential).
FT 123 EGF-like 2; calcium-binding (Potential).
FT 164 EGF-like 3.
FT 205 EGF-like 4.
FT 247 EGF-like 5; calcium-binding (Potential).
FT 288 EGF-like 6.
FT 334 EGF-like 7.
FT 375 EGF-like 8; calcium-binding (Potential).
FT 415 EGF-like 9.
FT 520 EGF-like 10.
FT 564 EGF-like 11.
FT 607 EGF-like 12.
FT 650 EGF-like 13.
FT 695 EGF-like 14.
FT 740 EGF-like 15.
FT 782 EGF-like 16.
FT 826 EGF-like 17.
FT 869 EGF-like 18.
FT 913 EGF-like 19.
FT 956 EGF-like 20.
FT 999 EGF-like 21.
FT 1042 EGF-like 22.
FT 1085 EGF-like 23.
FT 1128 EGF-like 24.
FT 1171 EGF-like 25.
FT 1214 EGF-like 26.
FT 1258 EGF-like 27.
FT 1301 EGF-like 28.
FT 1344 EGF-like 29.
FT 1387 EGF-like 30.
FT 1430 EGF-like 31.
FT 1473 EGF-like 32.
FT 1516 EGF-like 32.
FT 44 By similarity.
FT 74 By similarity.
FT 80 By similarity.
FT 107 By similarity.
FT 120 By similarity.
FT 137 By similarity.
FT 134 By similarity.
FT 149 By similarity.
FT 162 By similarity.
FT 179 By similarity.
FT 188 By similarity.
FT 203 By similarity.
FT 209 By similarity.
FT 220 By similarity.
FT 232 By similarity.
FT 245 By similarity.
FT 251 By similarity.
FT 262 By similarity.
FT 271 By similarity.
FT 286 By similarity.
FT 299 By similarity.
FT 312 By similarity.
FT 327 By similarity.
FT 349 By similarity.
FT 358 By similarity.
FT 360 By similarity.
FT 373 By similarity.
FT 389 By similarity.
FT 400 By similarity.
FT 411 By similarity.
FT 430 By similarity.
FT 439 By similarity.
FT 454 By similarity.
FT 537 By similarity.
FT 544 By similarity.
FT 555 By similarity.
FT 568 By similarity.
FT 580 By similarity.
FT 587 By similarity.
FT 598 By similarity.
FT 623 By similarity.
FT 630 By similarity.
FT 641 By similarity.
FT 668 By similarity.
FT DISULFID 654


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FT DISULFID 677 686 By similarity.
FT DISULFID 699 711 By similarity.
FT DISULFID 722 731 By similarity.
FT DISULFID 744 755 By similarity.
FT DISULFID 764 773 By similarity.
FT DISULFID 786 799 By similarity.
FT DISULFID 793 806 By similarity.
FT DISULFID 808 817 By similarity.
FT DISULFID 830 842 By similarity.
FT DISULFID 836 849 By similarity.
FT DISULFID 851 860 By similarity.
FT DISULFID 873 886 By similarity.
FT DISULFID 877 893 By similarity.
FT DISULFID 895 904 By similarity.
FT DISULFID 917 929 By similarity.
FT DISULFID 923 936 By similarity.
FT DISULFID 938 947 By similarity.
FT DISULFID 960 972 By similarity.
FT DISULFID 981 990 By similarity.
FT DISULFID 1003 1015 By similarity.
FT DISULFID 1009 1022 By similarity.
FT DISULFID 1024 1033 By similarity.
FT DISULFID 1046 1058 By similarity.
FT DISULFID 1052 1065 By similarity.
FT DISULFID 1067 1076 By similarity.
FT DISULFID 1089 1101 By similarity.
FT DISULFID 1095 1108 By similarity.
FT DISULFID 1110 1119 By similarity.
FT DISULFID 1132 1144 By similarity.
FT DISULFID 1138 1151 By similarity.
FT DISULFID 1153 1162 By similarity.
FT DISULFID 1175 1187 By similarity.
FT DISULFID 1179 1194 By similarity.
FT DISULFID 1196 1205 By similarity.
FT DISULFID 1218 1231 By similarity.
FT DISULFID 1240 1249 By similarity.
FT DISULFID 1262 1274 By similarity.
FT DISULFID 1268 1281 By similarity.
FT DISULFID 1283 1292 By similarity.
FT DISULFID 1305 1317 By similarity.
FT DISULFID 1311 1324 By similarity.
FT DISULFID 1326 1335 By similarity.
FT DISULFID 1348 1360 By similarity.
FT DISULFID 1354 1367 By similarity.
FT DISULFID 1369 1378 By similarity.
FT DISULFID 1391 1403 By similarity.
FT DISULFID 1397 1410 By similarity.
FT DISULFID 1412 1421 By similarity.
FT DISULFID 1434 1446 By similarity.
FT DISULFID 1440 1453 By similarity.
FT DISULFID 1455 1464 By similarity.
FT DISULFID 1477 1489 By similarity.
FT DISULFID 1498 1507 By similarity.
FT DISULFID 1520 1532 By similarity.
FT DISULFID 1541 1550 By similarity.
SO SEQUENCE 1574 AA; 165447 MW; 2B4833D8F77F6E7 CRC64;

Query Match 21.4%; Score 60.5; DB 1; Length 1574;
Best Local Similarity 32.2%; Pred. No. 2.2e+02;
Matches 19; Conservative 8; Mismatches 19; Indels 13; Gaps 4;

OY 5 AGCQNEYFDSLHACIPQCL-----RCSSTPPLT-----CQYRC--MASVTSVVG 51
DB 963 ACNCSAGAPCAVATGSCI-CPAGRWGPRCAOSCPLPLFGLNCSQICTCFNGASCDSVVG 1020
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DE Receptor protein kinase, putative.
GN ORFNames=251.t00016;
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=294381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HM-1:IMSS;
RX PubMed=15729342; DOI=10.1038/nature03291;
RA Loftus B.J., Anderson I., Davies R., Alemaek U.C., Samuelson J.,
RA Amedeo P., Roncaglia P., Bertman M., Hirt R.P., Mann B.J., Nozaki T.,
RA Sun B., Pop M., Duchene M., Ackers J., Tannich E., Leipzig M.,
RA Hofer M., Bruchhaus I., Willhoelt U., Bhattacharya A.,
RA Chillingworth T., Churcher C.M., Hance Z., Harris B., Harris D.,
RA Jagels K., Moule S., Mangall K.L., Ormond D., Squares R.,
RA Whitehead S., Quail M.A., Rabinowitsch E., Norbertczak H., Price C.,
RA Wang Z., Guillen N., Gluchrist C., Stroup S.E., Bhattacharya S.,
RA Lohia A., Foster P.G., Sichteritz-Ponten T., Weber C., Singh U.,
RA Mukherjee C., El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M.,
RA Barrell B.G., Fraser C.M., Hall N.;
RT "The genome of the protist parasite Entamoeba histolytica.";
RL Nature 433:865-868(2005).
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
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CC
EMBL; AAFB01000714; EAL44647.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001450; 4Fe4s_Fe_S_bd.
DR InterPro; IPR006210; BGP.
DR InterPro; IPR006212; Furin_repeat.
DR InterPro; IPR002350; Prot_inh_kazal.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001368; TNFR_c6.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF02420; AFP; 2.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00261; FU; 3.
DR PROSITE; PS00196; 4FE4S_FERREROXIN; UNKNOWN_1.
DR PROSITE; PS00282; KAZAL; UNKNOWN_1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
KW Kinase; Receptor.
SO SEQUENCE 1656 AA; 184722 MW; DC895410785B0056 CRC64;

Query Match 21.4%; Score 60.5; DB 2; Length 1656;
Best Local Similarity 28.6%; Pred. No. 2.3e+02;
Matches 12; Conservative 6; Mismatches 23; Indels 1; Gaps 1;

OY 7 QCQNEYFDSLHACIPQCLGSSNTPLTQCRCNCAVSNTS 48
DB 996 RCDGYYLTDLT-MCDPCIENCEQCNPNFTTQCKSSGYILNN 1036
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RESULT 97
O50S87_ENTHI PRELIMINARY; PRT; 1656 AA.
AC Q50S87;
DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 07-JUN-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
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RESULT 98
O57119_MOUSE PRELIMINARY; PRT; 1671 AA.
AC Q57119;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
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DE KIAA4041 protein (Fragment).
 GN Name=Celstr1; Synonyms=MKIAA4041;
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryonic tail;
 RA Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Koseki H., Hiraka S.,
 RA Suga Y., Nagase T., Ohara O., Koga H.,
 RT "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene.
 RT The Complete Nucleotide Sequences of Mouse KIAA-homologous cDNAs
 RT Identified by Screening of Terminal sequences of cDNA Clones Randomly
 RT Sampled from Size-Fractionated Libraries..";
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
 CC - FUNCTION: Receptor that may have an important role in cell/cell
 CC signaling during nervous system formation (By similarity).
 CC -----
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 CC -----
 DR EMBL: AC220170; BJD90355.1; -; mRNA.
 DR Ensembl: ENSMUSG0000016028; Mus musculus.
 DR MGI: MGI:1100883; Celstr1.
 DR GO: GO:0005615; Cytoplasmic space; RCA.
 DR GO: GO:0016021; C: integral to membrane; RCA.
 DR GO: GO:0042249; P: establishment of polarity of embryonic epit. .; IMP.
 DR GO: GO:0042472; P: inner ear morphogenesis; IMP.
 DR GO: GO:007626; P: locomotor behavior; IMP.
 DR InterPro: IPR008077; Angio_inhib.
 DR InterPro: IPR000152; Asx_hydroxyl_S.
 DR InterPro: IPR013320; Conn_like_subgrp.
 DR InterPro: IPR006210; EGF.
 DR InterPro: IPR000742; EGF_3.
 DR InterPro: IPR001881; EGF_Ca_bd.
 DR InterPro: IPR002049; EGF_lamln.
 DR InterPro: IPR006209; EGF_like.
 DR InterPro: IPR013032; EGF_like_reg.
 DR InterPro: IPR000832; GPCR_secretin.
 DR InterPro: IPR001879; hormone_recp.
 DR InterPro: IPR001791; laminin_G.
 DR InterPro: IPR012680; laminin_G_2.
 DR InterPro: IPR000203; PKD_cys_rich.
 DR Pfam: PF00002; 7tm_2; 1.
 DR Pfam: PF00008; EGF_5.
 DR Pfam: PF01825; GPS; 1.
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 DR Pfam: PF00053; Laminin_EGF_1.
 DR Pfam: PF02210; Laminin_G_2; 2.
 DR PRINTS: PR01694; BAIPRECTOR.
 DR PRINTS: PR00011; BGLAMININ.
 DR PRINTS: PR00249; GPCRSECRETIN.
 DR SMART: SM00181; EGF; 5.
 DR SMART: SM00180; EGF_lam; 1.
 DR SMART: SM00303; GPS; 1.
 DR SMART: SM00008; Hormr; 1.
 DR SMART: SM00282; LamG; 2.
 DR PROSITE: PS00010; ASX_HYDROXYL; 2.
 DR PROSITE: PS00022; EGF_1; 5.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS00026; EGF_3; 6.
 DR PROSITE: PS01248; EGF_LAM_1; 1.
 DR PROSITE: PS00027; G_PROTEIN_RECPT_F2_3; 1.
 DR PROSITE: PS00227; G_PROTEIN_RECPT_F2_4; 1.
 DR PROSITE: PS00261; G_PROTEIN_RECPT_F2_4; 1.
 DR PROSITE: PS00221; GPS; 1.
 DR PROSITE: PS00225; LAM_G_DOMAIN; 2.
 DR PROSITE: PS00025; LAM_G_DOMAIN; 2.
 DR EGF-like domain; laminin EGF-like domain.
 FT NON_TER 1
 SQ SEQUENCE 1671 AA; 183112 MW; 800598BAD02956F1 CRC64;

Query Match 21.4%; Score 60.5; DB 2; Length 1671;
 Best Local Similarity 28.3%; Pred. No. 2.3e+02;
 Matches 17; Conservative 5; Mismatches 19; Indels 19; Gaps 3;
 QY 7 QCSQNEYPFSLHACIPQL-----RCSNTPLPTQ-----RYCN-----ASYVN 47
 DB 634 QCKENYKPPADACLPCCPFHSGSHRACDMDTQCACPKGVIGRCNCRDNPFAVTS 693
 RESULT 99
 Q4SV9_TETNG PRELIMINARY; PRT; 1866 AA.
 ID Q4SV9_TETNG
 AC Q4SV9;
 DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2005, sequence version 1.
 DT 07-FEB-2006, entry version 4.
 DE Chromosome undetermined SCAR13714, whole genome shotgun sequence.
 DE (Fragment).
 GN ORFNames=GSTENG00011783001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 NCBI_TaxId=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15496914; DOI=10.1038/nature03025;
 RA Jallou O., Arny J.-M., Brunet F., Petit J.-L., Strange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozout-Costa C., Bernot A.,
 RA Nicoud S., Jaffe D., Fisher S., Lutfalla G., Dosat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Caselli V., Katinka M., Vacherie B.,
 RA Biemond C., Skalli Z., Catolico L., Poulin J., de Bernardis V.,
 RA Chaud C., Duprat S., Broctier P., Coutanceau J.-P., Gouzy J.,
 RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Querier F., Sautin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissbach J., Roest Croollins H.;
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype.";
 RL Nature 431:946-957 (2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC - CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -----
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 CC -----
 DR EMBL: CAE01013714; CAF95223.1; -; genomic_DNA.
 DR InterPro: IPR000884; TSP1.
 DR Pfam: PF00090; TSP_1; 10.
 DR SMART: SM00209; TSP1; 9.
 DR PROSITE: PS00092; TSP1; 11.
 FT NON_TER 1
 FT NON_TER 1
 FT NON_TER 1866
 SQ SEQUENCE 1866 AA; 207436 MW; 7179D6C88646483 CRC64;
 Query Match 21.4%; Score 60.5; DB 2; Length 1866;
 Best Local Similarity 31.1%; Pred. No. 2.6e+02;
 Matches 19; Conservative 11; Mismatches 16; Indels 15; Gaps 5;
 QY 2 LQMAQCQSN--EYFD--SLHAC-IPCOLRC-----SSNTPLPTQRYCNASVTNSV 49
 DB 177 VQKSGEAAQDAICFEYFEPKRLQACLPDQCVSNFSAWTP---CSKTCGLGLQRI 233
 QY 50 K 50

Db 234 R 234

RESULT 100

CELRL_MOUSE STANDARD; PRT; 3034 AA.

ID CELRL_MOUSE

AC 035161;

DT 02-AUG-2002, integrated into UniProtKB/Swiss-Prot.

DT 01-MAY-1999, sequence version 2.

DT 07-MAR-2006, entry version 61.

DE Cadherin EGF LAG seven-pass G-type receptor 1 precursor.

GN Name=Celst1;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridea; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA].

RX MEDLINE=99077689; PubMed=9858697; DOI=10.1016/S0925-4773(98)00153-1;

RA Hadjantonakis A.-K., Formstone C.J., Little P.F.R.;

RT "Celst1 is an evolutionarily conserved seven-pass transmembrane receptor and is expressed during mouse embryonic development.";

RL Mech. Dev. 78:91-95(1998).

RU [2]

RN TISSUE SPECIFICITY.

RP STRAIN=C57BL/6; TISSUE=Brain;

RX MEDLINE=97480720; PubMed=9339365; DOI=10.1006/geno.1997.4892;

RA Hadjantonakis A.-K., Sheward W.J., Hartmar A.J., de Galan L., Hoovers J.M.N., Little P.F.R.;

RT "Celst1, a neutral-specific gene encoding an unusual seven-pass transmembrane receptor, maps to mouse chromosome 15 and human chromosome 22qter.";

RT Genomics 45:97-104(1997).

RN [3]

RP DEVELOPMENTAL STAGE.

RX MEDLINE=21839555; PubMed=11850187; DOI=10.1016/S0925-4773(01)00623-2;

RA Tislar F., De-Backer O., Goffinet A.M., Lambert de Rouvroit C.A.;

RT "Developmental expression profiles of Celst (Flamingo) genes in the mouse.";

RL Mech. Dev. 112:157-160(2002).

RU [1]

CC -!- FUNCTION: Receptor that may have an important role in cell/cell signaling during nervous system formation.

CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.

CC -!- TISSUE SPECIFICITY: Expressed in the brain, where it is localized principally in the ependymal cell layer, choroid plexus and the area postrema. Also found in spinal chord and in the eye.

CC -!- DEVELOPMENTAL STAGE: First detected at E6. Predominantly expressed in the developing CNS, the emerging dorsal root ganglia and cranial ganglia. In the CNS, expression is uniform along the rostrocaudal axis. During gastrulation, it is expressed in the vicinity of the primitive streak, and becomes predominant in that area at late gastrulation. At E10, detected in ventricular zones (VZ), but not in marginal zones (MZ), and weakly in other structures. Between E12 and E15, a high expression is present in the VZ in all brain areas. No expression in differentiated neuronal fields. In the newborn and postnatal stages, expression remains restricted to the VZ. Also found weakly in fetal lungs, kidney and epithelia.

CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.

CC -!- LM-TM7 subfamily.

CC -!- SIMILARITY: Contains 9 cadherin domains.

CC -!- SIMILARITY: Contains 8 EGF-like domains.

CC -!- SIMILARITY: Contains 1 GPS domain.

CC -!- SIMILARITY: Contains 1 laminin EGF-like domain.

CC -!- SIMILARITY: Contains 2 laminin G-like domains.

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DR EMBL; AF031572; AAC6836.1; -, mRNA.

DR PIR; T14119; T14119.

DR HSP; P00749; IURK.

DR Ensembl; ENSMUSG0000016028; Mus musculus.

DR MGI; MGI:1100883; Celst1.

DR GO; GO:0005615; C:extracellular space; TAS.

DR GO; GO:0016021; C:integral to membrane; TAS.

DR GO; GO:0042249; P:establishment of polarity of embryonic epit. . .; IMP.

DR GO; GO:0042472; P:inner ear morphogenesis; IMP.

DR GO; GO:0007626; P:locomotory behavior; IMP.

DR InterPro; IPR000152; Asx hydroxyl_5.

DR InterPro; IPR002126; Cadherin.

DR InterPro; IPR013320; Cona_like_subgrp.

DR InterPro; IPR006210; EGF.

DR InterPro; IPR000742; EGF_3.

DR InterPro; IPR001881; EGF_Ca_bd.

DR InterPro; IPR002049; EGF_laminin.

DR InterPro; IPR006209; EGF_like.

DR InterPro; IPR013032; EGF_like_reg.

DR InterPro; IPR000832; GPCR_secretin.

DR InterPro; IPR001879; hormone_rcpt.

DR InterPro; IPR001791; Laminin_G.

DR InterPro; IPR012680; Laminin_G_2.

DR InterPro; IPR000203; PKD_cys_rich.

DR Pfam; PF00002; 7tm_2; 1.

DR Pfam; PF00028; Cadherin; 9.

DR Pfam; PF00008; EGF; 6.

DR Pfam; PF01825; GPS; 1.

DR Pfam; PF02793; HRM; 1.

DR Pfam; PF00053; Laminin EGF; 1.

DR Pfam; PF02210; Laminin_G_2; 2.

DR PRINTS; PR000205; CADHERIN.

DR PRINTS; PR00011; EGF_LAMININ.

DR PRINTS; PR00249; GPCRSECRETIN.

DR SMART; SM00112; CA; 8.

DR SMART; SM00181; EGF; 6.

DR SMART; SM00180; EGF_Lam; 1.

DR SMART; SM00303; GPS; 1.

DR SMART; SM00008; Horner; 1.

DR SMART; SM00282; Lams; 2.

DR PROSITE; PS00010; ASX_HYDROXYL; 2.

DR PROSITE; PS00232; CADHERIN_1; 7.

DR PROSITE; PS02068; CADHERIN_2; 9.

DR PROSITE; PS00022; EGF_1; 6.

DR PROSITE; PS01186; EGF_2; 2.

DR PROSITE; PS50026; EGF_3; 6.

DR PROSITE; PS01248; EGF_LAM_1; 1.

DR PROSITE; PS50027; EGF_LAM_2; 1.

DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; FALSE_NEG.

DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; FALSE_NEG.

DR PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.

DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.

DR PROSITE; PS50221; GPS; 1.

DR PROSITE; PS50025; LAM_G_DOMAIN; 2.

DR PROSITE; PS50025; LAM_G_DOMAIN; 2.

DR Calcium; Developmental protein; EGF-like domain;

DR G-protein coupled receptor; Glycoprotein; Hydroxylation;

DR Laminin EGF-like domain; Membrane; Receptor; Repeat; Signal;

DR Transducer; Transmembrane.

FT SIGNAL 1 29 Potential.

FT CHAIN 30 3034 Cadherin EGF LAG seven-pass G-type receptor 1.

FT TOPO_DOM 21 2484 /FtId=PRO_0000012915.

FT TRANSMEM 2485 2505 Extracellular (Potential).

FT TOPO_DOM 2506 2516 1 (Potential).

FT TRANSMEM 2517 2537 Cytoplasmic (Potential).

FT TOPO_DOM 2538 2542 2 (Potential).

FT TRANSMEM 2543 2563 Extracellular (Potential).

FT TOPO_DOM 2564 2587 3 (Potential).

FT TRANSMEM 2588 2608 Cytoplasmic (Potential).

FT TOPO_DOM 2609 2625 4 (Potential).

FT TRANSMEM 2626 2646 Extracellular (Potential).

FT TOPO_DOM 2647 2670 5 (Potential).

FT TRANSMEM 2671 2691 Cytoplasmic (Potential).

FT TOPO_DOM 2692 2694 6 (Potential).

FT TRANSMEM 2695 2715 Extracellular (Potential).

FT 7 (Potential).

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FT TOPO DOM 2716 3034 Cytoplasmic (Potential).
FT DOMAIN 261 368 Cadherin 1.
FT DOMAIN 369 474 Cadherin 2.
FT DOMAIN 475 580 Cadherin 3.
FT DOMAIN 581 702 Cadherin 4.
FT DOMAIN 703 804 Cadherin 5.
FT DOMAIN 805 907 Cadherin 6.
FT DOMAIN 908 1014 Cadherin 7.
FT DOMAIN 1015 1116 Cadherin 8.
FT DOMAIN 1121 1239 Cadherin 9.
FT DOMAIN 1318 1376 EGF-like 1; calcium-binding.
FT DOMAIN 1378 1414 EGF-like 2; calcium-binding.
FT DOMAIN 1418 1456 EGF-like 3; calcium-binding.
FT DOMAIN 1457 1661 Laminin G-like 1.
FT DOMAIN 1664 1700 EGF-like 4; calcium-binding.
FT DOMAIN 1704 1885 Laminin G-like 2.
FT DOMAIN 1887 1922 EGF-like 5; calcium-binding.
FT DOMAIN 1923 1961 EGF-like 6; calcium-binding.
FT DOMAIN 1962 1994 EGF-like 7; calcium-binding.
FT DOMAIN 1996 2031 EGF-like 8; calcium-binding.
FT DOMAIN 2031 2065 Laminin EGF-like.
FT DOMAIN 2423 2475 GP8.
FT COMBIAS 2674 2678 Poly-Leu.
FT MOD_RES 1681 1681 3-hydroxyaspartate (Potential).
FT MOD_RES 1904 1904 3-hydroxyaspartate (Potential).
FT CARBOHYD 236 236 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 561 561 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 649 649 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 793 793 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 1129 1129 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 1154 1154 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 1228 1228 N-linked (GlcNAc. . .) (Potential).
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FT CARBOHYD 1274 1274 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 1302 1302 N-linked (GlcNAc. . .) (Potential).
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FT CARBOHYD 1994 1994 N-linked (GlcNAc. . .) (Potential).
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FT CARBOHYD 2144 2144 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 2155 2155 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 2160 2160 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 2272 2272 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 2430 2430 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 2452 2452 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 2538 2538 N-linked (GlcNAc. . .) (Potential).
FT DISULFID 1322 1333 By similarity.
FT DISULFID 1327 1364 By similarity.
FT DISULFID 1366 1375 By similarity.
FT DISULFID 1382 1393 By similarity.
FT DISULFID 1387 1402 By similarity.
FT DISULFID 1404 1413 By similarity.
FT DISULFID 1422 1433 By similarity.
FT DISULFID 1427 1443 By similarity.
FT DISULFID 1445 1455 By similarity.
FT DISULFID 1635 1661 By similarity.
FT DISULFID 1679 1679 By similarity.
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Query Match 21.4%; Score 60.5; DB 1; Length 3034;
Best Local Similarity 28.3%; Pred. No. 4.4e+02;
Matches 17; Conservative 5; Mismatches 19; Indels 19; Gaps 3;
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QY 7 QCSQNYFPLSLHACTPPQL-----RCSSNTFPLTQ-----RYCN-----ASVTN 47
DB 2001 QCKENYTKPPADACLPCCCFPHGSHSRACDMDTGCACKPGVIGRCNCRCDNPFALVTS 2060
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Search completed: July 10, 2006, 16:44:08
Job time : 131.2 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: July 10, 2006, 16:41:19 ; Search time 15.6 seconds
(without alignments)
314.555 Million cell updates/sec

Title: US-10-077-137a-1_COPY_1_51
Perfect score: 283
Sequence: 1 MLOMAGOCSONEYFDSLHA.....TPPLTCORYCNASVTNSVKG 51

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------------|
| 1 | 283 | 100.0 | 184 | 2 | S43486 B-cell maturation |
| 2 | 70.5 | 24.9 | 1548 | 2 | S34583 serine proteinase |
| 3 | 69.5 | 24.6 | 5376 | 2 | T42215 zonadhesin - mouse |
| 4 | 68.5 | 24.2 | 1101 | 2 | T16840 hypothetical prote |
| 5 | 65.5 | 23.1 | 1299 | 2 | T43251 furin (EC 3.4.21.7 |
| 6 | 62.5 | 22.1 | 999 | 2 | T19275 hypothetical prote |
| 7 | 62 | 21.9 | 330 | 2 | T25169 hypothetical prote |
| 8 | 61.5 | 21.7 | 99 | 2 | S60231 gibberellin-regula |
| 9 | 61.5 | 21.7 | 483 | 2 | T24856 hypothetical prote |
| 10 | 61.5 | 21.7 | 520 | 2 | G88846 protein T12A7.2 (l |
| 11 | 60.5 | 21.4 | 1574 | 2 | T13954 MEGF6 protein - ra |
| 12 | 60.5 | 21.4 | 3034 | 2 | T14119 seven-pass transme |
| 13 | 59.5 | 21.0 | 388 | 2 | T31887 hypothetical prote |
| 14 | 59.5 | 21.0 | 388 | 2 | T31888 hypothetical prote |
| 15 | 59.5 | 21.0 | 388 | 2 | T31889 hypothetical prote |
| 16 | 59.5 | 21.0 | 445 | 2 | T31898 hypothetical prote |
| 17 | 59 | 20.8 | 758 | 2 | T15577 hypothetical prote |
| 18 | 58.5 | 20.7 | 1717 | 1 | A45558 epidermal growth f |
| 19 | 58.5 | 20.7 | 2533 | 2 | T28675 alpha-51D immobill |
| 20 | 58.5 | 20.7 | 2533 | 2 | T28675 alpha-51D-immobill |
| 21 | 58 | 20.5 | 63 | 2 | S07127 chymotrypsin/elast |
| 22 | 58 | 20.5 | 1513 | 2 | T21681 hypothetical prote |
| 23 | 58 | 20.5 | 1816 | 1 | S68960 laminin alpha-4 ch |
| 24 | 57.5 | 20.3 | 1680 | 2 | A43434 furin (EC 3.4.21.7 |
| 25 | 57 | 20.1 | 502 | 2 | T20130 hypothetical prote |
| 26 | 57 | 20.1 | 653 | 2 | G96675 hypothetical prote |
| 27 | 57 | 20.1 | 838 | 2 | T20125 hypothetical prote |
| 28 | 56.5 | 20.0 | 701 | 2 | S62460 hypothetical prote |
| 29 | 56 | 19.8 | 2476 | 2 | T34022 zonadhesin - pig |

| | | | | | |
|-----|------|------|------|---|-----------------------------|
| 30 | 56 | 19.8 | 2824 | 2 | T22759 hypothetical prote |
| 31 | 55.5 | 19.6 | 339 | 1 | KHRTB cathepsin B (EC 3. |
| 32 | 55.5 | 19.6 | 378 | 2 | B89588 protein R09f10.7 (|
| 33 | 55.5 | 19.6 | 815 | 1 | T05754 S-receptor kinase |
| 34 | 55.5 | 19.6 | 989 | 2 | T01519 hypothetical prote |
| 35 | 55 | 19.4 | 294 | 2 | T23682 hypothetical prote |
| 36 | 55 | 19.4 | 339 | 1 | KHMSB cathepsin B (EC 3. |
| 37 | 55 | 19.4 | 758 | 2 | S46625 finger protein YVL |
| 38 | 55 | 19.4 | 1620 | 2 | T27283 hypothetical prote |
| 39 | 54.5 | 19.3 | 392 | 2 | T27203 hypothetical prote |
| 40 | 54.5 | 19.3 | 419 | 2 | S69207 vascular endotheli |
| 41 | 54.5 | 19.3 | 493 | 2 | JCS486 membrane glycoprot |
| 42 | 54.5 | 19.3 | 879 | 2 | C90879 hypothetical prote |
| 43 | 54.5 | 19.3 | 879 | 2 | H64888 membrane protein Y |
| 44 | 54.5 | 19.3 | 879 | 2 | G85739 hypothetical prote |
| 45 | 54.5 | 19.3 | 2155 | 2 | T30197 alpha tectorin - m |
| 46 | 54 | 19.1 | 282 | 2 | S35754 slah-1A protein - |
| 47 | 54 | 19.1 | 282 | 2 | S35754 hypothetical prote |
| 48 | 54 | 19.1 | 474 | 2 | T27297 hypothetical prote |
| 49 | 54 | 19.1 | 497 | 2 | T27827 hypothetical prote |
| 50 | 54 | 19.1 | 1099 | 2 | T16822 myosin heavy chain |
| 51 | 54 | 19.1 | 1980 | 2 | S54307 myosin-IXb [simila |
| 52 | 54 | 19.1 | 2022 | 2 | AS9256 hypothetical prote |
| 53 | 53.5 | 18.9 | 255 | 2 | A84544 hypothetical prote |
| 54 | 53.5 | 18.9 | 332 | 2 | T21458 hypothetical prote |
| 55 | 53.5 | 18.9 | 356 | 2 | T21681 hypothetical prote |
| 56 | 53.5 | 18.9 | 915 | 2 | T21773 hypothetical prote |
| 57 | 53.5 | 18.9 | 927 | 2 | T21772 hypothetical prote |
| 58 | 53.5 | 18.9 | 1895 | 2 | T15881 hypothetical prote |
| 59 | 53.5 | 18.9 | 1935 | 2 | T39411 RNA helicase - fls |
| 60 | 53 | 18.7 | 98 | 2 | C89046 protein C10G8.4 (l |
| 61 | 53 | 18.7 | 274 | 2 | F86276 F14L17.2 protein - |
| 62 | 53 | 18.7 | 447 | 2 | A96639 protein T1F9.18 (l |
| 63 | 53 | 18.7 | 455 | 1 | GQHT1 tumor necrosis fac |
| 64 | 53 | 18.7 | 592 | 1 | JC1480 protein kinase C (|
| 65 | 53 | 18.7 | 596 | 2 | F88188 protein C18H9.7 (l |
| 66 | 53 | 18.7 | 654 | 2 | T30136 hypothetical prote |
| 67 | 53 | 18.7 | 712 | 1 | VCLJ54 env polyprotein pr |
| 68 | 53 | 18.7 | 859 | 1 | VCLJST env polyprotein pr |
| 69 | 53 | 18.7 | 1034 | 2 | JCS598 mucin - rat |
| 70 | 53 | 18.7 | 1077 | 2 | T41146 probable cysteine- |
| 71 | 53 | 18.7 | 1474 | 2 | D88550 protein ZC84.6 (lm |
| 72 | 53 | 18.7 | 2844 | 2 | S28291 hypothetical prote |
| 73 | 52.5 | 18.6 | 118 | 2 | S61051 myb-related transc |
| 74 | 52.5 | 18.6 | 378 | 2 | T51647 hypothetical prote |
| 75 | 52.5 | 18.6 | 389 | 2 | T29488 probable transamin |
| 76 | 52.5 | 18.6 | 397 | 2 | F72072 aspartate aminotra |
| 77 | 52.5 | 18.6 | 397 | 2 | C86552 mucin homolog - bo |
| 78 | 52.5 | 18.6 | 563 | 2 | A36054 viral capsid assoc |
| 79 | 52.5 | 18.6 | 847 | 2 | D72860 submaxillary mucin |
| 80 | 52.5 | 18.6 | 1589 | 2 | T42233 laminin alpha 5 ch |
| 81 | 52.5 | 18.6 | 3635 | 2 | T10053 trypsin inhibitor |
| 82 | 52 | 18.4 | 56 | 2 | JN0380 lysozyme (EC 3.2.1 |
| 83 | 52 | 18.4 | 141 | 2 | S20915 genome polyprotein |
| 84 | 52 | 18.4 | 180 | 2 | PC1305 hypothetical prote |
| 85 | 52 | 18.4 | 181 | 2 | T05301 tissue factor path |
| 86 | 52 | 18.4 | 304 | 1 | JC2264 probable alkaline |
| 87 | 52 | 18.4 | 420 | 2 | T30507 hypothetical prote |
| 88 | 52 | 18.4 | 547 | 2 | T34318 hypothetical prote |
| 89 | 52 | 18.4 | 689 | 2 | T52060 protein MEDEA (imp |
| 90 | 52 | 18.4 | 852 | 1 | VCLJGG env polyprotein pr |
| 91 | 52 | 18.4 | 869 | 2 | S53098 envelope polyprot |
| 92 | 52 | 18.4 | 1115 | 2 | S40241 G protein-coupled |
| 93 | 52 | 18.4 | 1483 | 2 | S30015 hypothetical prote |
| 94 | 52 | 18.4 | 1747 | 2 | T43162 vitellinogenin - gyp |
| 95 | 52 | 18.4 | 63 | 2 | S57816 antimicrobial pept |
| 96 | 51.5 | 18.2 | 424 | 2 | T14525 fibulin, splice fo |
| 97 | 51.5 | 18.2 | 685 | 2 | S78040 fibulin, splice fo |
| 98 | 51.5 | 18.2 | 705 | 2 | S34968 furin (EC 3.4.21.7 |
| 99 | 51.5 | 18.2 | 837 | 2 | S43656 hypothetical prote |
| 100 | 51.5 | 18.2 | 1808 | 2 | T15099 hypothetical prote |
| 101 | 51.5 | 18.2 | 2120 | 2 | T30243 alpha tectorin - c |
| 102 | 51 | 18.0 | 166 | 2 | H89044 protein B0238.12 (|

| | | | | | | | | | | | | | |
|-----|------|------|------|---|--------|---------------------|-----|------|------|-----|---|--------|---------------------|
| 687 | 44 | 15.5 | 439 | 2 | B72253 | conserved hypothet | 760 | 43.5 | 15.4 | 130 | 2 | C81154 | hypothetical prote |
| 688 | 44 | 15.5 | 453 | 2 | G86396 | protein T7N9.2 (Im | 761 | 43.5 | 15.4 | 140 | 2 | S20914 | lysozyme (EC 3.2.1 |
| 689 | 44 | 15.5 | 455 | 2 | E90316 | oxidoreductase [im | 762 | 43.5 | 15.4 | 140 | 2 | S41577 | lysozyme (EC 3.2.1 |
| 690 | 44 | 15.5 | 461 | 1 | KFHU | coagulation factor | 763 | 43.5 | 15.4 | 140 | 2 | S41574 | lysozyme (EC 3.2.1 |
| 691 | 44 | 15.5 | 462 | 1 | D85438 | hypothetical prote | 764 | 43.5 | 15.4 | 140 | 2 | S41573 | lysozyme (EC 3.2.1 |
| 692 | 44 | 15.5 | 467 | 1 | PABYC | acid phosphatase (| 765 | 43.5 | 15.4 | 183 | 3 | G84923 | hypothetical prote |
| 693 | 44 | 15.5 | 467 | 1 | S48996 | acid phosphatase (| 766 | 43.5 | 15.4 | 192 | 2 | B31926 | probable membrane |
| 694 | 44 | 15.5 | 467 | 2 | S53476 | acid phosphatase (| 767 | 43.5 | 15.4 | 213 | 3 | H88542 | protein ZK637.12 (|
| 695 | 44 | 15.5 | 468 | 2 | T33857 | hypothetical prote | 768 | 43.5 | 15.4 | 233 | 1 | C48560 | US6 protein - hum |
| 696 | 44 | 15.5 | 469 | 2 | H86421 | hypothetical prote | 769 | 43.5 | 15.4 | 250 | 2 | S06314 | regulatory protein |
| 697 | 44 | 15.5 | 470 | 2 | F71544 | probable mg++ tran | 770 | 43.5 | 15.4 | 252 | 2 | B33538 | inulin-like growth |
| 698 | 44 | 15.5 | 497 | 2 | T27169 | hypothetical prote | 771 | 43.5 | 15.4 | 254 | 2 | T48603 | inulin-like growth |
| 699 | 44 | 15.5 | 507 | 2 | T26530 | hypothetical prote | 772 | 43.5 | 15.4 | 272 | 1 | C64009 | ribonuclease homol |
| 700 | 44 | 15.5 | 513 | 2 | S28358 | presore vesicle p | 773 | 43.5 | 15.4 | 272 | 2 | A53748 | insulin-like growt |
| 701 | 44 | 15.5 | 542 | 2 | AG0341 | hypothetical prote | 774 | 43.5 | 15.4 | 292 | 2 | B42822 | cyclin D3 - human |
| 702 | 44 | 15.5 | 549 | 2 | H64992 | hypothetical prote | 775 | 43.5 | 15.4 | 292 | 2 | H81857 | hypothetical prote |
| 703 | 44 | 15.5 | 551 | 2 | S01793 | arylsulfatase (EC | 776 | 43.5 | 15.4 | 294 | 2 | T22058 | hypothetical prote |
| 704 | 44 | 15.5 | 551 | 2 | S07089 | arylsulfatase (EC | 777 | 43.5 | 15.4 | 297 | 2 | S66267 | buface antigen H |
| 705 | 44 | 15.5 | 588 | 2 | B65168 | probable adenine d | 778 | 43.5 | 15.4 | 299 | 2 | S68980 | leucyl aminopeptid |
| 706 | 44 | 15.5 | 588 | 2 | B91204 | probable adenine d | 779 | 43.5 | 15.4 | 324 | 2 | T18790 | hypothetical prote |
| 707 | 44 | 15.5 | 588 | 2 | D86050 | probable adenine d | 780 | 43.5 | 15.4 | 342 | 2 | B81086 | hypothetical prote |
| 708 | 44 | 15.5 | 602 | 2 | B46312 | pol polypeptide - | 781 | 43.5 | 15.4 | 347 | 2 | A38453 | anaerobic sulfite |
| 709 | 44 | 15.5 | 638 | 2 | AE1483 | B. subtilis fold p | 782 | 43.5 | 15.4 | 350 | 2 | A54420 | beta-galactoside a |
| 710 | 44 | 15.5 | 644 | 1 | KGHUHI | Kinnozen, Hmw pr | 783 | 43.5 | 15.4 | 353 | 2 | T09887 | DNA-binding protei |
| 711 | 44 | 15.5 | 655 | 2 | T16538 | hypothetical prote | 784 | 43.5 | 15.4 | 356 | 2 | G88968 | protein T2787.5 (l |
| 712 | 44 | 15.5 | 661 | 2 | B96596 | hypothetical prote | 785 | 43.5 | 15.4 | 371 | 2 | T01717 | hypothetical prote |
| 713 | 44 | 15.5 | 665 | 1 | VCWVKA | env polypeptide pr | 786 | 43.5 | 15.4 | 412 | 2 | T24023 | hypothetical prote |
| 714 | 44 | 15.5 | 667 | 2 | T01999 | hypothetical prote | 787 | 43.5 | 15.4 | 423 | 2 | T14531 | S-locus-specific g |
| 715 | 44 | 15.5 | 669 | 2 | T06702 | hypothetical prote | 788 | 43.5 | 15.4 | 423 | 2 | T14526 | S-locus-specific g |
| 716 | 44 | 15.5 | 704 | 2 | E97354 | hypothetical prote | 789 | 43.5 | 15.4 | 426 | 2 | T07810 | S-locus-specific g |
| 717 | 44 | 15.5 | 709 | 2 | B88553 | protein K04H4.2b (| 790 | 43.5 | 15.4 | 426 | 2 | T14532 | S-locus-specific g |
| 718 | 44 | 15.5 | 761 | 2 | H65083 | glycolate oxidase | 791 | 43.5 | 15.4 | 426 | 2 | T14527 | S-locus-specific g |
| 719 | 44 | 15.5 | 780 | 2 | A34102 | von Willebrand fac | 792 | 43.5 | 15.4 | 427 | 1 | VHNPV | nucleoprotein - p1 |
| 720 | 44 | 15.5 | 780 | 2 | T31548 | hypothetical prote | 793 | 43.5 | 15.4 | 428 | 2 | T07814 | S-locus-specific g |
| 721 | 44 | 15.5 | 782 | 2 | A61625 | tenascin-like prote | 794 | 43.5 | 15.4 | 428 | 2 | T14530 | S-locus-specific g |
| 722 | 44 | 15.5 | 787 | 2 | PN0677 | hypothetical prote | 795 | 43.5 | 15.4 | 428 | 2 | T14528 | S-locus-specific g |
| 723 | 44 | 15.5 | 854 | 1 | VCLJST | env polypeptide pr | 796 | 43.5 | 15.4 | 429 | 2 | T07809 | S-receptor kinase |
| 724 | 44 | 15.5 | 855 | 2 | JC7731 | membrane-bound arg | 797 | 43.5 | 15.4 | 429 | 2 | T14417 | S-locus-specific g |
| 725 | 44 | 15.5 | 857 | 2 | S19886 | env polypeptide E | 798 | 43.5 | 15.4 | 429 | 2 | T14534 | S-locus-specific g |
| 726 | 44 | 15.5 | 914 | 1 | JN0550 | iodide peroxidase | 799 | 43.5 | 15.4 | 430 | 2 | T14422 | S-locus-specific g |
| 727 | 44 | 15.5 | 914 | 1 | S07047 | iodide peroxidase | 800 | 43.5 | 15.4 | 430 | 2 | T14420 | S-locus-specific g |
| 728 | 44 | 15.5 | 915 | 1 | A48225 | subtilisin-like pr | 801 | 43.5 | 15.4 | 431 | 2 | T14415 | S-locus-specific g |
| 729 | 44 | 15.5 | 1107 | 2 | T15884 | hypothetical prote | 802 | 43.5 | 15.4 | 431 | 2 | T14426 | S-locus-specific g |
| 730 | 44 | 15.5 | 1135 | 2 | JQ2163 | hypothetical 126.5 | 803 | 43.5 | 15.4 | 434 | 2 | S04906 | S-locus-specific g |
| 731 | 44 | 15.5 | 1135 | 2 | JQ6065 | M polypeptide - Ha | 804 | 43.5 | 15.4 | 436 | 2 | A27827 | S-locus-specific g |
| 732 | 44 | 15.5 | 1142 | 2 | T30272 | hypothetical prote | 805 | 43.5 | 15.4 | 436 | 2 | T07816 | S-locus-specific g |
| 733 | 44 | 15.5 | 1166 | 1 | S06142 | protein-tyrosine k | 806 | 43.5 | 15.4 | 437 | 2 | J01109 | S-locus-specific g |
| 734 | 44 | 15.5 | 1181 | 2 | A43346 | 1-phosphatidylinos | 807 | 43.5 | 15.4 | 443 | 2 | D71405 | probable protein k |
| 735 | 44 | 15.5 | 1210 | 2 | A53183 | epidermal growth f | 808 | 43.5 | 15.4 | 450 | 2 | C66262 | F13K23.12 protein |
| 736 | 44 | 15.5 | 1255 | 1 | A24571 | protein-tyrosine k | 809 | 43.5 | 15.4 | 467 | 2 | T02238 | glucosyl transfera |
| 737 | 44 | 15.5 | 1454 | 2 | S53398 | hypothetical prote | 810 | 43.5 | 15.4 | 469 | 1 | S29126 | propeptin precursor |
| 738 | 44 | 15.5 | 1472 | 2 | H82802 | fibrillar assembly | 811 | 43.5 | 15.4 | 475 | 2 | H85156 | protein kinase [Im |
| 739 | 44 | 15.5 | 1522 | 2 | H88380 | protein T22F7.3 (I | 812 | 43.5 | 15.4 | 481 | 2 | S62427 | G-protein signalin |
| 740 | 44 | 15.5 | 1521 | 2 | T21214 | hypothetical prote | 813 | 43.5 | 15.4 | 484 | 2 | JC8020 | metalloproteinase- |
| 741 | 44 | 15.5 | 1521 | 2 | T50002 | hypothetical prote | 814 | 43.5 | 15.4 | 500 | 2 | AF0357 | conserved hypothet |
| 742 | 44 | 15.5 | 2139 | 2 | A44467 | voltage-dependent | 815 | 43.5 | 15.4 | 502 | 2 | S43123 | protein-tyrosine-p |
| 743 | 44 | 15.5 | 2143 | 2 | JH0427 | zinc finger protei | 816 | 43.5 | 15.4 | 509 | 2 | T00793 | hypothetical prote |
| 744 | 44 | 15.5 | 2150 | 1 | S27802 | hypothetical prote | 817 | 43.5 | 15.4 | 559 | 2 | B84428 | thrombomodulin pre |
| 745 | 44 | 15.5 | 2150 | 2 | T19450 | genome polypeptide | 818 | 43.5 | 15.4 | 577 | 2 | A60501 | env polypeptide - |
| 746 | 44 | 15.5 | 2182 | 1 | GNNYB1 | calcium channel pr | 819 | 43.5 | 15.4 | 586 | 1 | VCLJMP | probable thiamin A |
| 747 | 44 | 15.5 | 2220 | 2 | A45290 | hypothetical prote | 820 | 43.5 | 15.4 | 593 | 2 | A71361 | beta-transducin - |
| 748 | 44 | 15.5 | 2322 | 2 | T10542 | genome polypeptide | 821 | 43.5 | 15.4 | 595 | 2 | T39228 | protein-tyrosine-p |
| 749 | 44 | 15.5 | 3010 | 1 | GNWVTW | laminin alpha-1 ch | 822 | 43.5 | 15.4 | 596 | 1 | S62407 | complement C3b/C4b |
| 750 | 44 | 15.5 | 3712 | 1 | S18253 | antimicrobial pept | 823 | 43.5 | 15.4 | 613 | 2 | D84494 | probable Tail-like |
| 751 | 43.5 | 15.4 | 61 | 2 | S57815 | hypothetical 8.6K | 824 | 43.5 | 15.4 | 627 | 2 | S49788 | probable membrane |
| 752 | 43.5 | 15.4 | 76 | 2 | JE0003 | hypothetical prote | 825 | 43.5 | 15.4 | 633 | 2 | JC2005 | integrin beta-5 ch |
| 753 | 43.5 | 15.4 | 77 | 2 | T16222 | hypothetical prote | 826 | 43.5 | 15.4 | 656 | 2 | T21516 | hypothetical prote |
| 754 | 43.5 | 15.4 | 80 | 2 | H96775 | GAST1-like protein | 827 | 43.5 | 15.4 | 716 | 2 | S48813 | hypothetical prote |
| 755 | 43.5 | 15.4 | 95 | 2 | T45315 | hypothetical prote | 828 | 43.5 | 15.4 | 730 | 2 | A38308 | integrin beta-5 ch |
| 756 | 43.5 | 15.4 | 108 | 2 | H69834 | hypothetical prote | 829 | 43.5 | 15.4 | 799 | 2 | S65226 | probable membrane |
| 757 | 43.5 | 15.4 | 115 | 2 | H75086 | hypothetical prote | 830 | 43.5 | 15.4 | 810 | 2 | T21192 | hypothetical prote |
| 758 | 43.5 | 15.4 | 118 | 2 | S01141 | phospholipase A2 h | 831 | 43.5 | 15.4 | 813 | 2 | S51527 | S-receptor kinase |
| 759 | 43.5 | 15.4 | 124 | 2 | AE2874 | hypothetical prote | 832 | 43.5 | 15.4 | 849 | 1 | | |


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979 43 15.2 1367 1 IGHUR1 insulin-like growth
980 43 15.2 1372 2 T25933 hypothetical prote
981 43 15.2 1428 2 T08852 Iusterin A - Calif
982 43 15.2 1597 1 BVFSL sol protein, large
983 43 15.2 1597 2 T08428 gene small optic I
984 43 15.2 1743 2 T26859 hypothetical prote
985 43 15.2 1751 1 MMHUM laminin alpha-2 ch
986 43 15.2 1766 2 A42125 trophozoite cystei
987 43 15.2 1812 2 T49350 breast/ovarian can
988 43 15.2 2167 2 T34395 hypothetical prote
989 43 15.2 2352 2 T30201 Notch homolog prot
990 43 15.2 2524 2 A35844 Notch protein - Af
991 43 15.2 2588 2 T13442 NSD1 protein - mou
992 43 15.2 2610 2 T20968 hypothetical prote
993 43 15.2 3010 1 GNMVJC genome polyprotein
994 43 15.2 3061 1 UN0545 genome polyprotein
995 42.5 15.0 51 2 A42243 chitinase-related
996 42.5 15.0 63 2 S08191 metallothionein 2
997 42.5 15.0 68 2 B42243 GTP-binding regula
998 42.5 15.0 80 2 A84528 hypothetical prote
999 42.5 15.0 81 2 T15314 hypothetical prote
1000 42.5 15.0 98 1 KRGLBS keratin, feather -

```

ALIGNMENTS

RESULT 1

S43486 B-cell maturation factor - human

N:Alternate names: BCM protein; BCM protein; BEL protein

C:Species: Homo sapiens (man)

C:Date: 27-Jan-1995 #sequence revision 27-Jan-1995 #text_change 09-Jul-2004

C:Accession: S43486; S31208; S36661

R:Laabli, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.

Nucleic Acids Res. 22, 1147-1154, 1994

A:Title: The BCM gene, preferentially expressed during B lymphoid maturation, is bidire

A:Reference number: S43486; MUID:94218235; PMID:8165126

A:Accession: S43486

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-184 <LAa>

A:Cross-references: UNIPROT:Q02223; UNIPARC:UPI0000034D1B; EMBL:Z29574; NID:g471244; PID

R:Laabli, Y.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis,

EMBO J. 11, 3897-3904, 1992

A:Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;1

A:Reference number: S31208; MUID:93010984; PMID:1396583

A:Accession: S31208

A:Molecule type: mRNA

A:Residues: 1-184 <LA2>

A:Cross-references: UNIPARC:UPI0000034D1B; EMBL:Z14954; NID:g29407; PIDN:CAA78679.1; PID

A:Accession: S36661

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 4-184 <LA3>

A:Cross-references: UNIPARC:UPI0000046868; EMBL:Z14955

C:Genetics:

A:Gene: GDB:BCMA

A:Cross-references: GDB:135977; OMIM:109545

A:Map position: 16p13.1-16p13.1

A:Introns: 44/1; 93/1

C:Superfamily: human B-cell maturation factor

Query Match 100.0%; Score 283; DB 2; Length 184;

Best Local Similarity 100.0%; Pred. No. 8.5e-25;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 MCGAGGCGSNEYFDSLHACIPCOLRCSSNTPPLTCORICNASTYNSVK 51
Db 1 MCGAGGCGSNEYFDSLHACIPCOLRCSSNTPPLTCORICNASTYNSVK 51

```

RESULT 2

```

S34583
serine proteinase (EC 3.4.21.-) PC6B - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S34583
R:Nakagawa, T.; Murakami, K.; Nakayama, K.
FBS Lett. 327, 165-171, 1993
A:Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a f
A:Reference number: S34583; MUID:93327934; PMID:8335106
A:Accession: S34583
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1548 <NAK>
A:Cross-references: UNIPROT:Q04592; UNIPARC:UPI000016CF9E; GB:D17583; NID:g407344; PIDN:1
C:Keywords: hydrolase; serine proteinase

```

Query Match 24.9%; Score 70.5; DB 2; Length 1548;

Best Local Similarity 34.7%; Pred. No. 4.2;

Matches 17; Conservative 5; Mismatches 22; Indels 5; Gaps 1;

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OY 7 OCGSNEYFDSLHACIPCOLRCSSNTP-----LTQORYCNASTYNSVK 50
Db 1151 ECAVEYDEGSHRCPCPKKCSRCGSEDOCTCPREFTLNTTCVK 1199

```

RESULT 3

T42215 zonadhesin - mouse

N:Alternate names: sperm-specific membrane protein

C:Species: Mus musculus (house mouse)

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: T42215

R:Guo, Z.; Garbers, D.L.

J. Biol. Chem. 273, 3415-3421, 1998

A:Title: Species diversity in the structure of zonadhesin, a sperm-specific membrane prot

A:Reference number: Z22080; MUID:98123114; PMID:9452463

A:Accession: T42215

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-5376 <GAO>

A:Cross-references: UNIPROT:O88799; UNIPARC:UPI000002A15E; EMBL:U97068; NID:g3327420; PID

C:Genetics:

A:Gene: Zan

A:Map position: 5

C:Function:

A:Description: functions in multiple cell adhesion processes

A:Note: found exclusively on the apical region of the sperm head

C:Keywords: cell adhesion

Query Match 24.6%; Score 69.5; DB 2; Length 5376;

Best Local Similarity 36.8%; Pred. No. 16;

Matches 14; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

```

OY 7 OCGSNEYFDSLHACIPCOLRCSSNTP--PLTCORIC 41
Db 3299 QCPINSQFTDCLPSCVPSCSNRCVETSPSSCREGC 3336

```

RESULT 4

T16840 hypothetical protein T10E10.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C:Accession: T16840

R:Geiselt, C.

submitted to the EMBL Data Library, October 1995

A:Description: The sequence of C. elegans cosmid T10E10.

A:Reference number: Z18588

A:Accession: T16840

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1101 <GEI>

A:Cross-references: UNIPROT:Q22378; UNIPARC:UPI000017BB8F; EMBL:U39644; NID:g1049339; PID

A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:T10B10.4
A:introns: 99/2; 150/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3; 7
Query Match 24.2%; Score 68.5; DB 2; Length 1101;
Best Local Similarity 36.2%; Pred. No. 5.2;
Matches 17; Conservative 10; Mismatches 15; Indels 5; Gaps 3;

QY 7 GCSQNEVFDLSLHACIPCOLR--CSSNTPLTCQRCYNASVTVNSVKG 51
DB 350 GCSQSTVNSDLAVCVLAIONSQSSSTQOPVCS--C-SQVSSSCPG 393

RESULT 5
T43251
furin (EC 3.4.21.75) - fall armyworm
N:Alternate names: paired basic amino acid cleaving enzyme; proprotein convertase; serin
C:Species: Spodoptera frugiperda (fall armyworm)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43251
R:Cieplik, M.; Klenk, H.
Submitted to the EMBL Data Library, January 1996
A:Description: Cloning and functional characterization of FURIN from Spodoptera frugiper
A:Reference number: Z22368
A:Accession: T43251
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1299 <CIF>
A:Cross-references: UNIPROT:Q26489; UNIPARC:UPI0000083055; EMBL:Z68888; NID:G1167859; PI
A:Experimental source: clone Sfurin 6; ovary
C:Function:
A:Description: responsible for the endoproteolytic processing of proproteins with specif
C:Keywords: hydrolase; serine proteinase

Query Match 23.1%; Score 65.5; DB 2; Length 1299;
Best Local Similarity 34.0%; Pred. No. 13;
Matches 18; Conservative 8; Mismatches 14; Indels 13; Gaps 4;

QY 8 GSONEYFDLSLHACIPCOLRCS----SNTPPLTCQRCYNAS--VTNSVKG 51
DB 1150 GSRPLRIDRLNNQCVFC--CSERGVTNTPTPTDC-CHCNPENGEICINSSVAG 1198

RESULT 6
T19275
hypothetical protein F34D10.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T19275; T21723
R:Harris, B.
Submitted to the EMBL Data Library, September 1994
A:Reference number: Z19099
A:Accession: T19275
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-999 <MIL>
A:Cross-references: UNIPROT:O17969; UNIPARC:UPI0000079A41; EMBL:Z237139; PIDN:CAA85494.1;
A:Experimental source: clone C14B1
R:Keshav, J.
Submitted to the EMBL Data Library, June 1994
A:Reference number: Z19464
A:Accession: T21723
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-999 <M12>
A:Cross-references: UNIPARC:UPI0000079A41; EMBL:Z24799; PIDN:CAA84320.1; GSPDB:GN00021;
A:Experimental source: clone F34D10
C:Genetics:
A:Gene: CESP:F34D10.2
A:Map position: 3
A:introns: 20/3; 40/3; 72/1; 234/3; 387/3; 457/1; 523/2; 541/3; 682/1; 784/2; 822/2; 870

Query Match 22.1%; Score 62.5; DB 2; Length 999;
Best Local Similarity 42.5%; Pred. No. 23;
Matches 17; Conservative 2; Mismatches 20; Indels 1; Gaps 1;

QY 13 YFDSLHACIPCOLR--RCSNTPLTCQRCYNASVTVNSVKG 51
DB 516 YEDSLKTCIGRAFRRVKMTPPLRIQSYFVSSTPGLDG 555

RESULT 7
T25169
hypothetical protein T23F1.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T25169
R:Wilkinson, J.
Submitted to the EMBL Data Library, October 1996
A:Reference number: Z19990
A:Accession: T25169
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-330 <MIL>
A:Cross-references: UNIPROT:O18118; UNIPARC:UPI000006118C; EMBL:Z81129; PIDN:CAB03405.1;
A:Experimental source: clone T23F1
C:Genetics:
A:Gene: CESP:T23F1.6
A:Map position: 5
A:introns: 16/3
C:Superfamily: gliadin

Query Match 21.9%; Score 62; DB 2; Length 330;
Best Local Similarity 29.2%; Pred. No. 10;
Matches 14; Conservative 7; Mismatches 19; Indels 8; Gaps 2;

QY 8 GSONEYFDLSLHACIP----COLRCSNTPLP---TCQRCYNASVTN 47
DB 59 CASSQOYQLQTSQCMPACQSCSQOCOSNTNTQCOPTCQSCQTSN 106

RESULT 8
S60231
gibberellin-regulated protein GAS3 precursor - Arabidopsis thaliana
N:Alternate names: GAS1 protein homolog
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 09-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C:Accession: S60231
R:Herzog, M.; Dorne, A.M.; Grelliet, F.
Plant Mol. Biol. 27, 743-752, 1995
A:Title: GAS3, a gibberellin-regulated gene family from Arabidopsis thaliana related to
A:Reference number: S60229; MUID:95244835; PMID:7727751
A:Accession: S60231
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-99 <HER>
A:Cross-references: UNIPROT:P46687; UNIPARC:UPI0000000D66; EMBL:U11764; NID:G887934; PIDN
C:Genetics:
A:Gene: GAS3
C:Superfamily: gibberellin-regulated protein GAS2
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-99/Product: gibberellin-regulated protein GAS3 #status predicted <MAT>

Query Match 21.7%; Score 61.5; DB 2; Length 99;
Best Local Similarity 35.6%; Pred. No. 4.1;
Matches 16; Conservative 7; Mismatches 17; Indels 5; Gaps 2;

QY 6 GCSQNEVFDLSLHACIPCOLRCSNTPLTCQRY----CNASVT 46
DB 47 GRCSSSRPNLCIRACNSCYRNC-VPPGTGNHHLCPCVASIT 90

RESULT 9
T24856
hypothetical protein T12A7.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T24856
R:Lemard, N.
Submitted to the EMBL Data Library, June 1996
A:Reference number: Z19943
A:Accession: T24856
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-483 <M11>
A:Cross-references: UNIPROT:Q22423, UNIPARC:UPI000008213D, EMBL:Z73911, PIDN:CAA98142.2;
A:Experimental source: clone T12A7
C:Genetics:
A:Gene: CESP:T12A7.2
A:Map position: 4
A:Introns: 36/3; 71/1; 146/1; 255/2; 287/2; 340/3; 387/1; 449/2

Query Match 21.7%; Score 61.5; DB 2; Length 483;
Best Local Similarity 31.8%; Pred. No. 16;
Matches 14; Conservative 5; Mismatches 20; Indels 5; Gaps 1;

Qy 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVNSVKG 51
Db 108 CMNDGTFNHTLGRV-----CTSNMVGEHCIFRCNSGVNKTSG 146

RESULT 10
G88846
protein T12A7.2 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G88846
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see webites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: G88846
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-520 <STO>
A:Cross-references: UNIPROT:Q22423, UNIPARC:UPI000017A62A; GB:chr_IV; PIDN:CAA98142.1; F
C:Genetics:
A:Gene: T12A7.2
A:Map position: 4

Query Match 21.7%; Score 61.5; DB 2; Length 520;
Best Local Similarity 31.8%; Pred. No. 17;
Matches 14; Conservative 5; Mismatches 20; Indels 5; Gaps 1;

Qy 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVNSVKG 51
Db 145 CMNDGTFNHTLGRV-----CTSNMVGEHCIFRCNSGVNKTSG 183

RESULT 11
T13954
MEGF6 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13954
R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A:Reference number: Z14126; MUID:98360089; PMID:9693030
A:Accession: T13954
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1574 <NAK>
A:Cross-references: UNIPROT:O88281, UNIPARC:UPI0000043BEE; EMBL:AB011532; NID:G3449293;
A:Experimental source: strain Sprague-Dawley; brain
C:Genetics:

A:Gene: MEGF6
Query Match 21.4%; Score 60.5; DB 2; Length 1574;
Best Local Similarity 32.2%; Pred. No. 56;
Matches 19; Conservative 8; Mismatches 19; Indels 13; Gaps 4;

Qy 5 AGQSQNEYFDSLHACIPCOL-----RCSSNTPPLT---CQRYC---NASVNSVKG 51
Db 963 ACNCGAGAPCDVAVGSCI-CPAGRWGPRCAOSCPPLTRGLNCSQICTFNGASCDSTVG 1020

RESULT 12
T14119
seven-pass transmembrane receptor protein precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T14119
R:Hadjantonakis, A.K.; Formstone, C.J.; Little, P.F.R.
Submitted to the EMBL Data Library, October 1997
A:Description: The Celser family of novel evolutionarily conserved seven-pass transmembrat
A:Reference number: Z17881
A:Accession: T14119
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-3034 <HAD>
A:Cross-references: UNIPROT:O35161, UNIPARC:UPI00002931C; EMBL:AF031572; NID:G3800735; 1
C:Genetics:
A:Gene: Celser1
A:Map position: 15
C:Keywords: transmembrane protein
F:1-26/Domains: signal sequence #status predicted <SIG>
F:27-3034/Product: seven-pass transmembrane receptor protein

Query Match 21.4%; Score 60.5; DB 2; Length 3034;
Best Local Similarity 28.3%; Pred. No. 99;
Matches 17; Conservative 5; Mismatches 19; Indels 19; Gaps 3;

Qy 7 QCSQNEYFDSLHACIPCOL-----RCSSNTPPLTCQ-----RYCN-----ASVTN 47
Db 2001 QCKENYKRPADQCLPCDCPRHSGHSRACMDITQCAKCKRGVIGQCNCRCNDNPAEYTS 2060

RESULT 13
T31887
hypothetical protein C03A7.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T31887
R:Greco, T.; Bradshaw, H.; Elliott, G.
Submitted to the EMBL Data Library, July 1997
A:Description: The sequence of C. elegans cosmid C03A7.
A:Reference number: Z21096
A:Accession: T31887
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-388 <GRE>
A:Cross-references: UNIPROT:O16500, UNIPARC:UPI000007BC52; EMBL:AF016451; PIDN:AAB66001.1
A:Experimental source: strain Bristol N2; clone C03A7
C:Genetics:
A:Gene: CESP:C03A7.4
A:Map position: 5
A:Introns: 75/3
C:Superfamily: gliadin

Query Match 21.0%; Score 59.5; DB 2; Length 388;
Best Local Similarity 31.9%; Pred. No. 22;
Matches 15; Conservative 4; Mismatches 15; Indels 13; Gaps 2;

Qy 3 QNAGQSQNEYFDSLHACIPCOLRC-SSNTPPLTCQRYCNASVNS 48
Db 316 QCAPQCEQS-----CQDQCVQDQDPAQCQTRCQSSCSNS 350

RESULT 14
T31888
hypothetical protein C03A7.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T31888
R:Greco, T.; Bradshaw, H.; Elliott, G.
A:Description: The sequence of C. elegans cosmid C03A7.
A:Reference number: Z21096
A:Accession: T31888
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-388 <GRE>
A:Cross-references: UNIPROT:O16501; UNIPARC:UPI0000077D46; EMBL:AF016451; PIDN:AAB65996.
C:Genetics:
A:Gene: CESP:C03A7.7
A:Map position: 5
A:Introns: 75/3
C:Superfamily: gliadin

Query Match 21.0%; Score 59.5; DB 2; Length 388;
Best Local Similarity 31.9%; Pred. No. 22;
Matches 15; Conservative 4; Mismatches 15; Indels 13; Gaps 2;

OY 3 OMAGGCSONEYFDSLHACIPCOLRC-SSNTPLTCORCMASVTNS 48
Db 316 QCAPQCEQS-----CQGCVCQQQPPAQCQTACSSCSNS 350

RESULT 15
T31889
hypothetical protein C03A7.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T31889
R:Greco, T.; Bradshaw, H.; Elliott, G.
A:Description: The sequence of C. elegans cosmid C03A7.
A:Reference number: Z21096
A:Accession: T31889
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-438 <GRE>
A:Cross-references: UNIPROT:O16502; UNIPARC:UPI000007AF62; EMBL:AF016451; PIDN:AAB65995.
C:Genetics:
A:Gene: CESP:C03A7.8
A:Map position: 5
A:Introns: 75/3
C:Superfamily: gliadin

Query Match 21.0%; Score 59.5; DB 2; Length 438;
Best Local Similarity 31.9%; Pred. No. 24;
Matches 15; Conservative 4; Mismatches 15; Indels 13; Gaps 2;

OY 3 OMAGGCSONEYFDSLHACIPCOLRC-SSNTPLTCORCMASVTNS 48
Db 366 QCAPQCEQS-----CQGCVCQQQPPAQCQTACSSCSNS 400

RESULT 16
T31898
hypothetical protein C03A7.14 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T31898
R:Greco, T.; Bradshaw, H.; Elliott, G.
A:Description: The sequence of C. elegans cosmid C03A7.
A:Reference number: Z21096
A:Accession: T31898

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-445 <GRE>
A:Cross-references: UNIPROT:O16511; UNIPARC:UPI000007B691; EMBL:AF016451; PIDN:AAB66007.1
A:Experimental source: strain Bristol N2; clone C03A7
C:Genetics:
A:Gene: CESP:C03A7.14
A:Map position: 5
A:Introns: 18/3; 75/3
C:Superfamily: gliadin

Query Match 21.0%; Score 59.5; DB 2; Length 445;
Best Local Similarity 31.9%; Pred. No. 25;
Matches 15; Conservative 4; Mismatches 15; Indels 13; Gaps 2;

OY 3 OMAGGCSONEYFDSLHACIPCOLRC-SSNTPLTCORCMASVTNS 48
Db 373 QCAPQCEQS-----CQGCVCQQQPPAQCQTACSSCSNS 407

RESULT 17
T15577
hypothetical protein C23G10.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 31-Dec-2004
C:Accession: T15577
R:Latreille, P.
A:Description: The sequence of C. elegans cosmid C23G10.
A:Reference number: Z18372
A:Accession: T15577
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-758 <LAT>
A:Cross-references: UNIPROT:Q9GVR5; UNIPARC:UPI000017925B; EMBL:U39851; NID:G1055062; PII
A:Introns: 47/3; 237/3; 293/2; 405/3; 487/1; 577/3; 694/3

Query Match 20.8%; Score 59; DB 2; Length 758;
Best Local Similarity 42.9%; Pred. No. 44;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 15 DSLHACIPCOLRCSSNTPL 35
Db 260 ESVFPLVPAEIRCSADGPEL 280

RESULT 18
A45558
epidermal growth factor receptor homolog precursor - fluke (Schistosoma mansoni)
N:Contains: protein-tyrosine kinase (EC 2.7.1.112)
C:Species: Schistosoma mansoni
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A45558; S27836
R:Shoemaker, C.B.; Ramachandran, H.; Land, A.; dos Reis, M.G.; Stein, L.D.
Mol. Biochem. Parasitol. 53, 17-32, 1992
A>Title: Alternative splicing of the Schistosoma mansoni gene encoding a homologue of epi
A:Reference number: A45558; MUID:92365727; PMID:1501637
A:Accession: A45558
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1717 <SHO>
A:Cross-references: UNIPROT:Q26566; UNIPARC:UPI000007DCD7; EMBL:M86396; NID:G160957; PIDN
A>Note: sequence extracted from NCBI backbone (NCBIP:111129)
C:Genetics:
A:Gene: SBR
C:Superfamily: fluke epidermal growth factor receptor homolog 1; protein kinase homology
C:Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; phosphoprotein;
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-1717/Product: epidermal growth factor receptor homolog 1 #status predicted <MAT>
F:1018-1323/Domain: protein kinase homology <KIN>
F:1026-1034/Region: protein kinase ATP-binding motif

Query Match 20.8%; Score 59; DB 1; Length 1717;
Best Local Similarity 39.1%; Pred. No. 89;
Matches 9; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 7 QCSQNEYPDSLHACIPCOLRCS 29
DB 645 ECPRTYIDPQTRHCLPCNCS 667

RESULT 19
T28675
alpha-51D immobilization antigen - Parametium tetraurelia
C/Species: Parametium tetraurelia
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T28675
R/Schwegmann, K.J.
Submitted to the EMBL Data Library, March 1996
A/Reference number: Z20506
A/Accession: T28675
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-2533 <SCH>
A/Cross-references: UNIPROT:P90589; UNIPARC:UPI0000078A73; EMBL:X96400; PIDN:CAA65264.1
C/Genetics:
A/Gene: alpha-51D
A/Genetic code: SGC5
A/Introns: 280/3; 538/2; 1248/2
C/Superfamily: G surface protein

Query Match 20.7%; Score 58.5; DB 2; Length 2533;
Best Local Similarity 20.7%; Pred. No. 1.4e+02;
Matches 17; Conservative 7; Mismatches 23; Indels 35; Gaps 2;

QY 5 AGCCQNEVF-----DSLHACIPCOLRCSNTPPLTCQR----- 39
DB 1661 AGACTNKKCYDNVTATSDSECSYLSGCVTRGTGCI PNSEPTSYRGTKLQCELFKFTG 1720

QY 40 -----YCNASVTNSVKG 51
DB 1721 LDANKNPIYECSDATNTATG 1742

RESULT 20
T28674
alpha-51D-immobilization antigen - Parametium tetraurelia
C/Species: Parametium tetraurelia
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T28674
R/Schmidt, H.J.
Submitted to the EMBL Data Library, March 1995
A/Reference number: Z20505
A/Accession: T28674
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-2533 <SCH>
A/Cross-references: UNIPROT:Q27183; UNIPARC:UPI000007E3B2; EMBL:X85135; NID:G728634; PID
A/Genetic code: SGC5
A/Note: alpha-51D
C/Superfamily: G surface protein

Query Match 20.7%; Score 58.5; DB 2; Length 2533;
Best Local Similarity 20.7%; Pred. No. 1.4e+02;
Matches 17; Conservative 7; Mismatches 23; Indels 35; Gaps 2;

QY 5 AGCCQNEVF-----DSLHACIPCOLRCSNTPPLTCQR----- 39
DB 1661 AGACTNKKCYDNVTATSDSECSYLSGCVTRGTGCI PNSEPTSYRGTKLQCELFKFTG 1720

QY 40 -----YCNASVTNSVKG 51
DB 1721 LDANKNPIYECSDATNTATG 1742

RESULT 21
S07127
chymotrypsin/elastase inhibitor - common roundworm
C/Species: Ascaris lumbricoideis (common roundworm)
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C/Accession: S07127
R/Babin, D.R.; Peanasky, R.J.; Goos, S.M.
Arch. Biochem. Biophys. 232: 143-161, 1996
A/Title: The isoforms of chymotrypsin/elastase from Ascaris lumbricoideis: the prima
A/Reference number: S07127; MUID:84255715; PMID:6564898
A/Accession: S07127
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-63 <BAB>
A/Cross-references: UNIPARC:UPI000012D146
C/Superfamily: roundworm trypsin inhibitor

Query Match 20.5%; Score 58; DB 2; Length 63;
Best Local Similarity 36.6%; Pred. No. 6.9;
Matches 15; Conservative 5; Mismatches 13; Indels 8; Gaps 4;

QY 8 CSQNEYPDSLHACIPCOLRC--SSNP-PLTCQR--YCNAS 44
DB 5 CGPNEVWTE---CTGCEMKCGPDENTPCPLMCRSPSCCS 41

RESULT 22
T23681
hypothetical protein M02G9.1 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T23681
R/Matthews, L.
Submitted to the EMBL Data Library, November 1996
A/Reference number: Z19781
A/Accession: T23681
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1513 <WIL>
A/Cross-references: UNIPROT:O17970; UNIPARC:UPI0000076B6D; EMBL:Z81573; PIDN:CAB04625.1;
A/Experimental source: clone M02G9
C/Genetics:
A/Gene: CESP:M02G9.1
A/Map position: 2
A/Introns: 23/3; 71/3; 121/3; 183/1; 1083/3; 1141/3; 1408/1; 1449/1

Query Match 20.5%; Score 58; DB 2; Length 1513;
Best Local Similarity 43.8%; Pred. No. 1e+02;
Matches 14; Conservative 3; Mismatches 13; Indels 2; Gaps 2;

QY 15 DSLHAC-IPCOLRC--SSNPPLTCQR--YCNAS 44
DB 141 DSCQNVCONVCGACVSONSPPAVCQYTCROS 172

RESULT 23
S68960
laminin alpha-4 chain precursor - human
N/Alternate names: laminin A4
C/Species: Homo sapiens (man)
C/Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 31-Dec-2004
C/Accession: S68960; S65926; S49149; S40150; I53516
R/Richards, A.; Al-Imara, L.; Pope, F.M.
Eur. J. Biochem. 238: 813-821, 1996
A/Title: The complete cDNA sequence of laminin alpha-4 and its relationship to the other
A/Reference number: S68960; MUID:96300249; PMID:8706685
A/Accession: S68960
A/Molecule type: mRNA
A/Residues: 1-1816 <RIC>
A/Cross-references: UNIPROT:Q16363; UNIPROT:Q14731; UNIPARC:UPI0000016B53; EMBL:X91171; P
A/Experimental source: tissue type heart

Riivaniemi, A.; Sainio, K.; Sariola, H.; Tryggvason, K.
FEBS Lett. 365, 183-188, 1995
A>Title: Primary structure and expression of a novel human laminin alpha-4 chain.
A/Reference number: 153516; MUID:95300971; PMID:7781776
A/Accession: S65926
A/Molecule type: mRNA
A/Residues: 1-142, 'P', 144-177, 'F', 179-490, 'Y', 492-1056, 'P', 1058-1816 <ITV>
A/Cross-references: UNIPARC:UPI000003498C; EMBL:S78569; NID:91042081; PIDN:AA834635.1; F
R:Richards, A.J.; Al-Ismara, L.; Carter, N.; Leverisha, M.; Lloyd, J.C.; Pope, F.M.
Submitted to the EMBL Data Library, December 1993
A/Description: Localisation of the gene (LAMA4) to chromosome 6q21 and isolation of a pa
A/Reference number: S49149
A/Accession: S49149
A/Molecule type: mRNA
A/Residues: 236-1816 <R12>
A/Cross-references: UNIPARC:UPI000016ABEA; EMBL:X76939; NID:9509805; PIDN:CAAS4258.1; PI
R:Richards, A.J.; Al-Ismara, L.; Carter, N.; Lloyd, J.C.; Pope, F.M.
Submitted to the EMBL Data Library, February 1993
A/Description: Isolation of a partial cDNA encoding a protein homologous to laminin A. A
A/Reference number: S40150
A/Accession: S40150
A/Molecule type: mRNA
A/Residues: 1403-1541, 'S', 1543-1816 <R13>
A/Cross-references: UNIPARC:UPI00000709C9; EMBL:X70904; NID:9437804; PIDN:CAAS0261.1; PI
C/Genetics: GDB:LAMA4; LAMA3
A/Map position: 6q21-6q21
A/Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C/Function: Laminins interact with cells and with other basement membrane proteins to promote
A/Description: Laminin G repeat homology; Laminin-type EGF-like homology
C/Keywords: basement membrane; cell binding; coiled coil; extracellular matrix; glycoprotein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-1816/Product: laminin alpha-4 chain #status predicted <MAT>
F:82-129/Domain: laminin-type EGF-like homology <LE1>
F:132-184/Domain: laminin-type EGF-like homology <LE2>
F:187-338/Domain: laminin-type EGF-like homology <LE3>
F:241-265/Domain: laminin-type EGF-like homology #status atypical <LE4>
F:717-719/Region: cell attachment (R-G-D) motif
F:862-1031/Domain: laminin G repeat homology <LG1>
F:1068-1223/Domain: laminin G repeat homology <LG2>
F:1252-1398/Domain: laminin G repeat homology <LG3>
F:1488-1636/Domain: laminin G repeat homology <LG4>
F:1665-1816/Domain: laminin G repeat homology <LG5>
F:104, 215, 308, 458, 524, 550, 571, 574, 631, 639, 735, 751, 754, 780, 803, 1086, 1261, 1359, 1411/Bindin
F:266, 269/Disulfide bonds: interchain #status predicted

Query Match 20.5%; Score 58; DB 1; Length 1816;
Best Local Similarity 21.0%; Pred. No. 1.2e+02;
Matches 13; Conservative 13; Mismatches 20; Indels 16; Gaps 2;
QY 5 AGCGSQNVEYFDSLHACIPQ-----LRGSNPPPLTCQRYCNASTVNSV 49
DB 64 AEKCNMG-FFHTLSGECVPCDCNGNSNECLDSSGVCVHCORNTTGEHCXCLDGYLDT 122

QY 50 KG 51
DB 123 RG 124

RESULT 24
A4434
furin (EC 3.4.21.75) 2 - fruit fly (*Drosophila melanogaster*)
C/Species: *Drosophila melanogaster*
C/Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: A43434
R:Roebroeck, A.J.; Creemers, J.W.; Pauli, I.G.; Kurzik-Dumke, U.; Rentrop, M.; Gateff, E.
J. Biol. Chem. 267, 17208-17215, 1992
A>Title: Cloning and functional expression of Dfurin2, a subtilisin-like proprotein proc
A/Reference number: A44344; MUID:92381036; PMID:1512259
A/Accession: A43434
A/Status: preliminary

A/Molecule type: mRNA
A/Residues: 1-1680 <ROB>
A/Cross-references: UNIPROT:P30432; UNIPARC:UPI000015BC03; GB:M94375; NID:9157461; PID:9
A/Note: sequence extracted from NCBI backbone (NCBIN:111933, NCBI:P.111934)
C/Genetics:
A/Gene: FlyBase:Fur2
A/Cross-references: FlyBase:FBgn0004598
C/Keywords: hydrolase; serine proteinase; transmembrane protein
F:409-652/Domain: subtilisin homology <SBT>
F:418, 457, 638/Active site: Asp, His, Ser #status predicted

Query Match 20.3%; Score 57.5; DB 2; Length 1680;
Best Local Similarity 34.3%; Pred. No. 1.3e+02;
Matches 12; Conservative 5; Mismatches 17; Indels 1; Gaps 1;
QY 8 CSQNEVYFDSLHACIPQRLCS-NTPLTCQRYC 41
DB 1199 CSSEFYSQVEGQCRPCASCSGSCNPADTCTSC 1233

RESULT 25
T20130
hypothetical protein CS0H2.3b - *Caenorhabditis elegans*
C/Species: *Caenorhabditis elegans*
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T20130
R:McMurray, A.
Submitted to the EMBL Data Library, June 1996
A/Reference number: Z19226
A/Accession: T20130
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-502 <MIL>
A/Cross-references: UNIPROT:O17692; UNIPARC:UPI000007CDBF; EMBL:Z73971; PIDN:CAA98256.1;
A/Experimental source: clone CS0H2
C/Genetics:
A/Gene: C50H2.3b
A/Map position: 5
A/Introns: 72/1; 122/1; 152/3; 188/1; 209/1; 255/1; 301/1; 339/1; 424/1

Query Match 20.1%; Score 57; DB 2; Length 502;
Best Local Similarity 34.7%; Pred. No. 52;
Matches 17; Conservative 5; Mismatches 15; Indels 12; Gaps 3;
QY 4 MAGCQSQNVEYFDSLHACIPQ-----RCSSNT-----PPLTCQRYCNA 43
DB 70 MNCQMQQRYF--HASLTERQFWFGGRSDSRNIFDEELTCQWLCES 115

RESULT 26
G96675
hypothetical protein T23K8.9 [imported] - *Arabidopsis thaliana*
C/Species: *Arabidopsis thaliana* (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: G96675
R:Thiel, G.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A/Reference number: A66141; MUID:21016719; PMID:11130712
A/Accession: G96675
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-653 <STO>
A/Cross-references: UNIPROT:Q9S948; UNIPARC:UPI00000AACE7; GB:AE005173; NID:94646199; PI
C/Genetics:
A/Gene: T23K8.9

Proc. Natl. Acad. Sci. U.S.A. 80, 3666-3670, 1983
 A>Title: Homology of amino acid sequences of rat liver cathepsins B and H with that of P.
 A:Reference number: A00976, PMID:83221657, PMID:6574504
 A:Accession: A00977

A:Molecule type: protein
 A:Residues: 80-126,129-158, 'G',160-333 <TAK>
 A:Cross-references: UNIPARC:UPI0000172C7A
 R:San Segundo, B.; Chan, S.-J.; Steiner, D.F.
 Proc. Natl. Acad. Sci. U.S.A. 82, 2320-2324, 1985
 A>Title: Identification of cDNA clones encoding a precursor of rat liver cathepsin B.
 A:Reference number: 159019, PMID:85190489, PMID:2986112
 A:Accession: 159019
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 69-339 <RES>
 A:Cross-references: UNIPARC:UPI00001708F9; GB:M11305; NID:g203647; PIDN:AAA40993.1; PID:
 C:Function: broad specificity endopeptidase and peptidyl dipeptidase
 A:Pathway: intracellular protein degradation
 C:Superfamily: papain
 C:Keywords: cysteine proteinase; glycoprotein; hydrolase; lysosome; protein degradation
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:18-79/Domain: propeptide #status predicted <PRO>
 F:80-126/Domain: light chain #status experimental <CHL>
 F:80-126,129-333/Product: cathepsin B #status experimental <MAT>
 F:129-333/Domain: heavy chain #status experimental <CHH>
 F:129-122,105-150,141-207,142-146,179-211,187-198/Disulfide bonds: #status predicted
 F:108-276,298/Active site: Cys, His, Asn #status predicted
 F:192/Binding site: carboxylate (Asn) (covalent) #status experimental

Query Match 19.6%; Score 55.5; DB 1; Length 339;
 Best Local Similarity 25.5%; Pred. No. 55;
 Matches 12; Conservative 7; Mismatches 21; Indels 7; Gaps 1;

QY 11 NEYFDSLHACIPCOLRCSSNTPPLT-----CORYCNASTVNSVK 50
 Db 174 NSHIGCLPYTIPCEHHVNGSRPCTGEGDTPKCNKCEAGYSTSYK 220

RESULT 32
 B89588
 Protein R09F10.7 [imported] - Caenorhabditis elegans
 N:Alternate names: protein R09F10.2
 C:Species: Caenorhabditis elegans
 C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C:Accession: B89588, C89588
 R:anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A>Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
 A:Reference number: A75000; PMID:99069613; PMID:9851916
 A>Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
 A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
 A:Accession: B89588
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-378 <STO>
 A:Cross-references: UNIPROT:Q27383; UNIPARC:UPI0000083585; GB:chr_X; PIDN:AAC69096.1; PI
 A>Note: glutamine-rich protein
 A:Accession: C89588
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-378 <ST2>
 A:Cross-references: UNIPARC:UPI0000083585; GB:chr_X; PIDN:AAC69090.1; PID:g1465856; GSPD
 C:Genetics: glutamine-rich protein
 A:Gene: R09F10.7, R09F10.2
 A:Map position: X
 C:Superfamily: gliadin

Query Match 19.6%; Score 55.5; DB 2; Length 378;
 Best Local Similarity 29.8%; Pred. No. 61;
 Matches 14; Conservative 6; Mismatches 14; Indels 13; Gaps 2;

QY 3 QWAGCCSQNEYPDSLHACIPCOLRCSSNTPPLT-CORYCNASTVNS 48
 Db 306 QCAPQCEQS-----CQQCCVQQCCVQACQCSQSCSS 340

RESULT 33
 T05754
 S-receptor kinase (EC 2.7.1.1-) M4122.110 precursor - Arabidopsis thaliana
 N:Alternate names: protein M4122.110
 C:Species: Arabidopsis thaliana (mouse-ear cross)
 C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 31-Dec-2004
 C:Accession: T05754
 R:Bevan, M.; Reichert, B.J.; Barel, E.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X.; Schuel
 submitted to the Protein Sequence Database, June 1998
 A:Reference number: Z15450
 A:Accession: T05754
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-815 <BEV>
 A:Cross-references: UNIPROT:O81833; UNIPARC:UPI00000489FA; EMBL:AL030978
 A:Experimental source: cultivar Columbia; BAC clone M4122
 C:Genetics:
 A:Map position: 4
 A:introns: 471/1; 516/3; 587/1; 666/2; 716/3
 A>Note: M4122.110
 C:Function:
 A:Description: involved in preventing fertilization between plants having the same S-loc
 C:Superfamily: S-locus receptor-like kinase SRK; protein kinase homology: S-locus-specifi
 C:Keywords: ATP; glycoprotein; magnesium; phosphotransferase; receptor; serine/threonine-
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-815/Product: S-receptor kinase #status predicted <MAT>
 F:33-431/Domain: S-locus-specific glycoprotein homology <SSG>
 F:442-461/Domain: transmembrane #status predicted <TM>
 F:498-778/Domain: protein kinase homology <KIN>
 F:506-514/Region: protein kinase ATP-binding motif
 F:53,249,265,385/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:528,644,625,627/Active site: Lys, Glu, Asp, Lys #status predicted
 F:630,634/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 19.6%; Score 55.5; DB 1; Length 815;
 Best Local Similarity 35.7%; Pred. No. 12e+02;
 Matches 10; Conservative 5; Mismatches 10; Indels 3; Gaps 1;

QY 24 COLRCSSNTPPLTCORYCNASTVNSVK 51
 Db 378 CKIKCSSN---CSCRAVANTDIREGKG 402

RESULT 34
 T01519
 hypothetical protein T10M13.17.1 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cross)
 C>Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
 C:Accession: T01519
 R:Johnson, A.F.; de la Baetide, M.; Lodhi, M.; Hoffman, J.; Hasegawa, A.; Gnoj, L.; Gorte
 submitted to the EMBL Data Library, May 1997
 A:Description: The sequence of the Arabidopsis thaliana T10M13 BAC.
 A:Reference number: Z14346
 A:Accession: T01519
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-989 <JOH>
 A:Cross-references: UNIPROT:O9ZU00; UNIPARC:UPI00000A0E3D; EMBL:AF001308; NID:g2104523; I
 A:Experimental source: cultivar Columbia
 C:Genetics:
 A:Map position: 4S
 A:introns: 31/3
 A>Note: T10M13.17.1

Query Match 19.6%; Score 55.5; DB 2; Length 989;
 Best Local Similarity 41.9%; Pred. No. 14e+02;
 Matches 13; Conservative 3; Mismatches 10; Indels 5; Gaps 2;

QY 8 CSQNEYPDSLHACIPIC---QLRCSNTP 34
 Db 540 CARN-IDBRLFHGSCPCNFTLDRCLVNP 569

RESULT 35
 723682
 hypochelical protein M0269.3 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C/Accession: 723682

A/Reference number: 219781
 A/Accession: 723682

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-294 <MTL>
 A/Cross-references: UNIPROT:Q9XUS0; UNIPARC:UPI0000076A9F; EMBL:281573; PIDD:CAA04626.1;

A/Experimental source: clone M0269

C/Genetics:

A/Map position: 2
 A/Introns: 20/3; 76/2; 182/3; 223/3

Query Match 19.4%; Score 55; DB 2; Length 294;
 Best Local Similarity 37.3%; Pred. No. 56;
 Matches 22; Conservative 3; Mismatches 20; Indels 14; Gaps 5;

QY 3 QMAGCCSQ--NEYFSLHACIPCOLRCS--NTPEL--TCOR-----YCNA--SVTN 47
 Db 72 QCSNOCNOQCTSIITSSGPFSSCOSACSSACTPTCIRTCCORNCNMLCNGNSNCTN 130

RESULT 36

KHMSB
 cathepsin B (EC 3.4.22.1) precursor - mouse

N/Alternate names: preprocathepsin B
 C/Species: Mus musculus (house mouse)

C/Date: 31-Mar-1992 #sequence_revision 26-Apr-1996 #text_change 09-Jul-2004

C/Accession: A38458; A49826; B26498; S12901; PS0360

R/Qian, F.; Frankfurter, A.; Chan, S.-J.; Steiner, D.F.

A/Title: The structure of the mouse cathepsin B gene and its putative promoter.

A/Reference number: A38458; MUID:91190267; PMID:2012677

A/Accession: A38458

A/Molecule type: DNA

A/Residues: 1-339 <QIA>
 A/Cross-references: UNIPROT:P10605; UNIPARC:UPI0000018A4; GB:W63999

R/Qian, F.; Frankfurter, A.; Steiner, D.F.; Bajkowski, A.S.; Chan, S.J.

A/Title: Characterization of multiple cathepsin B mRNAs in murine B16 melanoma.

A/Reference number: A49826; MUID:92082172; PMID:1746502

A/Accession: A49826

A/Molecule type: mRNA

A/Residues: 1-339 <QI2>
 A/Cross-references: UNIPARC:UPI0000018A4; GB:S69034; NID:9239906; PIDD:AA820536.1; PII

A/Experimental source: B16 melanoma

A/Note: sequence extracted from NCBI backbone (NCBI:69034, NCBI:69039)

R/Chan, S.-J.; San Segundo, B.; McCormick, M.B.; Steiner, D.F.

A/Title: Nucleotide and predicted amino acid sequences of cloned human and mouse prepro

A/Reference number: A26498; MUID:87017021; PMID:3463996

A/Accession: B26498

A/Molecule type: mRNA

A/Residues: 1-159, 'N', 161-173, 'D', 175-176, 'I', 178-283, 'V', 285-339 <CHA>
 A/Cross-references: UNIPARC:UPI000016CCE0; GB:M14222; NID:9192841; PIDD:AAA37494.1; PII:

R/Ferrara, M.; Wojcik, F.; Rhaissi, H.; Mordier, S.; Roux, M.P.; Bechet, D.

A/Title: Gene structure of mouse cathepsin B.

A/Reference number: S12901; MUID:91032179; PMID:2226854

A/Accession: S12901

A/Molecule type: DNA

A/Residues: 1-159, 'N', 161-173, 'D', 175-176, 'I', 178-283, 'V', 285-339 <FER>

A/Cross-references: UNIPARC:UPI000016CCE0

R/Fieremert, C.; Closs, E.I.; Silbermann, M.; Erle, V.; Strauss, P.G.

A/Title: Isolation of a cathepsin B-encoding cDNA from murine osteogenic cells.

A/Reference number: P60360; MUID:91365255; PMID:1889751

A/Accession: P60360

A/Status: translation not shown

A/Molecule type: mRNA

A/Residues: 314-339 <FRI>

A/Cross-references: UNIPARC:UPI000016CCE1; EMBL:X54966; NID:950596; PIDD:CAA8713.1; PII:

C/Genetics:

A/Note: single copy gene

C/Function:

A/Description: broad specificity endopeptidase and peptidyl dipeptidase

A/Pathway: intracellular protein degradation

C/Superfamily: papain

C/Keywords: cysteine proteinase; glycoprotein; hydrolase; lysosome; protein degradation

F.1-17/Domain: signal sequence #status predicted <SIG>

F.80-339/Product: cathepsin B #status predicted <MAT>

F.38,192/Binding site: carboxylate (asn) (covalent) #status predicted

F.93-122,105-150,141-207,142-146,179-211,187-198/Disulfide bonds: #status predicted

F.108,278,298/Active site: Cys, His, Asn #status predicted

Query Match 19.4%; Score 55; DB 1; Length 339;
 Best Local Similarity 25.0%; Pred. No. 63;
 Matches 16; Conservative 7; Mismatches 17; Indels 24; Gaps 2;

QY 11 NEYFSLHACIPCOLRCSNTPPLT-----CORYNA-----SVT 46
 Db 174 NSHVGCLPYTTPCEHHVNGSRPCTGSDTPRCNKSCEAGYSBPKEDKHFGYTSYSVS 233

QY 47 NSVK 50
 Db 234 NSVK 237

RESULT 37
 S46625
 finger protein YJL206C - yeast (Saccharomyces cerevisiae)

N/Alternate names: probable membrane protein YJL206C; protein J0316

C/Species: Saccharomyces cerevisiae

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Oct-2004

C/Accession: S46625; S56993

R/Pumelle, B.; Coster, F.; Goffeau, A.

A/Title: The sequence of a 36 kb segment on the left arm of yeast chromosome X identifies

ae gene ACO1 and two homologues to chromosome III genes.

A/Reference number: S46621; MUID:95274326; PMID:7754713

A/Accession: S46625

A/Molecule type: DNA

A/Status: nucleic acid sequence not shown

A/Residues: 1-758 <PUN>

A/Cross-references: UNIPROT:P39529; UNIPARC:UPI000013B60A; EMBL:X77688; NID:91183992; PII

R/Pumelle, B.; Coster, F.; Goffeau, A.

A/Title: submitted to the Protein Sequence Database, September 1995

A/Reference number: S56977

A/Accession: S56993

A/Molecule type: DNA

A/Residues: 1-758 <PUN>

A/Cross-references: UNIPARC:UPI000013B60A; EMBL:Z49481; NID:91015584; PIDD:CAA89502.1; PII

A/Title: F42-18/Domain: GAL4 zinc binuclear cluster homology <GAL4>

C/Keywords: DNA binding; nucleus; transcription regulation; transmembrane protein; zinc

Query Match 19.4%; Score 55; DB 2; Length 758;
 Best Local Similarity 43.8%; Pred. No. 1.3e+02;
 Matches 14; Conservative 2; Mismatches 6; Indels 10; Gaps 2;

QY 20 ACIPC---QIRCSNTPPLTCQRYCNASVTNS 48
DB 46 ACIACRKRKVRCSGNIPCRLCQ-----TNS 70

RESULT 38
T27283
hypothetical protein Y64G10A.f - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T27283
R/Inscough, R.
submitted to the EMBL Data Library, September 1999
A/Reference number: Z20336
A/Accession: T27283
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1620 <MIL>
A/Cross-references: UNIPARC:UPI000017BCB4; EMBL:AL10498; NID:e1542303; PIDN:CA854471.1;
A/Experimental source: clone Y64G10A
C/Genetics:
A/Gene: CESP:Y64G10A.f
A/Intons: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 625/1; 7

Query Match 19.4%; Score 55; DB 2; Length 1620;
Best Local Similarity 25.6%; Pred. No. 2.4e+02;
Matches 11; Conservative 7; Mismatches 17; Indels 8; Gaps 1;

QY 8 CSONEYFDSLHACI-----PCQLRCSNTPPLTCQRYCN 42
DB 1409 CENGVCDSSTGSCVCPGYIGTKCEIACQSDRFPTCEKCN 1451

RESULT 39
T27303
hypothetical protein Y68A4A.10 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T27303
R/Steward, C.
submitted to the EMBL Data Library, January 1998
A/Reference number: Z20340
A/Accession: T27303
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-392 <MIL>
A/Cross-references: UNIPROT:Q9XXP6; UNIPARC:UPI000007BED1; EMBL:AL021503; PIDN:CA16424.
A/Experimental source: clone Y68A4A
C/Genetics:
A/Gene: CESP:Y68A4A.10
A/Map position: 5
A/Intons: 45/2; 74/3; 139/3; 175/2; 190/3; 241/3; 305/3; 356/3

Query Match 19.3%; Score 54.5; DB 2; Length 392;
Best Local Similarity 40.0%; Pred. No. 81;
Matches 10; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

QY 20 ACIPCOLRCSNTPPLTCQRYCNAS 44
DB 189 SCLPCO-TCASFTDPMSEKATCTAT 212

RESULT 40
S69207
vascular endothelial growth factor C precursor - human
N/Alternate names: FLT4 ligand DHM
C/Species: Homo sapiens (man)
C/Date: 27-Apr-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C/Accession: S69207; S61795; S71443; S69208; G02659
R/Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksela, EMO J. 15, 1751, 1996
A/Title: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is a ligand for
A/Reference number: S69207; MUID:96203094; PMID:8612600

A/Accession: S69207
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-419 <JOU>
A/Cross-references: UNIPROT:P49767; UNIPARC:UPI0000001C2A; EMBL:X94216; NID:g1177488; PII
A/Note: the nucleotide sequence was submitted to the EMBL data library, December 1995
A/Note: only a part of the translation is shown
R/Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksela, C
EMO J. 15, 290-298, 1996
A/Title: A novel vascular endothelial growth factor, VEGF-C, is a ligand for the FLT4 (V
A/Reference number: S61795; MUID:96178224; PMID:8617204
A/Accession: S61795
A/Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 70-419 <JOU1>
A/Cross-references: UNIPARC:UPI0000150795
A/Note: this sequence has been revised in reference S69207
A/Accession: S71443
A/Molecule type: protein
A/Residues: 'X', 104-120 <JOU2>
A/Cross-references: UNIPARC:UPI000014E2AF
R/lee, J.; Gray, A.; Yuan, J.; Luch, S.M.; Avraham, H.; Wood, W.I.
submitted to the EMBL Data Library, December 1995
A/Description: Vascular endothelial growth factor related protein (VRP): A ligand and spe
A/Reference number: S69208
A/Accession: S69208
A/Molecule type: mRNA
A/Residues: 1-419 <LEF>
A/Cross-references: UNIPARC:UPI000001C2A; EMBL:U43142; NID:g1150988; PIDN:AA85214.1; P
R/Morris, J.C.
submitted to the EMBL Data Library, May 1996
A/Reference number: H01557
A/Accession: G02659
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-419 <MOR>
A/Cross-references: UNIPARC:UPI000001C2A; EMBL:U58111; NID:g1373426; PIDN:AAB02909.1; P
C/Genetics:
A/Gene: GDB:VEGFC; VRP
A/Cross-references: GDB:3890883; OMIM:601528
F/1-12/Domain: signal sequence #status predicted <SIG>
F/13-102/Domain: propeptide #status predicted <PRO>
F/103-419/Product: vascular endothelial growth factor C #status experimental <MAT>

Query Match 19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 86;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSONEYFDSLHACIPCOLRCSNTP--PLTCQRYCNAS 44
DB 327 QCGANREFDENCCQCV-CRRTCPRNQPLNPKACACCTES 365

RESULT 41
JC5486
membrane glycoprotein CD30 homolog precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
C/Accession: JC5486
R/Aizawa, S.; Satoh, H.; Horie, R.; Ito, K.; Choi, S.H.; Takeuchi, H.; Watanabe, T.
Gene 182, 155-162, 1996
A/Title: Cloning and characterization of a cDNA for rat CD30 homolog and chromosomal ass
A/Reference number: JC5486; MUID:97136705; PMID:8982082
A/Contents: T cell
A/Accession: JC5486
A/Molecule type: mRNA
A/Residues: 1-493 <ALIZ>
A/Cross-references: UNIPROT:P97525; UNIPARC:UPI000003170F0; DBJ:D42117; NID:g1817523; PII
C/superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolog
F/1-16/Domain: signal sequence #status predicted <SIG>
F/19-93/Product: membrane glycoprotein CD30 homolog #status predicted <MAT>
F/278-304/Domain: transmembrane #status predicted <TM>

A:Molecule type: DNA
A:Residues: 1-915 <WIL>
A:Cross-references: UNIPROT:002364; UNIPARC:UPI000002A1C9; EMBL:Z81527; P1DN:CAB04280.1;
A:Experimental source: clone F35E12
R:Steward, C.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19870
A:Accession: T24297
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-915 <W12>
A:Cross-references: UNIPARC:UPI000002A1C9; EMBL:Z81110; P1DN:CAB03263.1; GSPDB:GN00023;
A:Experimental source: clone T01D3
C:Genetics:
A:Gene: CESP:T01D3.6b
A:Map position: 5
A:introns: 38/2; 87/3; 128/2; 242/2; 374/3; 404/3; 722/3; 830/3; 845/1

Query Match 18.9%; Score 53.5; DB 2; Length 915;
Best Local Similarity 26.0%; Pred. No. 2.2e+02;
Matches 13; Conservative 4; Mismatches 20; Indels 13; Gaps 1;

Qy 5 AGCCSNEYFDSLHACIP-----COLRCSSNTPPLTCORIC 41
Db 453 AERKTEFTYFLQYCOLALPQVANNQWRAQINCPLACPLNHPSTCTSSC 502

RESULT 57
T21772
hypothetical protein T01D3.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T21772; T24296
R:Steward, C.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19470
A:Accession: T21772
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-927 <WIL>
A:Cross-references: UNIPROT:002364; UNIPARC:UPI0000086677; EMBL:Z81527; P1DN:CAB04279.1;
A:Experimental source: clone F35E12
R:Steward, C.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19870
A:Accession: T24296
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-927 <W12>
A:Cross-references: UNIPARC:UPI0000086677; EMBL:Z81110; P1DN:CAB03262.1; GSPDB:GN00023;
A:Experimental source: clone T01D3
C:Genetics:
A:Gene: CESP:T01D3.6
A:Map position: 5
A:introns: 38/2; 87/3; 128/2; 242/2; 374/3; 416/3; 734/3; 842/3; 857/1

Query Match 18.9%; Score 53.5; DB 2; Length 927;
Best Local Similarity 26.0%; Pred. No. 2.2e+02;
Matches 13; Conservative 4; Mismatches 20; Indels 13; Gaps 1;

Qy 5 AGCCSNEYFDSLHACIP-----COLRCSSNTPPLTCORIC 41
Db 465 AFKCTFTYFLQYCOLALPQVANNQWRAQINCPLACPLNHPSTCTSSC 514

RESULT 58
T15881
hypothetical protein D1044.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T15881
R:Pauley, A.
submitted to the EMBL Data Library, June 1994

A:Description: The sequence of C. elegans cosmid D1044.
A:Reference number: Z18423
A:Accession: T15881
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1895 <PAU>
A:Cross-references: UNIPARC:UPI000004CAE8; EMBL:U00065; NID:g495661; P1D:g495684; P1DN:A
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:D1044.3
A:introns: 35/2; 63/2; 150/1; 191/3; 207/2; 405/3; 551/3; 629/1; 764/1; 933/1; 959/2; 103

Query Match 18.9%; Score 53.5; DB 2; Length 1895;
Best Local Similarity 26.5%; Pred. No. 4e+02;
Matches 13; Conservative 12; Mismatches 17; Indels 7; Gaps 3;

Qy 6 GQCSQNE-YFDSLHACIP-----COL-RCSSNTPPLTCORICNMSVTN 47
Db 1465 GQCSNQVYNNQYNTVPISGQCQITQCLGNSQCMNSFCQCPSTTN 1513

RESULT 59
T39411
RNA helicase - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T39411
R:Lyne, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Badcock, K.; Churcher, C.M.
submitted to the EMBL Data Library, April 1998
A:Reference number: Z21852
A:Accession: T39411
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1935 <LYN>
A:Cross-references: UNIPROT:060072; UNIPARC:UPI000013A2C9; EMBL:AL022600; P1DN:CA118663.1;
A:Experimental source: strain 972h-; cosmid c13G1
C:Genetics:
A:Gene: SPDB:SPBC13G1.10C
A:Map position: 2

Query Match 18.9%; Score 53.5; DB 2; Length 1935;
Best Local Similarity 37.2%; Pred. No. 4.1e+02;
Matches 16; Conservative 7; Mismatches 9; Indels 11; Gaps 3;

Qy 1 MLCQMGQCS-----QNEY--FDSLHACIPCOLRCSS-SNT 32
Db 820 ITALLSQCSFQIKSRNHRHRELSMNSRQCLRDSISNT 862

RESULT 60
C89046
protein C10G8.4 (imported) - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: C89046
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_eleg
A:Accession: C89046
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <STO>
A:Cross-references: UNIPROT:Q94162; UNIPARC:UPI000007C506; GB:chr_V; P1DN:AB09171.1; P1I
C:Genetics:
A:Gene: C10G8.4
A:Map position: 5

Query Match 18.7%; Score 53; DB 2; Length 98;
Best Local Similarity 34.8%; Pred. No. 37;
Matches 16; Conservative 3; Mismatches 21; Indels 6; Gaps 2;

[illegible]

DB 194 QMSGNGILITVYAHDDKKFKSLVSCMNPNTLSIFLDAPTLECYXYDCAKTIINV 246

RESULT 63
GQHTU1

tumor necrosis factor receptor 1 precursor [validated] - human
N.Alternate names: p55 tumor necrosis factor receptor; TNF receptor type 1
N.Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein
C.Species: Homo sapiens (man)
C.Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 09-Jul-2004
C.Accession: A38208, A34899, A34900, A36555, G36555, A38281, S12057, J10758, A60231, A38-
R.Fuchs, P.J. Strehl, S.J. Dvorzak, M., Himmeler, A./ Ambros, P.F.
Genomics 13, 219-224, 1992
A.Title: Structure of the human TNF receptor 1 (p60) gene (TNFRF1) and localization to chr
A.Reference number: A38208; MUID:92250049; PMID:1315717
A.Accession: A38208

A.Molecule type: DNA
A.Residues: 1-455 <FUC>
A.Cross-references: UNIPROT:P19438; UNIPARC:UPI000002CE11; GB:M75864; GB:M75865; GB:M7586
R.Iloetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lesslauer
Cell 61, 351-359, 1990
A.Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor recep
A.Reference number: A34899; MUID:90235284; PMID:2158662
A.Accession: A34899

A.Molecule type: mRNA
A.Residues: 1-455 <LOE>
A.Cross-references: UNIPARC:UPI000002CE11; GB:M58286; GB:M33480; NID:g339753; PIDN:AAA36
A.Experimental source: placenta
A.Note: part of this sequence, including the amino end of the mature protein, confirmed b
R.Schnall, T.U.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanga, T.; C
Cell 61, 361-370, 1990
A>Title: Molecular cloning and expression of a receptor for human tumor necrosis factor.
A.Reference number: A34900; MUID:90235285; PMID:2158653
A.Accession: A34900

A.Molecule type: mRNA
A.Residues: 1-455 <SCH>
A.Cross-references: UNIPARC:UPI000002CE11; GB:M33294; NID:g339744; PIDN:AAAO3210.1; PID:g
R.Himmeler, A.; Maurer-Fogy, I.; Kroenke, M.; Schmeutlich, F.; Pfizenmaier, K.; Lantz, M.; C
DNA Cell Biol. 9, 705-715, 1990
A>Title: Molecular cloning and expression of human and rat tumor necrosis factor recepto
A.Reference number: A36555; MUID:91090841; PMID:1702293
A.Accession: A36555

A.Molecule type: mRNA
A.Residues: 1-455 <HIM>
A.Cross-references: UNIPARC:UPI000002CE11; GB:M63121; NID:g339755; PIDN:AAA36754.1; PID:g
A.Accession: C36555

A.Molecule type: Protein
A.Residues: 30-38,41-53,'X','55-79,'XX','82-94,'NK','XX','100-104,107-128,162-167,'X',169-20
A.Cross-references: UNIPARC:UPI000002D38; UNIPARC:UPI000002D836; UNIPARC:UPI0001736DE;
A>Note: The purified protein, called tumor necrosis factor binding protein, is a soluble
Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990
R.Gray, P.W.; Barrett, K.; Chanly, D.; Turner, M.; Feldmann, M.
A>Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of rec
A.Reference number: A38281; MUID:91017509; PMID:2170974
A.Accession: A38281

A.Molecule type: mRNA
A.Residues: 1-455 <GRA>
A.Cross-references: UNIPARC:UPI000002CE11; GB:M37764
A>Note: The authors translated the codon TAG for residue 371 as Thr. AAG for residue 372 as
R.Nophar, Y.; Kempner, O.; Brakelbusch, C.; Engelmann, H.; Zwang, R.; Adierka, D.; Holtmann,
EMBO J. 9, 3269-3278, 1990
A>Title: Soluble forms of tumor necrosis factor receptors (TNF-Ss). The cDNA for the type
le form of the receptor.
A.Reference number: S12057; MUID:91006021; PMID:1598610
A.Accession: S12057

A.Molecule type: mRNA
A.Residues: 1-455 <NOP>
A.Cross-references: UNIPARC:UPI000002CE11; EMBL:X55313; NID:g37223; PIDN:CMA39021.1; PID:
A>Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, we
R.Kempner, O.; Wallach, D.
Gene 134, 209-216, 1993

A>Title: Cloning and partial characterization of the promoter for the human p55 tumor necr
A.Reference number: J10758; MUID:94085779; PMID:8262379

A:Accession: J070758
A:Molecule type: DNA
A:Residues: 1-13 <KEM>
A:Cross-references: UNIPARC:UPI0000155CFB
R:Secklinger, P.; Vey, E.; Turcatti, G.; Wangfield, P.; Dayer, J.M.
Eur. J. Immunol. 20, 1167-1174, 1990
A:Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequence
A:Reference number: A60231; MUID:90292116; PMID:2113477
A:Accession: A60231
A:Molecule type: protein
A:Residues: 41-43, 'X', 45-53, 'X', 55-57 <SEC>
A:Cross-references: UNIPARC:UPI0000072FDB
R:Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucchi III, J.A.; Jeffes, E.W.B.; Le
Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
A:Title: Purification and characterization of an inhibitor (soluble tumor necrosis factor
inhibitor).
A:Reference number: A38258; MUID:91062364; PMID:2174164
A:Accession: A38258
A:Molecule type: protein
A:Residues: 41-60 <GAT>
A:Cross-references: UNIPARC:UPI00001736E1
A:Experimental source: cancer patient serum
R:Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thyseil, H.; Grubb, A.; Adolf, G.
Eur. J. Haematol. 42, 270-275, 1989
A:Title: Isolation and characterization of a tumor necrosis factor binding protein from
A:Reference number: A60594; MUID:89171156; PMID:2924890
A:Accession: A60594
A:Molecule type: protein
A:Residues: 41-43, 'X', 45-53, 'V', 55-57, 'XK', 60 <OLS>
A:Cross-references: UNIPARC:UPI00001736E2
A:Experimental source: renal failure patient urine
R:Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A:Reference number: A35010; MUID:90110215; PMID:215136
A:Accession: A35010
A:Molecule type: protein
A:Residues: 41-45 <ENG>
A:Cross-references: UNIPARC:UPI00001736E3
A:Experimental source: normal urine
R:Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
Biotechnol. Biochem. 58, 2266-2269, 1994
A:Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified from
A:Reference number: J02404; MUID:95128033; PMID:7765720
A:Accession: J02404
A:Molecule type: protein
A:Residues: 41-53, 'X', 55-144, 'X', 146-150, 'X', 152-186, 'X', 188-201 <KAJ>
A:Cross-references: UNIPARC:UPI00001736E4
A:Experimental source: urine
A:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
C:Genetics:
A:Gene: GDB:TNFR1
A:Cross-references: GDB:125913; OMIM:191190
A:Map position: 12P13.2-12P13.2
A:Intons: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolo
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-45/Domain: tumor necrosis factor receptor 1 #status predicted <MAT>
F:30-21/Domain: extracellular #status predicted <EXT>
F:41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status
F:44-82/Domain: NGF receptor repeat homology <NG1>
F:84-126/Domain: NGF receptor repeat homology <NG2>
F:127-157/Domain: NGF receptor repeat homology <NG3>
F:166-196/Domain: NGF receptor repeat homology <NG4>
F:212-234/Domain: transmembrane #status predicted <MEM>
F:235-455/Domain: intracellular #status predicted <INT>
F:54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Oy 8 CSONE---YFPSLHACIPCOLRCSNTPPLTCQRYCNASVT 46
 |::||:||||:|:
Dn 127 CRKQYRHYSSENIFFCFCNCST-CLANGTVHLSCDCKKNVTVT 167

RESULT 64

JCI1480
protein kinase C (EC 2.7.1.1-) zeta - mouse
C:Species: Mus musculus (house mouse)
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-Oct-2004
A:Accession: JCI1480
R:Goodnight, J.; Kazanietz, M.G.; Blumberg, P.M.; Mushinski, J.F.; Mischnak, H.
Gene 122, 305-311, 1992
A>Title: The cDNA sequence, expression pattern and protein characteristics of mouse protei
A:Reference number: JCI1480; MUID:93138400; PMID:1487145
A:Accession: JCI1480
A:Molecule type: mRNA
A:Residues: 1-592 <GOO>
A:Cross-references: UNIPROT:Q02956; UNIPARC:UIP0000029ADD; GB:M94632; NID:g200498; PIDN:f
A:Experimental source: brain
C:Superfamily: protein kinase C, zeta/iota types; protein kinase C zinc-binding repeat h
C:Keywords: ATP; photobol ester binding; phosphotransferase; serine/threonine-specific ptc
F:i11-180/domain: protein kinase C zinc-binding repeat homology <KI>
F:250-518/domain: protein kinase homology <KIN>
F:258-266/Region: protein kinase ATP-binding motif
F:281/Active site: Lys #status predicted

Query Match
Best Local Similarity 18.7%; Score 53; DB 1; Length 592;
Matches 15; Conservative 8; Mismatches 14; Indels 6; Gaps 3;

Oy 6 GGCGSNEY-FDSLHACIPCQL----RCSSNTPLTCCORYCA 43
 |::|:~::~:|:~:|
Dn 145 GGCGSERIWGLSRGGYRCINCRLVKRKCHV-LVPYLTCRRHMDS 186
 |::|:~::~:|:~:|

RESULT 65

F88188
proteIn ClB9.7 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: F88188
R:Anonymous. The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A>Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; MUID:99069613; PMID:9851916
A>Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: F88188
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-596 <STO>
A:Cross-references: UNIPROT:Q09485; UNIPARC:UIP00000816F3; GB:chr_II; PID:g722386; GSDB:
A:Genetics: C
A:Map position: 2

Query Match
Best Local Similarity 18.7%; Score 53; DB 2; Length 596;
Matches 11; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

Oy 8 CSONEYFDLSLHACIPCQLRCSNTPPLTCORYN 42
 |::|:~::~:|:~:|
Dn 54 CDGCFEGMLSYALSQMOLATPDNDNSAKKEAFIN 88
 |::|:~::~:|:~:|

RESULT 66

TJ30136
hypothetical protein CI4Cl1.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: TJ30136
:/DN, Z.: Gattung, S.

submitted to the EMBL Data Library, March 1996
 A:Description: The sequence of C. elegans cosmid C14C11.
 A:Reference number: Z20742
 A:Accession: T30135
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-654 <DU2>
 A:Cross-references: UNIPROT:Q17982; UNIPARC:UPI000017B77E; EMBL:U53141; PIDN:AAA96110.1;
 A:Experimental source: strain Bristol N2; clone C14C11
 C:Genetics:
 A:Gene: CEP-14C11.8
 A:Map position: 5
 A:introns: 50/3; 98/3; 155/3; 182/3; 229/3; 318/3; 365/3; 522/3; 543/3; 586/3

Query Match 18.7%; Score 53; DB 2; Length 654;
 Best Local Similarity 37.1%; Pred. No. 1.9e+02;
 Matches 13; Conservative 5; Mismatches 15; Indels 2; Gaps 2;

Qy 15 DSLHACIP-CQLRCSSNTPPLT-CQRYCNASVTN 47
 Db 532 NNCVQACQPCQCOQCQSVNQCVCQSCQSCGN 566

RESULT 67
 VCLJ54
 env polyprotein precursor - human immunodeficiency virus type 2 (isolate ST/24.1C/2)
 N:Alternate names: coat polyprotein
 N:Contains: surface glycoprotein gp120; transmembrane glycoprotein gp41
 C:Species: human immunodeficiency virus type 2, HIV-2
 A>Note: host Homo sapiens (man)
 C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
 C:Accession: M42535
 R:Multigene, M.U.: Yamshchikov, G.V.; Rlter Jr., G.D.; Gao, F.; Jin, M.U.; Nail, C.D.; S
 J. Vitol. 66, 3971-3975, 1992
 A:Title: Cytoplasmic domain truncation enhances fusion activity by the exterior glycopro
 A:Reference number: M42535; MUID:92260681; PMID:1583738
 A:Accession: A42535
 A:Molecule type: DNA
 A:Residues: 1-712 <MU2>
 A:Cross-references: UNIPROT:P32536; UNIPARC:UPI000012A033; GB:M86924; NID:g325760; PIDN:
 C:Genetics:
 A:Gene: env
 C:Superfamily: type E retrovirus env polyprotein
 C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-712/Product: env polyprotein #status predicted <ENV>
 F:20-501/Product: surface glycoprotein gp120 #status predicted <SGG>
 F:506-712/Product: transmembrane glycoprotein gp41 #status predicted <TPG>
 F:507-523/Region: hydrophobic
 F:675-694/Domain: transmembrane #status predicted <TMN>
 F:36,69,78,113,137,145,160,173,200,232,235,242,266,272,283,294,304,359,392,402,4

Query Match 18.7%; Score 53; DB 1; Length 712;
 Best Local Similarity 29.3%; Pred. No. 2e+02;
 Matches 12; Conservative 7; Mismatches 12; Indels 10; Gaps 1;

Qy 19 HACIPOLRCSSNT-----PPLTCQRYCNASVTNSV 49
 Db 409 HNYVPCHIKQIINTMHKVGKNVYLPFRREGQLTNCSTVTSTII 449

RESULT 68
 VCLJ57
 env polyprotein precursor - human immunodeficiency virus type 2 (isolate ST)
 N:Alternate names: coat polyprotein
 N:Contains: surface glycoprotein gp120; transmembrane glycoprotein gp41
 C:Species: human immunodeficiency virus type 2, HIV-2
 A>Note: host Homo sapiens (man)
 C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Sep-1994
 C:Accession: H33943
 R:Kumar, P.; Hui, J.; Kappes, J.C.; Haggarty, B.S.; Hoxle, J.A.; Arya, S.K.; Shaw, G.M.;
 J. Virol. 64, 890-901, 1990
 A:Title: Molecular characterization of an attenuated human immunodeficiency virus type 2

A:Reference number: A33943; MUID:90112662; PMID:2296086
 A:Accession: H33943
 A:Molecule type: genomic RNA
 A:Residues: 1-859 <KIM>
 A:Cross-references: UNIPARC:UPI0000174A3A; EMBL:M86924
 C:Genetics:
 A:Gene: env
 C:Superfamily: type E retrovirus env polyprotein
 C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-859/Product: env polyprotein #status predicted <ENV>
 F:20-501/Product: surface glycoprotein gp120 #status predicted <SGG>
 F:506-859/Product: transmembrane glycoprotein gp41 #status predicted <TPG>
 F:507-523/Region: hydrophobic
 F:675-694/Domain: transmembrane #status predicted <TMN>
 F:36,69,78,113,137,145,160,173,186,200,232,235,242,266,272,283,294,304,359,392,40

Query Match 18.7%; Score 53; DB 1; Length 859;
 Best Local Similarity 29.3%; Pred. No. 2.3e+02;
 Matches 12; Conservative 7; Mismatches 12; Indels 10; Gaps 1;

Qy 19 HACIPOLRCSSNT-----PPLTCQRYCNASVTNSV 49
 Db 409 HNYVPCHIKQIINTMHKVGKNVYLPFRREGQLTNCSTVTSTII 449

RESULT 69
 JCS598
 mucin - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 09-Jul-2004
 C:Accession: JCS598
 R:Inatcom, T.; Tisale, A.S.; Zhan, Q.; Spurr-Michaud, S.; Gipson, I.K.
 Biochem. Biophys. Res. Commun. 236, 789-797, 1997
 A:Title: Cloning of rat Muc5AC mucin gene: Comparison of its structure and tissue distrib
 A:Reference number: JCS598; MUID:97396181; PMID:9245735
 A:Accession: JCS598
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-1034 <INA>
 A:Cross-references: UNIPROT:Q35888; UNIPARC:UPI00000E7779; GB:U83139; NID:g2315984; PIDN:
 A:Note: translation not complete
 C:Comment: This protein is a high molecular weight glycoprotein which is a major componen
 ntestinal tract and reproductive tract.
 C:Genetics:
 A:Gene: Muc5A
 F:45-149/Domain: von Willebrand factor type C repeat homology <VWC>
 F:762-830/Domain: von Willebrand factor type C repeat homology <VWC>

Query Match 18.7%; Score 53; DB 2; Length 1034;
 Best Local Similarity 40.0%; Pred. No. 2.7e+02;
 Matches 16; Conservative 5; Mismatches 15; Indels 4; Gaps 2;

Qy 1 MLQWAGCQSQNEYFDSLHA---CIPCOLRCSSNTPPLTC 37
 Db 560 MLDLEVCSGELTYASLCAAGVCIPMRSH-TNNITCPFTC 598

RESULT 70
 T41146
 probable cysteine-rich transcription regulator - fission yeast (Schizosaccharomyces pombe
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: T41146
 R:Hilbert, H.; Duesterhoeft, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, October 1998
 A:Reference number: Z21973
 A:Accession: T41146
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1077 <HLI>
 A:Cross-references: UNIPROT:Q74853; UNIPARC:UPI000006A9D7; EMBL:AL031907; PIDN:CAA21417.1
 A:Experimental source: strain 972h-, cosmid c18

C:Genetics:
A:Gene: SPDB:SPC18.03
A:Map position: 3
F:193-252/Domain: RING finger homology <RNF>

Query Match 18.7%; Score 53; DB 2; Length 1077;
Best Local Similarity 29.5%; Pred. No. 2.8e+02;
Matches 13; Conservative 7; Mismatches 14; Indels 10; Gaps 2;

QY 2 LQMGCGCQNEVFDLSLHACIPQQLRCSNTPTLTCORCNMSV 45
DB 495 LSCGTCSET-----LTIPC--RCTANVQVTCBQLONGFI 528

RESULT 71
D88550
protein ZC84.6 [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: D88550
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A:Reference number: A/5000; WUID:99069613; PMID:9851916
A>Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C_ele
A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A:Accession: D88550
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-1474 <STO>
A:Cross-references: UNIPROT:O62504; UNIPARC:UPI00000781E7; GB:chr_III; PIDN:CAA979570.1;
C:Genetics:

A:Gene: ZC84.6
A:Map position: 3

Query Match 18.7%; Score 53; DB 2; Length 1474;
Best Local Similarity 35.9%; Pred. No. 3.7e+02;
Matches 14; Conservative 5; Mismatches 16; Indels 4; Gaps 3;

QY 3 QMAGCQONE--YFDSLHACIPQC-LRGS-SNTPTLTC 37
DB 518 ROSSCPANFECYFDGNMHGCCPTKAFCTSLSPSPKTC 556

RESULT 72
S28291

hypothetical protein ZC84.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S28291
R:Thomas, K.

submitted to the EMBL Data Library, December 1992

A:Reference number: S28285
A:Accession: S28291
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-2844 <THO>
A:Cross-references: UNIPROT:Q03610; UNIPARC:UPI000017BCB9; EMBL:Z19157

C:Genetics:
A:Residues: 14/1; 32/3; 57/1; 192/3; 277/1; 398/1; 439/1; 474/1; 497/1; 813/1; 1135/1; 12
A:introns: 14/1; 32/3; 57/1; 192/3; 277/1; 398/1; 439/1; 474/1; 497/1; 813/1; 1135/1; 12
F:220-274/Domain: animal Kunitz-type proteinase inhibitor homology <BP11>
F:343-395/Domain: animal Kunitz-type proteinase inhibitor homology <BP12>
F:442-492/Domain: animal Kunitz-type proteinase inhibitor homology <BP13>
F:546-596/Domain: animal Kunitz-type proteinase inhibitor homology <BP14>
F:654-706/Domain: animal Kunitz-type proteinase inhibitor homology <BP15>
F:1662-1716/Domain: animal Kunitz-type proteinase inhibitor homology <BP16>
F:1787-1839/Domain: animal Kunitz-type proteinase inhibitor homology <BP17>
F:1845-1895/Domain: animal Kunitz-type proteinase inhibitor homology <BP18>
F:1952-2004/Domain: animal Kunitz-type proteinase inhibitor homology <BP19>
F:2097-2152/Domain: animal Kunitz-type proteinase inhibitor homology <BP10>

Query Match 18.7%; Score 53; DB 2; Length 2844;

Best Local Similarity 35.9%; Pred. No. 6.5e+02;
Matches 14; Conservative 5; Mismatches 16; Indels 4; Gaps 3;

QY 3 QMAGCQONE--YFDSLHACIPQC-LRGS-SNTPTLTC 37
DB 1924 ROSSCPANFECYFDGNMHGCCPTKAFCTSLSPSPKTC 1962

RESULT 73
S61051

hypothetical protein YDL162c - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein D1510
C:Species: Saccharomyces cerevisiae
C:Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C:Accession: S61051; S67714
R:Pohl, T.M.

submitted to the EMBL Data Library, November 1995

A:Reference number: S61010
A:Accession: S61051
A:Molecule type: DNA
A:Residues: 1-118 <POH>

A:Cross-references: UNIPROT:Q12307; UNIPARC:UPI000006A6BC; EMBL:Z67750; NID:G1061256; PII
R:Pohl, T.M.
submitted to the Protein Sequence Database, July 1996

A:Reference number: S67708
A:Accession: S67714
A:Molecule type: DNA
A:Residues: 1-118 <POH>

A:Cross-references: UNIPARC:UPI000006A6BC; EMBL:Z74210; NID:G1431255; PIDN:CAA98735.1; P
A:Experimental source: strain S288C
C:Genetics:

A:Cross-references: SGD:S0002321
A:Map position: 4L
C:Superfamily: Saccharomyces hypothetical protein YDL162c

Query Match 18.6%; Score 52.5; DB 2; Length 118;
Best Local Similarity 34.4%; Pred. No. 49;
Matches 11; Conservative 4; Mismatches 10; Indels 7; Gaps 2;

QY 8 GSONEYFDSLHACIP---COLRCSNTPTL 35
DB 72 CNRNSYCSRMFYCCLTLSSFSLRC--VPPL 100

RESULT 74
T51647

mbd-related transcription factor MYB33 [imported] - Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C:Accession: T51647
R:Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Denekamp, M.; Greco, R.; J
; Paz-Ares, J.; Weisshaar, B.
Plant J. 16, 263-276, 1998

A:Title: Towards functional characterisation of the members of the R2R3-MYB gene from Ara
A:Reference number: Z14349; WUID:9839469; PMID:9839469
A:Accession: T51647
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 1-378 <KRA>
A:Cross-references: UNIPROT:Q9ZTE7; UNIPARC:UPI00000477EF; EMBL:AF062875; PIDN:AA03597.1

A:Experimental source: cultivar Columbia
C:Genetics:
A:Gene: MYB33
A:Map position: III
C:Keywords: transcription factor

Query Match 18.6%; Score 52.5; DB 2; Length 378;
Best Local Similarity 23.5%; Pred. No. 1.3e+02;
Matches 16; Conservative 9; Mismatches 20; Indels 23; Gaps 2;

QY 6 GCGSQNEVFDLSLHACIPQQLRCSNTPTLTCORCN 42
DB 136 GNCASSPRYENFMTPTIPSSKRLMESELLYPCCSSITIKOFSSPFOFRNTSPQITSKTCS 195

OY 43 ASVTSVK 50
|||
Db 196 FSVPCDVE 203

RESULT 75

T29468

hypothetical protein M01H9.2 - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T29468

R:Pauley, A.; Gattung, S.

submitted to the EMBL Data Library, September 1996

A:Description: The sequence of *C. elegans* cosmid M01H9.

A:Reference number: Z20626

A:Accession: T29468

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-389 <PAU>

A:Cross-references: UNIPROT:Q95018; UNIPARC:UPI000007DA14; EMBL:U70853; PIDD:AA09143.1;

A:Experimental source: strain Bristol N2; clone M01H9

C:Genetics:

A:Gene: CESP:M01H9.2

A:Map position: 4

A:Introns: 51/1; 96/1; 121/3; 209/2; 319/1

Query Match 18.6%; Score 52.5; DB 2; Length 389;
Best Local Similarity 34.1%; Pred. No. 1.4e+02;

Matches 14; Conservative 5; Mismatches 15; Indels 7; Gaps 2;

OY 8 SONEYPDSLHACT-----PCQLRCSSNTPLTCQRYCN 42

Db 317 CSGYQCIDSIKIDCAEVKAKGACKLSVASEYCPRTCE-YCN 356

RESULT 76

F72072

probable transaminase (EC 2.6.1.-) aspc [similarity] - *Chlamydomonas reinhardtii* (strainC:Species: *Chlamydomonas reinhardtii*, *Chlamydomonas reinhardtii*

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C:Accession: F72072

R:Kaltman, S.; Mitchell, W.; Marathe, R.; Lammell, C.; Fan, J.; Olinger, L.; Grimwood, J.;

Nature Genet. 21, 385-389, 1999

A:Title: Comparative genomes of *Chlamydomonas reinhardtii* and *C. trachomatis*.

A:Reference number: A72000; MUID:9920606; PMID:10192388

A:Accession: F72072

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-397 <ARN>

A:Cross-references: UNIPROT:Q92856; UNIPARC:UPI00000D40BB; GB:AE001634; GB:AE001363; NID

C:Genetics:

A:Gene: aspc

C:Superfamily: aspartate transaminase

C:Keywords: aminotransferase

Query Match 18.6%; Score 52.5; DB 2; Length 397;
Best Local Similarity 29.3%; Pred. No. 1.4e+02;

Matches 17; Conservative 6; Mismatches 18; Indels 17; Gaps 2;

OY 9 SONEYPDSLHACT-----ACIPQQLRCSSNTPL---LTCQRYCNASVTNSV 49

Db 337 SDEAFDFELHGYHIAVTPGHSFGSCGQGFVRFPSALTPOPIALACDRLCTASLKETM 394

RESULT 77

C86552

aspartate aminotransferase [imported] - *Chlamydomonas reinhardtii* (strain J138)C:Species: *Chlamydomonas reinhardtii*, *Chlamydomonas reinhardtii*

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: C86552

R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is

Nucleic Acids Res. 28, 2311-2314, 2000

A:Title: Comparison of whole genome sequences of *Chlamydomonas reinhardtii* J138.

A:Reference number: A86491; MUID:20303049; PMID:10871362

A:Accession: C86552

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-397 <STO>

A:Cross-references: UNIPROT:Q92856; UNIPARC:UPI00000D40BB; GB:BA000008; NID:98978865; PII

A:Experimental source: strain J138

C:Genetics:

A:Gene: aspc

C:Superfamily: aspartate transaminase

Query Match 18.6%; Score 52.5; DB 2; Length 397;
Best Local Similarity 29.3%; Pred. No. 1.4e+02;

Matches 17; Conservative 6; Mismatches 18; Indels 17; Gaps 2;

OY 9 SONEYPDSLHACT-----ACIPQQLRCSSNTPL---LTCQRYCNASVTNSV 49

Db 337 SDEAFDFELHGYHIAVTPGHSFGSCGQGFVRFPSALTPOPIALACDRLCTASLKETM 394

RESULT 78

A36054

mucin homolog - bovine

C:Species: *Bos primigenius taurus* (cattle)

C:Date: 16-Nov-1990 #sequence_revision 16-Nov-1990 #text_change 09-Jul-2004

C:Accession: A36054

R:Bhargava, A.K.; Molach, J.T.; Davidson, E.A.; Bhavananadan, V.P.

Proc. Natl. Acad. Sci. U.S.A. 87, 6798-6802, 1990

A:Title: Cloning and cDNA sequence of a bovine submaxillary gland mucin-like protein cont

A:Reference number: A36054; MUID:90370871; PMID:2204065

A:Accession: A36054

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-563 <BHA>

A:Cross-references: UNIPROT:P98091; UNIPARC:UPI000012F8DE; GB:M36192; NID:9163400; PIDD:J

Query Match 18.6%; Score 52.5; DB 2; Length 563;
Best Local Similarity 25.0%; Pred. No. 1.9e+02;

Matches 18; Conservative 11; Mismatches 20; Indels 23; Gaps 4;

OY 1 MLOMAGQCSQNEYPF---SLHACIPQ-----LRC-SSNTPL-----LTC 37

Db 491 MARCGECKKTKIKYDIFOLKNSCLCCQEBNREYREIDLPDGGITPYRYRHITSCG 550

OY 38 QRYCNASVTNSV 49

Db 551 LDICQGSMTSTV 562

RESULT 79

D72860

viral capsid associated protein - Autographa californica nuclear polyhedrosis virus

C:Species: Autographa californica nuclear polyhedrosis virus, AcNPV

A:Note: dsDNA virus

C:Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004

C:Accession: D72860

R:AYres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.

Virology 202, 586-605, 1994

A:Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.

A:Reference number: A72850; MUID:94303173; PMID:8030224

A:Accession: D72860

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-847 <AYR>

A:Cross-references: UNIPROT:Q06670; UNIPARC:UPI000013921A; GB:L22858; NID:9510708; PIDD:J

C:Genetics:

A:Gene: Ac-P95

Query Match 18.6%; Score 52.5; DB 2; Length 847;
Best Local Similarity 31.2%; Pred. No. 2.6e+02;

Matches 10; Conservative 7; Mismatches 12; Indels 3; Gaps 1;

A:Molecule type: mRNA
A:Residues: 1-180 <STU>
A:Cross-references: UNIPROT:O81277; UNIPARC:UPI0000033AP1; DDBJ:D14596; NID:g303576; PID
A:Experimental source: blood
C:Superfamily: hepatitis C virus genome polypeptide
C:Keywords: capsid protein; envelope protein; glycoprotein; polypeptide; transmembrane
F:53-64,74-84,91-103,109-118,155-164/Region: hypervariable region #status predicted
F:123-154/Domain: transmembrane #status predicted <TM>
F:157,70,95,166/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.4%; Score 52; DB 2; Length 180;
Best Local Similarity 29.3%; Pred. No. 80;
Matches 17; Conservative 8; Mismatches 21; Indels 12; Gaps 4;

Qy 4 MAGCCSONE---EYFDSLHA--CIPC-----QLRCSSNTPPLTCORCNASVNSVK 50
Db 64 LTNDCSNSIYEADVILHAPGCVPCVODGNTSTCTWTFVTVAVRVYCAT-TASIR 120

RESULT 85
T05301
hypothetical protein F26P21.50 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T05301
R:Bevan, M.; Terry, N.; Ardiles, W.; Buyschaert, C.; Dasseville, R.; De Clerck, R.; De
ewes, H.W.; Mayer, K.F.X.; Schueller, C.
submitted to the Protein Sequence Database, October 1998
A:Reference number: Z15407
A:Accession: T05301
A:Molecule type: DNA
A:Residues: 1-181 <BEV>
A:Cross-references: UNIPROT:O82636; UNIPARC:UPI0000045180; EMBL:AL031804
A:Experimental source: cultivar Columbia; BAC clone F26P21
C:Genetics:
A:Map position: 4
A:introns: 48/3; 84/3; 140/3
A:Note: F26P21.50
C:Superfamily: Arabidopsis thaliana hypothetical protein F26P21.50

Query Match 18.4%; Score 52; DB 2; Length 181;
Best Local Similarity 27.7%; Pred. No. 80;
Matches 13; Conservative 6; Mismatches 16; Indels 12; Gaps 2;

Qy 2 LOMAGCCSONEY-----FDSLHACIPCOLRCSSNTPPTC 37
Db 18 LQPSGGCDSDSNFPLYFKVTRYPFHSQFYALAKCF-RCEVTPKERC 63

RESULT 86
JC2264
tissue factor pathway inhibitor precursor - rhesus macaque
N:Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation inhib
C:Species: Macaca mulatta (rhesus macaque)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: JC2264
R:Kamei, S.; Kamikubo, Y.; Hamuro, T.; Fujimoto, H.; Ishihara, M.; Yonemura, H.; Miyamot
J. Biochem. 115, 708-714, 1994
A:Title: Amino acid sequence and inhibitory activity of rhesus monkey tissue factor path
A:Reference number: JC2264; MUID:94375417; PMID:8089087
A:Accession: JC2264
A:Molecule type: mRNA
A:Residues: 1-304 <KAM>
A:Cross-references: UNIPROT:Q28864; UNIPARC:UPI0000136C90; GB:S73337; NID:g685016; PIDN:
A:Experimental source: liver
C:Comment: This protein inhibits the activities of factor Xa and tissue factor-factor VI
C:Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
C:Keywords: anticoagulant; glycoprotein; serine proteinase inhibitor
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-304/Product: tissue factor pathway inhibitor #status predicted <MAT>
F:54-104/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F:125-175/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F:217-267/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>

F:54-104,63-87,79-100,125-175,134-158,150-171,217-267,226-250,242-263/Disulfide bonds: #
F:64/Inhibitory site: lys (coagulation factor VII/tissue factor complex) #status predict
F:135/Inhibitory site: Arg (coagulation factor X) #status predicted
F:145,159,256/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:122/Inhibitory site: Arg (unidentified proteinase) #status predicted

Query Match 18.4%; Score 52; DB 1; Length 304;
Best Local Similarity 32.5%; Pred. No. 1.2e+02;
Matches 13; Conservative 6; Mismatches 17; Indels 4; Gaps 2;

Qy 6 GQCCSONE--YFDSLHACIPCOLR-CSSNTPPLTCORVC 41
Db 224 GLCRANENRFYNSVIGRCRPFKYSQCGGNENFTSKREC 263

RESULT 87
T30507
probable alkaline exonuclease - Lymantria dispar nuclear polyhedrosis virus
C:Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30507
R:Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohn
Virology 253, 17-34, 1999
A:Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria di
A:Reference number: Z20836; MUID:99124785; PMID:9887315
A:Accession: T30507
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-420 <KUZ>
A:Cross-references: UNIPROT:O9YWH1; UNIPARC:UPI00000F0FCB; EMBL:AF081810; NID:g3822234; I
C:Superfamily: OPMNPV alkaline exonuclease

Query Match 18.4%; Score 52; DB 2; Length 420;
Best Local Similarity 27.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 8; Mismatches 22; Indels 2; Gaps 1;

Qy 3 QMAGCCSONEYFDSLHACIPCOLRCSSNTPP--LTCRCYNAS 44
Db 293 QLRALASGLYYDGHVLCVSCNGRFFTSAPPARLTLEHRCGAN 336

RESULT 88
T34338
hypothetical protein K03A1.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T34338
R:Nhan, M.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid K03A1.
A:Reference number: Z21505
A:Accession: T34338
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-547 <NHA>
A:Cross-references: UNIPARC:UPI000017BA83; EMBL:U41625; PIDN:AAA8324.1; CESP:K03A1.3
A:Genes: CESP:K03A1.3
A:introns: 33/3; 50/2; 95/1; 116/3; 181/2; 293/3; 342/1; 371/3; 390/2; 451/1; 484/2

Query Match 18.4%; Score 52; DB 2; Length 547;
Best Local Similarity 40.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 8 CSQNEFDSLHACIPCOLR 27
Db 85 CQKTFADGIGHKCFYCOLR 104

RESULT 89
T52060
protein MEDRA [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)


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A:Residues: 1-1483 <PAS>
A:Cross-references: UNIPROT:P33202, UNIPARC:UPI0000137AD6, GB:S53418, NID:g263497, PIDD:
A:Experimental source: strain S288C
R:Boyer, J.; Pascolo, S.; Richard, G.F.; Ghazvini, M.; Colleau, L.; Thierry, A.; Monnia
A:Reference number: S37813
A:Accession: S37821
A:Molecule type: DNA
A:Residues: 1-1483 <BOY>
A:Cross-references: UNIPARC:UPI0000137AD6, EMBL:Z28010, NID:g485992, PIDD:CAA8145.1, PI
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:UPD4
A:Cross-references: SGD:S0001493, MIPS:YKL010c
A:Map position: 11L

Query Match          18.4%; Score 52; DB 2; Length 1483;
Best Local Similarity 34.3%; Pred. No. 4.8e+02;
Matches 12; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Py      6 GGCGONEYPDSLHACIPCCORCSSNTPPLTCORY 40
       |||||::||::||::||::||::||::||::||
Db     496 GVTSNGEKFPDSLVQCLPILVEITYTNADPFVRRY 530

RESULT 94
T43162
vitellogenin - gypsy moth
C:Species: Lymantria dispar (gypsy moth)
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43162; T43268
R:Hitemach, S.T.; Lehtoma, K.
submitted to the EMBL Data Library, June 1996
A:Description: Gypsy moth vitellogenin mRNA.
A:Reference number: Z22321
A:Accession: T43162
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-1747 <HIR>
A:Cross-references: UNIPROT:Q25269, UNIPARC:UPI000007E826; EMBL:U60186; NID:g1399940; PID
R:Hitemach, S.; Lehtoma, K.
Arch. Insect Biochem. Physiol. 36, 151-164, 1997
A>Title: Structure of the gypsy moth vitellogenin gene.
A:Reference number: Z22378; MUID:97468497; PMID:9327584
A:Accession: T43268
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-819; 'O', 821-1747 <Hi2>
A:Cross-references: UNIPARC:UPI0000084020; EMBL:U90756; NID:g2894826; PID:g2894827; PIDD
C:Genetics:
A:Insertions: 11/1, 725/2, 796/3, 1120/1, 1410/1; 1477/2
C:Superfamily: Boll weevil vitellogenin

Query Match          18.4%; Score 52; DB 2; Length 1747;
Best Local Similarity 29.4%; Pred. No. 5.6e+02;
Matches 10; Conservative 6; Mismatches 6; Indels 12; Gaps 1;

Py      23 PCQLR-----CSSNTPLPTCORYCNAS 44
       |||::||::||::||::||::||::||::||
Db     1663 PCOVONQVYHENGEICITTTPIISACOSCHSS 1696

RESULT 95
S57816
antimicrobial peptide 2 precursor - garden four-o'clock
C:Species: Mirabilis jalapa (garden four-o'clock)
C>Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: S57816; A42316
R:De Bolle, M.F.C.; Eggensmont, K.; Duncan, R.E.; Osborn, R.W.; Terras, F.R.G.; Broekaert
Plant Mol. Biol. 28, 713-721, 1995
A>Title: Cloning and characterization of two cDNA clones encoding seed-specific antimicro
A:Reference number: S57815; MUID:95375234; PMID:7647302
A:Accession: S57816

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A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-63 <DEB>
A:Cross-references: UNIPROT:E25404; UNIPARC:UPI000020D6AF; EMBL:U15539; NID:G558664; PIDD
R:Cammue, B.P.; De Bolle, M.F.; Terras, F.R.; Proost, P.; Van Damme, J.; Rees, S.B.; Vank
J. Biol. Chem. 267, 2228-2233, 1992
A:Title: Isolation and characterization of a novel class of plant antimicrobial peptides
A:Accession: A42316; MUID:92129292; PMID:1133929
A:Status: preliminary
A:Molecule type: protein
A:Residues: 28-63 <CAM>
A:Cross-references: UNIPARC:UPI0000034E9D
A:Note: sequence extracted from NCBI backbone (NCBIP.78217)

Query Match 18.2%; Score 51.5; DB 2; Length 63;
Best Local Similarity 38.5%; Pred. No. 37;
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

Oy 17 ILHACTPCQLRCSSNT-PLTLCQRC 41
::|||::|||::|||::|||
Db 24 MIEACTIGNGRCNENVPVCCGFC 49

RESULT 96
T14525
S-locus-specific glycoprotein - wild cabbage (fragment)
N:Alternate names: S glycoprotein
C:Species: Brassica oleracea (wild cabbage)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #ext_change 31-Dec-2004
C:Accession: T14525
R:Kusaba, M.; Nishio, T.; Saita, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A:Title: Striking sequence similarity in inter- and intra-specific comparisons o f class
mechanism.
A:Reference number: Z18078; MUID:97352858; PMID:9207151
A:Accession: T14525
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-424 <KUS>
A:Cross-references: UNIPROT:Q23834; UNIPARC:UPI00000A9E33; EMBL:D85200; NID:G2351131; PIDD
C:Superfamily: S-locus glycoprotein; S-locus-specific glycoprotein homology
C:Keywords: glycoprotein

Query Match 18.2%; Score 51.5; DB 2; Length 424;
Best Local Similarity 39.3%; Pred. No. 1.9e+02;
Matches 11; Conservative 3; Mismatches 11; Indels 3; Gaps 1;

Oy 24 COLRCSSNTPPLTCQRCYNASVTNSKVG 51
|||::|||::|||::|||
Db 369 CEKRLSD---CNCCTAYANADIRNSGTG 393

RESULT 97
S78040
fibulin, splice form C precursor - mouse
N:Alternate names: basement-membrane protein BM-90
C:Species: Mus musculus (house mouse)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #ext_change 09-Jul-2004
C:Accession: S78040; S78560; S36440
R:Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.
Eur. J. Biochem. 215, 733-740, 1993
A:Title: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-dependent
A:Reference number: S34968; MUID:93358897; PMID:8354280
A:Accession: S78040
A:Molecule type: mRNA
A:Residues: 1-685 <PAN>
A:Cross-references: UNIPROT:Q08879; UNIPARC:UPI0000176527; EMBL:X70854
R:Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.
Submitted to the EMBL Data Library, January 1993
A:Description: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-depe
A:Reference number: S36440
A:Accession: S78560

A.Molecule type: mRNA
A.Residues: 1-39, 'P', 41-685 <CHU>
A.Cross-references: UNIPARC:UPI000002A96F; EMBL:X70854
C.Genetics: 568/3
A.Introns: 568/3
C.Superfamily: fibulin-1; EGF homology
C.Keywords: alternative splicing; basement membrane; calcium binding; extracellular matrix
F.1-29/Domain: signal sequence #status predicted <Sig>
F.30-685/Product: fibulin, splice form C #status predicted <MAT>
F.98,537,541/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.2%; Score 51.5; DB 2; Length 685;
Best Local Similarity 23.2%; Pred. No. 2.8e+02;
Matches 13; Conservative 6; Mismatches 24; Indels 13; Gaps 2;

QY 7 OCSQNEYPFLHACIP-----COLRCSNTPPLTCORVCNASVTSVK 51
DB 385 ECKAGYFPGISRTCTVDINECQRYPGRLCGHKCENTPGSFHCS--CSAGFRUSVDG 438

RESULT 98
S34968
fibulin, splice form D precursor - mouse
N.Alternate names: basement-membrane protein BM-90; calcium-binding protein BM-90
C.Species: Mus musculus (house mouse)
C.Date: 10-Dec-1993 #sequence revision 10-Nov-1995 #text_change 09-Jul-2004
C.Accession: S34968; S36441; S13814
R.Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.
Eur. J. Biochem. 215, 733-740, 1993
A.Title: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-dependent
A.Reference number: S34968; MUID:93358897; PMID:8354280
A.Accession: S34968
A.Molecule type: mRNA
A.Residues: 1-705 <PAN>
A.Cross-references: UNIPROT:Q08879; UNIPARC:UPI000017651E
R.Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.
submitted to the EMBL Data Library, January 1993
A.Description: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-dep
A.Reference number: S36440
A.Accession: S36441
A.Molecule type: mRNA
A.Residues: 1-39, 'P', 41-705 <PAN>
A.Cross-references: UNIPARC:UPI0000028FD1; EMBL:X70854; NID:G396820; PIDN:CAA50207.1; PI
R.Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.
submitted to the EMBL Data Library, January 1993
A.Description: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-dep
A.Reference number: S36440
A.Accession: S36441
A.Molecule type: mRNA
A.Residues: 1-39, 'P', 41-705 <PAN>
A.Cross-references: UNIPARC:UPI0000011EBB0; UNIPARC:UPI000017651F; UNIPARC:UPI0000176520;
525; UNIPARC:UPI0000176526
C.Superfamily: fibulin-1; EGF homology
C.Keywords: alternative splicing; basement membrane; calcium binding; extracellular matr
F.1-29/Domain: signal sequence #status predicted <Sig>
F.30-705/Product: fibulin, splice form D #status predicted <MAT>
F.98,537,541/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.2%; Score 51.5; DB 2; Length 705;
Best Local Similarity 23.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 6; Mismatches 24; Indels 13; Gaps 2;

QY 7 OCSQNEYPFLHACIP-----COLRCSNTPPLTCORVCNASVTSVK 51
DB 385 ECKAGYFPGISRTCTVDINECQRYPGRLCGHKCENTPGSFHCS--CSAGFRUSVDG 438

RESULT 99
S43656
furin (EC 3.4.21.75) 2 - great pond snail
N.Alternate names: furin homolog
C.Species: Lymnaea stagnalis (great pond snail)

C.Date: 19-Mar-1997 #sequence revision 19-Mar-1997 #text_change 09-Jul-2004
C.Accession: S43656
R.Smit, A.B.; Spiker, S.; Nagle, G.T.; Knock, S.L.; Kurosky, A.; Geraerts, W.P.M.
FEBS Lett. 343, 27-31, 1994
A.Title: Structural characterization of a Lymnaea putative endoprotease related to human
A.Reference number: S43656; MUID:94215700; PMID:8163012
A.Accession: S43656
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-837 <SMI>
A.Cross-references: UNIPROT:Q26352; UNIPARC:UPI000007EA10; GB:S69833; NID:G546392; PID:G
C.Superfamily: Kexin; subtilisin homology
C.Keywords: hydrolase; serine proteinase
F.159-397/Domain: subtilisin homology <SRT>

Query Match 18.2%; Score 51.5; DB 2; Length 837;
Best Local Similarity 32.6%; Pred. No. 3.4e+02;
Matches 14; Conservative 9; Mismatches 17; Indels 3; Gaps 2;

QY 12 EYFDSLHACIPCOLRCSNT-PPLTCORYCNA--SVTSVK 51
DB 667 EGFYTMNDWCFPCISCATCIGPMLTDCRSCPSGHQHQVKG 709

RESULT 100
T15099
hypothetical protein W03F8.5 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 20-Sep-1999 #sequence revision 20-Sep-1999 #text_change 31-Dec-2004
C.Accession: T15099
R.Johnson, D.; Bradshaw, H.; Keppeler, D.
submitted to the EMBL Data Library, December 1997
A.Description: The sequence of C. elegans cosmid W03F8.
A.Reference number: Z18293
A.Accession: T15099
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-1808 <JOH>
A.Cross-references: UNIPROT:Q44565; UNIPARC:UPI000007A125; EMBL:AF039041; NID:G2736380; I
A.Experimental source: strain Bristol N2; clone W03F8
C.Genetics: 4
A.Gene: CBSP.W03F8.5
A.Map position: 4
A.Introns: 99/2; 255/2; 365/2; 435/3; 565/2; 975/2; 1055/2; 1602/3; 1719/3; 1766/1
C.Superfamily: laminin-type EGF-like homology
F.797-842/Domain: laminin-type EGF-like homology <LEG>

Query Match 18.2%; Score 51.5; DB 2; Length 1808;
Best Local Similarity 21.6%; Pred. No. 6.5e+02;
Matches 19; Conservative 8; Mismatches 22; Indels 39; Gaps 4;

QY 3 OMAGGOSQNEY-----PDSLHACIP-----QLRCS-- 29
DB 981 ECKGEGQAHMWSPREVGTCRCDCNGNIDMAMGSCDAATGECCLKLHTHGAOCENC 1040

QY 30 -----SNTPLTCOR-VCNASVTSVK 51
DB 1041 VDGYYGDAKLKTCQRCVCNDELGTNSTKG 1068

Search completed: July 10, 2006, 16:42:05
Job time : 25.6 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:40:38 ; Search time 72 Seconds
(without alignments)
323.862 Million cell updates/sec

Title: US-10-077-137a-1_COPY_1_51
Perfect score: 283
Sequence: 1 MlOMAGQCSQNEYPFSLHA.....TPPLTCORYCNASVTSVWG 51

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

A_Geneseq.8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 283 | 100.0 | 52 | 9 | AEC02032 Amino aci |
| 2 | 283 | 100.0 | 184 | 3 | AAB08843 Amino aci |
| 3 | 283 | 100.0 | 184 | 3 | AA94001 A human B |
| 4 | 283 | 100.0 | 184 | 4 | AAE09241 Human BCM |
| 5 | 283 | 100.0 | 184 | 4 | AA711979 Human B C |
| 6 | 283 | 100.0 | 184 | 4 | AAE06698 Human BAF |
| 7 | 283 | 100.0 | 184 | 4 | AAE00506 Human B C |
| 8 | 283 | 100.0 | 184 | 5 | ABB81487 Human BCM |
| 9 | 283 | 100.0 | 184 | 5 | ABP54694 Metastati |
| 10 | 283 | 100.0 | 184 | 5 | AAE28961 Human B-C |
| 11 | 283 | 100.0 | 184 | 6 | AAE35216 Human B-C |
| 12 | 283 | 100.0 | 184 | 6 | ADA49361 Human BCM |
| 13 | 283 | 100.0 | 184 | 6 | ABP60552 Human tum |
| 14 | 283 | 100.0 | 184 | 6 | ABP97717 Amino aci |
| 15 | 283 | 100.0 | 184 | 7 | ADD67527 Human Lyl |
| 16 | 283 | 100.0 | 184 | 7 | ADG43715 Human B-C |
| 17 | 283 | 100.0 | 184 | 8 | ADK00756 Native hu |
| 18 | 283 | 100.0 | 184 | 8 | ADQ44442 Neutrokin |
| 19 | 283 | 100.0 | 184 | 8 | ADP56014 Human PRO |
| 20 | 283 | 100.0 | 184 | 9 | ADW03432 Human BCM |
| 21 | 283 | 100.0 | 184 | 9 | ADZ67760 Human tum |
| 22 | 283 | 100.0 | 184 | 9 | AEA23348 Tumor ant |
| 23 | 283 | 100.0 | 184 | 9 | AEC02031 Amino aci |

| | | | | | |
|----|------|-------|------|---|--------------------|
| 24 | 283 | 100.0 | 302 | 4 | AAE06699 Mouse IgG |
| 25 | 283 | 100.0 | 302 | 4 | AAE0507 Human BCM |
| 26 | 283 | 100.0 | 302 | 7 | ADG43717 Human B-C |
| 27 | 277 | 97.9 | 184 | 4 | ABR40082 Human Gen |
| 28 | 274 | 96.8 | 288 | 5 | ABG95060 Human tra |
| 29 | 269 | 95.1 | 51 | 5 | AAE15485 Human B-C |
| 30 | 269 | 95.1 | 181 | 5 | AAE15484 Human BCM |
| 31 | 269 | 95.1 | 283 | 5 | AAE15488 Human BCM |
| 32 | 257 | 90.8 | 296 | 9 | AAE02042 Amino aci |
| 33 | 249 | 88.0 | 58 | 5 | AAE15501 Human B C |
| 34 | 230 | 81.3 | 40 | 9 | ADZ67761 Human tum |
| 35 | 215 | 76.0 | 38 | 9 | AEC02033 Amino aci |
| 36 | 206 | 72.8 | 157 | 4 | AAE60700 Human BAF |
| 37 | 201 | 71.0 | 34 | 5 | AAE15486 Human B-C |
| 38 | 201 | 71.0 | 34 | 6 | ADA49366 Human BCM |
| 39 | 197 | 69.6 | 34 | 9 | AEC02026 Formula I |
| 40 | 196 | 69.3 | 34 | 9 | AEC02027 Formula I |
| 41 | 194 | 68.6 | 34 | 9 | AEC02028 Formula I |
| 42 | 194 | 68.6 | 34 | 9 | AEC02017 Formula I |
| 43 | 192 | 67.8 | 34 | 9 | AEC02025 Formula I |
| 44 | 192 | 67.8 | 34 | 9 | AEC02024 Formula I |
| 45 | 191 | 67.5 | 34 | 9 | AEC02020 Formula I |
| 46 | 189 | 66.8 | 34 | 9 | AEC02018 Formula I |
| 47 | 189 | 66.8 | 34 | 9 | AEC02029 Formula I |
| 48 | 182 | 64.3 | 34 | 9 | AEC02019 Formula I |
| 49 | 181 | 64.0 | 185 | 3 | ABO8844 Amino aci |
| 50 | 181 | 64.0 | 185 | 4 | AA711980 Murine B |
| 51 | 181 | 64.0 | 185 | 5 | AAE15490 Mouse B C |
| 52 | 181 | 64.0 | 185 | 9 | ADZ67762 Mouse tum |
| 53 | 181 | 64.0 | 281 | 5 | AAE15489 Mouse BCM |
| 54 | 158 | 55.8 | 42 | 6 | ABJ38417 TAL-1 re |
| 55 | 151 | 53.4 | 26 | 7 | AD153060 Human BCM |
| 56 | 104 | 36.7 | 117 | 5 | AAE15491 Human-mur |
| 57 | 90.5 | 32.0 | 24 | 5 | AAE15492 Human-mur |
| 58 | 71.5 | 25.3 | 249 | 3 | AA94006 A murine |
| 59 | 71.5 | 25.3 | 249 | 7 | ABM85744 Mouse pro |
| 60 | 71.5 | 25.3 | 249 | 9 | ADZ67773 Mouse tum |
| 61 | 71.5 | 25.3 | 249 | 9 | AEAS5078 Tumor nec |
| 62 | 70.5 | 24.9 | 1548 | 7 | ADC71568 Mouse sub |
| 63 | 70.5 | 24.9 | 1877 | 7 | ABB80243 Murine su |
| 64 | 68.5 | 24.2 | 332 | 6 | AAE35228 Human TAC |
| 65 | 68.5 | 24.2 | 1569 | 8 | ADR18921 Human muc |
| 66 | 68.5 | 24.2 | 2240 | 8 | ADR18914 Mature Hu |
| 67 | 68.5 | 24.2 | 2258 | 8 | ADR18913 Human muc |
| 68 | 68.5 | 24.2 | 2264 | 8 | ADR18915 His-tagge |
| 69 | 67.5 | 23.9 | 37 | 5 | AAU10951 Human AGP |
| 70 | 67.5 | 23.9 | 48 | 9 | ADZ67772 Human tum |
| 71 | 67.5 | 23.9 | 59 | 5 | AAE15500 Human TAC |
| 72 | 67.5 | 23.9 | 166 | 2 | AAE75785 Human TAC |
| 73 | 67.5 | 23.9 | 166 | 5 | AAE15494 Human TAC |
| 74 | 67.5 | 23.9 | 171 | 8 | ADN03188 Human TAC |
| 75 | 67.5 | 23.9 | 265 | 4 | AAE09244 Human TAC |
| 76 | 67.5 | 23.9 | 266 | 6 | ABP97723 Amino aci |
| 77 | 67.5 | 23.9 | 266 | 9 | ABP97723 Amino aci |
| 78 | 67.5 | 23.9 | 291 | 5 | AAU10949 Human AGP |
| 79 | 67.5 | 23.9 | 292 | 2 | ADZ67771 Human tum |
| 80 | 67.5 | 23.9 | 293 | 2 | AAW75783 Human Lym |
| 81 | 67.5 | 23.9 | 293 | 3 | AAE36312 Human neu |
| 82 | 67.5 | 23.9 | 293 | 3 | AAE94000 A transme |
| 83 | 67.5 | 23.9 | 293 | 4 | AAE09240 Human TAC |
| 84 | 67.5 | 23.9 | 293 | 4 | AAE17914 Human tum |
| 85 | 67.5 | 23.9 | 293 | 5 | AAO14130 Human tra |
| 86 | 67.5 | 23.9 | 293 | 5 | ABE81488 Human TAC |
| 87 | 67.5 | 23.9 | 293 | 5 | AAU99512 Human TAC |
| 88 | 67.5 | 23.9 | 293 | 5 | AAE28962 Human TAC |
| 89 | 67.5 | 23.9 | 293 | 5 | AAU75408 Tumor ne |
| 90 | 67.5 | 23.9 | 293 | 5 | AAU09900 Human AGP |
| 91 | 67.5 | 23.9 | 293 | 5 | AAE15493 Human tra |
| 92 | 67.5 | 23.9 | 293 | 5 | ABG71496 Human tum |
| 93 | 67.5 | 23.9 | 293 | 6 | AAE35211 Human TAC |
| 94 | 67.5 | 23.9 | 293 | 6 | ABP60551 Human tum |
| 95 | 67.5 | 23.9 | 293 | 6 | ABP97716 Amino aci |
| 96 | 67.5 | 23.9 | 293 | 6 | AAO29592 Human DIT |

| | | | | | | |
|------|----|------|-----|----|----------|---------------------|
| 973 | 51 | 18.0 | 200 | 10 | AAE28750 | Aae28750 Lead Cere |
| 974 | 51 | 18.0 | 209 | 5 | AA018662 | AA018662 Hepatitis |
| 975 | 51 | 18.0 | 209 | 6 | ABP55558 | ABP55558 Hepatitis |
| 976 | 51 | 18.0 | 209 | 6 | AAE32871 | AAE32871 Hepatitis |
| 977 | 51 | 18.0 | 209 | 7 | ADD55516 | ADD55516 Hepatitis |
| 978 | 51 | 18.0 | 209 | 8 | ADP71098 | ADP71098 Hepatitis |
| 979 | 51 | 18.0 | 210 | 5 | AA018669 | AA018669 Hepatitis |
| 980 | 51 | 18.0 | 210 | 7 | ADD55536 | ADD55536 Hepatitis |
| 981 | 51 | 18.0 | 210 | 8 | ADP71118 | ADP71118 HCV E1 pr |
| 982 | 51 | 18.0 | 212 | 5 | AA018660 | AA018660 Hepatitis |
| 983 | 51 | 18.0 | 212 | 7 | ADD55512 | ADD55512 Hepatitis |
| 984 | 51 | 18.0 | 212 | 8 | ADP71094 | ADP71094 HCV E1 pr |
| 985 | 51 | 18.0 | 213 | 2 | AAW46619 | AAW46619 Pseudom |
| 986 | 51 | 18.0 | 217 | 7 | AB081895 | AB081895 Pseudom |
| 987 | 51 | 18.0 | 239 | 5 | AA018666 | AA018666 Hepatitis |
| 988 | 51 | 18.0 | 239 | 7 | ADD55530 | ADD55530 Hepatitis |
| 989 | 51 | 18.0 | 239 | 8 | ADP71112 | ADP71112 HCV E1 pr |
| 990 | 51 | 18.0 | 247 | 7 | ABO77990 | ABO77990 Pseudom |
| 991 | 51 | 18.0 | 252 | 8 | ADY07374 | ADY07374 Plant full |
| 992 | 51 | 18.0 | 263 | 5 | AA018661 | AA018661 Hepatitis |
| 993 | 51 | 18.0 | 263 | 7 | ADD55514 | ADD55514 Hepatitis |
| 994 | 51 | 18.0 | 263 | 8 | ADP71086 | ADP71086 HCV E1 pr |
| 995 | 51 | 18.0 | 326 | 2 | AAE27866 | AAE27866 Myxoma VI |
| 996 | 51 | 18.0 | 326 | 2 | AAE85072 | AAE85072 Myxoma VI |
| 997 | 51 | 18.0 | 334 | 4 | AAU60378 | AAU60378 Propionib |
| 998 | 51 | 18.0 | 334 | 4 | ABM56897 | ABM56897 Propionib |
| 999 | 51 | 18.0 | 348 | 4 | AB61240 | AB61240 Chinese h |
| 1000 | 51 | 18.0 | 348 | 6 | AB032676 | AB032676 Secreted |

ALIGNMENTS

RESULT 1
AEC02032
ID AEC02032 standard; peptide; 52 AA.
XX
AC AEC02032;
XX
DT 20-OCT-2005 (first entry)
XX
DE Amino acid sequence of an extracellular domain of BCMA.
XX
DE APRIL; BAPF; immune disorder; immunomodulator; antiinflammatory; cancer;
XX
KW cytostatic; neoplasm; immunosuppressive; therapeutic;
XX
KW B-cell maturation antigen; BCMA.
XX
OS Synthetic.
XX
PN WO2005075511-A1.
XX
PD 18-AUG-2005.
XX
PF 04-AUG-2004; 2004WO-US025247.
XX
XX 29-JAN-2004; 2004US-0540271P.
XX
PA (GETH) GENENTECH INC.
XX
PI Kelley RF, Patel D;
XX
XX WPI; 2005-555932/56.
XX
PT New polypeptides that inhibit APRIL and/or BAPF binding to BCMA, useful
XX
PT for treating immune-related disease, cancer or T-cell mediated disease
XX
PT such as graft rejection, graft versus host disease (GVHD) and
XX
PT inflammation.
XX
PS Disclosure; SEQ ID NO 21; 140pp; English.
XX
XX The specification describes polypeptides that bind APRIL or BAPF. The
XX
XX polypeptides inhibit APRIL or BAPF binding to B-cell maturation antigen
XX
XX (BCMA). APRIL and BAPF are tumor necrosis family (TNF) members. The

polypeptides of the invention are useful for treating immune-related diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic lupus erythematosus; cancer such as leukemia, lymphoma, or multiple sclerosis; or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and inflammation. The present sequence represents an extracellular domain of BCMA.

Sequence 52 AA;

Query Match 100.0%; Score 283; DB 9; Length 52;
Best Local Similarity 100.0%; Pred. No. 3.9e-26;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQWAGGCSQNEFYDSLHACTIPCOLRCSNTPTTCORYCNASVTNSVKG 51
DB 1 MLQWAGGCSQNEFYDSLHACTIPCOLRCSNTPTTCORYCNASVTNSVKG 51

RESULT 2
AAB08843
ID AAB08843 standard; peptide; 184 AA.
XX
AC AAB08843;
XX
DT 02-JAN-2001 (first entry)
XX
XX Amino acid sequence of human.

BCMA; necrosis factor- κ B activator; NF- κ B; gene expression; cancer;
KW anti-cell death gene; apoptosis; viral infection; inflammatory response;
KW rheumatoid arthritis; inflammatory bowel disease; septic shock.
XX
OS Homo sapiens.

Key location/Qualifiers
FH 57..77
FT Domain /note="putative transmembrane domain"
FT

PN WO20050633-A1.

PD 31-AUG-2000.

PF 24-FEB-2000; 2000WO-US004925.

PR 24-FEB-1999; 99US-0121485P.

PA (GENO) GEN HOSPITAL CORP.

PI Seed B, Ting A;

XX WPI; 2000-558405/51.

Identifying a modulator of gene expression for drug designing, by
PT contacting a compound library with a cell expressing an anti-cell death
PT gene and reporter gene, and determining alteration in reporter gene
PT expression.

PS Claim 32; Fig 7A; 53pp; English.

The present sequence represents a BCMA (not defined) polypeptide. BCMA is
CC a necrosis factor (NF)- κ B activator. The method of the invention is used
CC to identify compounds which modulate BCMA activity (and thus NF- κ B
CC activity). The specification describes a method of identifying a
CC polypeptide which increases gene expression from a promoter. The method
CC involves contacting a library of with a cell which expresses a
CC recombinant anti-cell death gene and a reporter gene operably linked to
CC the promoter, and then determining whether the expression of the reporter
CC gene is altered as a result of contact with library. The method is useful
CC for identifying polypeptides which increase or decrease gene expression
CC from a promoter. The BCMA polypeptide or nucleic acid are useful for
CC preparing a pharmaceutical composition for treating cancer, apoptosis,
CC viral infections, inflammatory response, such as rheumatoid arthritis,
CC inflammatory bowel disease or septic shock. BCMA is useful for

CC identifying compounds that modulate NF-kB expression and thus for drug
CC designing
XX
SQ Sequence 184 AA;
Query Match 100.0%; Score 283; DB 3; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MLOMAGQCSQNEYFDSLHACIPCOLRCSNTPPLTCQRYCNASTVNSVKG 51
Db 1 MLOMAGQCSQNEYFDSLHACIPCOLRCSNTPPLTCQRYCNASTVNSVKG 51
RESULT 3
ID AAY94001 standard; protein; 184 AA.
XX AAY94001;
AC
XX 20-OCT-2000 (first entry)
DT
XX
XX A human BCMA protein, a B cell protein related to TACI.
DE
XX
XX Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
KW ztnf4 activity; antibody production; autoimmune disease; amyloidosis;
KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;
KW renal neoplasia; multiple myeloma; lymphoma; light chain neuropathy;
KW immune response; immunosuppression; graft rejection; joint pain;
KW graft versus host disease; inflammation; swelling; anaemia; septic shock;
KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;
KW renal artery stenosis; occlusion; cholesterol; renal emboli.
XX
XX Homo sapiens.
OS
XX
XX WO200040716-A2.
PN
XX
XX 13-JUL-2000.
PD
XX
XX 07-JAN-2000; 2000WO-US000396.
XX
XX 07-JAN-1999; 99US-00226533.
PR
XX
XX (ZYMO) ZYMOGENETICS INC.
PA
XX
XX Gross JA, Xu W, Madden K, Yee DP;
PI
XX
XX MPI: 2000-452538/39.
DR
XX
XX N-PSDB; AAS58559.
PT
XX
XX Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,
PT renal disease, graft versus host disease, and inflammation, comprises
PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide.
XX
XX
XX Disclosure; Page 152; 175pp; English.
PS
XX
XX The present sequence represents a human BCMA protein, a B cell protein
CC related to transmembrane activator and CAML-interactor (TACI) receptor.
CC TACI is a tumour necrosis factor (TNF) receptor. The extracellular
CC domains of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell
CC protein) receptor contain a cysteine rich domain, and are used for
CC inhibiting ztnf4 activity. ztnf4 is a TNF ligand. They may also be used
CC for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated
CC with activated or resting B lymphocytes, effector T-cells, or with
CC antibody production. The antibody production is associated with an
CC autoimmune disease selected from systemic lupus erythematosus, myasthenia
CC gravis, multiple sclerosis and rheumatoid arthritis. The ztnf4 activity
CC and BR43x2, TACI or BCMA receptor-ligand engagement is associated with
CC asthma, bronchitis, emphysema, end stage renal failure,
CC glomerulonephritis, vasculitis, nephritis, pyelonephritis, renal

CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy,
CC amyloidosis, moderating immune response, immunosuppression, graft
CC rejection, graft versus host disease, inflammation, insulin dependent
CC diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or
CC septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies,
CC agonists or antagonists can be used to treat hypertension, renal artery
CC stenosis, or occlusion, and cholesterol or renal emboli
XX
SQ Sequence 184 AA;
Query Match 100.0%; Score 283; DB 3; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MLOMAGQCSQNEYFDSLHACIPCOLRCSNTPPLTCQRYCNASTVNSVKG 51
Db 1 MLOMAGQCSQNEYFDSLHACIPCOLRCSNTPPLTCQRYCNASTVNSVKG 51
RESULT 4
ID AAE09241 standard; protein; 184 AA.
XX AAE09241;
AC
XX 19-NOV-2001 (first entry)
DT
XX
XX Human BCMA protein.
DE
XX
XX Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;
KW TACI; BCMA; therapy; cancer; leukemia; myeloma; lymphoma;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.
XX
XX Homo sapiens.
OS
XX
XX WO200160397-A1.
PN
XX
XX 23-AUG-2001.
PD
XX
XX 28-NOV-2000; 2000WO-US032378.
XX
XX 16-FEB-2000; 2000US-0182938P.
PR
XX
XX 22-AUG-2000; 2000US-0226986P.
XX
XX (GENT) GENENTECH INC.
PA
XX
XX Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Masters SA, Pitti RM;
PI
XX
XX Yan M;
PI
XX
XX MPI: 2001-541628/60.
DR
XX
XX N-PSDB; AAD15902.
PT
XX
XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
PT activity, for treating autoimmune disorders and cancer, comprises
PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
PT antagonists.
XX
XX
XX Example 2; Fig 2; 160pp; English.
PS
XX
XX The invention relates to methods of using one or more agonists or
CC antagonists to modulate the activity of the members of TNF (tumour
CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g.
CC TACI or BCMA. The method is useful for treating pathological conditions
CC or diseases associated with increased TALL-1 and APRIL expression or
CC activity. TALL-1 and APRIL antagonists are used to block the interaction
CC between APRIL and TALL-1 with TACI or BCMA. They are useful for treating
CC a mammal suffering from cancer such as leukaemia, lymphoma, myeloma,
CC cancers of lung and colon and autoimmune diseases e.g. rheumatoid
CC arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The
CC present sequence is human BCMA protein
XX
XX Sequence 184 AA;
SQ

```
Query Match      100.0%; Score 283; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 MLQWAGGCSQNEYPDSLHACIPCOLRCSNTPTTCQRYCNASYTVNSVKG 51
Db      1 MLQWAGGCSQNEYPDSLHACIPCOLRCSNTPTTCQRYCNASYTVNSVKG 51

RESULT 5
ID      AAY71979 standard; protein; 184 AA.
XX
AC      AAY71979;
XX
XX      28-MAR-2001 (first entry)
DT
XX
DE      Human B cell maturation factor (BCMA) protein.
XX
KM      Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
KM      Tumour necrosis factor and Apol-related leucocyte expressed ligand 1;
KM      therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
KM      systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
KM      thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
KM      haemolytic anaemia; Grave's disease; myasthenia gravis; chromosome 16;
KM      post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;
KM      B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.
XX
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
FT      Domain      1..62
FT      /label= Extracellular_domain
XX
PN      WO200068378-A1.
XX
XX      16-NOV-2000.
PD
XX
PF      05-MAY-2000; 2000MO-US012266.
XX
PR      06-MAY-1999; 99US-0132892P.
PR      01-MAY-2000; 2000US-0201012P.
XX
PA      (NAGE-) NAT JEWISH MEDICAL & RES CENT.
XX
PI      Shu HS;
XX
XX      WPI, 2001-016094/02.
XX      N-PSDB; AAD02125.
DR
XX
XX      Isolated TALL-1 protein is used to identify compounds that regulate B
XX      lymphocyte proliferation, used to treat B lymphocyte associated
XX      autoimmune disorders.
XX
PS      Claim 37; Page 104-105; 112pp; English.
XX
XX      The present invention relates to Tumour necrosis factor (TNF) and Apol-
XX      related leucocyte expressed ligand 1 (TALL-1) nucleic acid molecules,
XX      proteins (including homologues) and their antibodies. The invention in
XX      particular relates to methods for regulating the interaction between TALL
XX      -1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to
XX      regulate monocyte, macrophage and B lymphocyte mediated immune responses.
XX      TALL-1 protein is useful for identifying compounds that regulate B
XX      lymphocyte proliferation. It is also useful for treating B lymphocyte
XX      associated autoimmune disorders like rheumatoid arthritis, systemic lupus
XX      erythematosus (SLE), insulin dependent diabetes mellitus, multiple
XX      sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic
XX      anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome,
XX      pemphigus vulgaris, acute rheumatic fever, post-streptococcal
XX      glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its
XX      corresponding nucleic acid sequence are also useful in diagnostic assays.
XX      The present sequence is a human B cell maturation factor (BCMA) protein.
XX      It is the receptor for TALL-1 protein. BCMA gene is located on chromosome
```

```
CC      16. In human tissues, BCMA is expressed by spleen and lymph nodes but not
CC      by brain, muscle, heart, lung, kidney, pancreas, testis and placenta.
CC      BCMA mRNA is absent in the pro-B lymphocyte stage but its expression
CC      increases with B lymphocyte maturation
XX
SQ      Sequence 184 AA:
XX
OY      1 MLQWAGGCSQNEYPDSLHACIPCOLRCSNTPTTCQRYCNASYTVNSVKG 51
Db      1 MLQWAGGCSQNEYPDSLHACIPCOLRCSNTPTTCQRYCNASYTVNSVKG 51

RESULT 6
ID      AAB60698 standard; protein; 184 AA.
XX
AC      AAB60698;
XX
XX      22-MAY-2001 (first entry)
DT
XX
DE      Human BAFF receptor (BAFF-R).
XX
KM      Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
KM      immune-related disorder; B-cell growth inhibitor; BCMA;
KM      B-cell maturation inhibitor; immunoglobulin production inhibitor;
KM      autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
KM      renal disorder; immunosuppressive disorder; HIV infection;
KM      organ transplantation; antiinflammatory; systemic lupus erythematosus;
KM      autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
KM      B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
KM      lymphoma; gene therapy; cancer; tumour.
XX
XX      Homo sapiens.
XX
OS
XX
XX      WO200112812-A2.
XX
XX      22-FEB-2001.
PD
XX
PF      16-AUG-2000; 2000MO-US022507.
XX
PR      17-AUG-1999; 99US-0149378P.
PR      11-FEB-2000; 2000US-0181684P.
PR      18-FEB-2000; 2000US-0183536P.
XX
PA      (BIOJ ) BIOGEN INC.
PA      (APOT-) APOTEC R & D SA.
XX
PI      Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P,
PI      Thompson J;
XX
XX      WPI, 2001-202866/20.
XX      N-PSDB; AAF59998.
DR
XX
XX      Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
XX      lympho-proliferative disorder by administering BAFF-receptor polypeptide,
XX      chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.
XX
PS      Claim 20; Fig 1; 59pp; English.
XX
XX      The invention relates to the use of a BAFF receptor (BAFF-R, also known
XX      as BCMA) protein, or a BAFF-R fusion protein as an agent for the
XX      treatment of a variety of immune-related disorders. BAFF-R is a member of
XX      the TNF (tumour necrosis factor) family, acting as an immunoregulatory
XX      agent, and also plays a role in the development of hypertension and
XX      related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-
XX      specific antibodies can be used for inhibiting B-cell growth, dendritic
XX      cell-induced B-cell growth and maturation, and immunoglobulin production,
XX      and in the treatment of autoimmune disorders, B-cell lymphoproliferative
XX      disorders, hypertension and renal disorders. The BAFF-R proteins may also
```

CC be used in the treatment of immunosuppressive disorders and HIV
CC infection, and in patients undergoing organ transplantation. The BAFF-R
CC proteins or BAFF-R specific antibodies may be used for treating,
CC suppressing or altering an immune response involving a signalling pathway
CC between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R
CC inhibits B-cell growth and maturation it is useful for treating diseases
CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
CC human BAFF-R may be used in gene therapy to treat tumours, lymphomas,
CC autoimmune disorders and inherited B-cell-associated disorders. The
CC present sequence represents human BAFF-R

SQ Sequence 184 AA;

Query Match 100.0%; Score 283; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLOMAGQCSQNEYFDSLHACIPCOLRCSNTPLTCORVCNASTVNSVKG 51
1 MLOMAGQCSQNEYFDSLHACIPCOLRCSNTPLTCORVCNASTVNSVKG 51

Db 1 MLOMAGQCSQNEYFDSLHACIPCOLRCSNTPLTCORVCNASTVNSVKG 51

RESULT 7
AAE00506
ID AAE00506 standard; protein; 184 AA.

AC AAE00506;

DT 31-JUL-2001 (first entry)

DE Human B cell maturation protein (BCMA).

XX Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytosolic;
XX gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
XX carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
XX systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
XX B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;
XX organ transplantation; HIV; human immunodeficiency virus; TNF;
XX tumour necrosis factor; BCMA; B cell maturation protein.

OS Homo sapiens.

PN WO200124811-A1.

PD 12-APR-2001.

PF 05-OCT-2000; 2000WO-US027579.

PR 06-OCT-1999; 99US-0157933P.

PR 11-FEB-2000; 2000US-0181807P.

PR 30-JUN-2000; 2000US-0215688P.

PA (BIOJ) BIOGEN INC.

PA (APOT) APOTEC R & D SA.

PI Schneider P, Thompson J, Cachero T, Ambrose C, Rennett P,

DR WPI, 2001-266242/27.

DR N-PSDB; AAD03844.

XX Treating a mammal for a condition associated with undesired cell
XX proliferation such as cancer or carcinoma, comprises administering a
XX composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R)
XX antagonist.

PS Claim 3; Fig 3A; 85pp; English.

XX The invention relates to a method of treating a mammal for a condition
XX associated with undesired cell proliferation such as cancer or carcinoma.
XX The method involves administering a composition comprising A
XX Proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell

CC maturation protein (BCM or BCMA) antagonist that antagonises the
CC interaction between APRIL and its cognate receptor(s). This method is
CC useful for treating undesired cell proliferation such as cancer or
CC carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
CC prostate carcinoma, and other carcinomas whose proliferation is modulated
CC by APRIL. It is also useful for treating autoimmune diseases (Grave's
CC disease, systemic lupus erythematosus-SLE), hypertension, cardiovascular
CC diseases, renal disorders, B-cell lympho-proliferative disorders,
CC immunosuppressive diseases, organ transplantation, inflammation and human
CC immunodeficiency virus (HIV), and for treating, suppressing or altering
CC an immune response involving a signalling pathway between APRIL-R and its
CC ligand. APRIL-R DNA is also useful in gene therapy. The present sequence
CC is human APRIL-R also referred as BCMA or BCM protein

SQ Sequence 184 AA;

Query Match 100.0%; Score 283; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLOMAGQCSQNEYFDSLHACIPCOLRCSNTPLTCORVCNASTVNSVKG 51
1 MLOMAGQCSQNEYFDSLHACIPCOLRCSNTPLTCORVCNASTVNSVKG 51

Db 1 MLOMAGQCSQNEYFDSLHACIPCOLRCSNTPLTCORVCNASTVNSVKG 51

RESULT 8
ABB81487
ID ABB81487 standard; protein; 184 AA.

AC ABB81487;

DT 02-SEP-2002 (first entry)

DE Human BCMA receptor related protein SEQ ID NO:7.

XX Human; Ztnfr12; tumour necrosis factor receptor; cytosolic;
XX immunosuppressive; dermatological; antiinflammatory; antidiabetic;
XX neuroprotective; antirheumatic; antiarthritic; antiasclerotic;
XX nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
XX autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
XX multiple sclerosis; insulin dependent diabetes mellitus; asthma;
XX rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
XX glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
XX light chain neuropathy; hypertension; large vessel disease;
XX graft-versus host disease; graft rejection; Crohn's disease.

OS Homo sapiens.

PN WO200238766-A2.

PD 16-MAY-2002.

PF 05-NOV-2001; 2001WO-US047018.

PR 07-NOV-2000; 2000US-0246449P.

PR 20-DEC-2000; 2000US-0257131P.

PR 28-JUN-2001; 2001US-0301715P.

PR 29-AUG-2001; 2001US-0315565P.

PA (ZYMO) ZYMOGENETICS INC.

PI Gross JA, Xu W, Henne RM, Grant FJ,

DR WPI, 2002-508212/54.

XX Novel isolated human tumor necrosis factor receptor polypeptide, termed
XX Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage
XX renal failure or renal disease and lymphoma.

PS Disclosure; Page 135-136; 154pp; English.

XX The present invention describes a human tumour necrosis factor receptor

CC designated, ztnfr12 (1). (1) has cytostatic, immunosuppressive,
CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
CC antirheumatic, antiallergic, antistatic, nephrotoxic and hypotensive
CC activities, and can be used in gene therapy. (1) can be used for
CC inhibiting, in a mammal, the activity of a ligand that binds ztnfr12
CC (e.g. ztnf4), for treating disorders and diseases associated with B
CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
CC inhibiting the proliferation of tumour cells. (1) is useful for treating
CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
CC leukaemia, nephritis, and pyelonephritis, and for treating renal
CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
CC amyloidosis, hypertension, large vessel diseases, graft-versus host
CC disease, graft rejection and Crohn's disease. (1) is useful for
CC modulating the immune system, for regulating B cell responses and
CC development, for modulating development of other cells, antibody
CC production and cytokine production, and for modulating T and B cell
CC communication. The present sequence represents a protein which is given
CC in the exemplification of the present invention

CC
XX
SQ

Query Match 100.0%; Score 283; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQMGAGCSQNEYPDSLHACIPQRLCSSNTPPLTCORYNASVTVSKG 51
Db 1 MLQMGAGCSQNEYPDSLHACIPQRLCSSNTPPLTCORYNASVTVSKG 51

RESULT 9
ABP54694
ID ABP54694 standard; protein; 184 AA.

XX
AC
XX
ABP54694;

DT 30-DEC-2002 (first entry)

XX
DE Metastatic colorectal cancer-associated polypeptide.

XX
KW Colorectal cancer; metastasis; differential expression; cytostatic;
XX
diagnosis; gene therapy; vaccine.

OS
XX
Homo sapiens.

XX
PN WO20026677-A2.

XX
PD 06-SEP-2002.

XX
PF 27-FEB-2002; 2002WO-US006001.

XX
PR 27-FEB-2001; 2001US-0272206P.

XX
PR 02-APR-2001; 2001US-0281149P.

XX
PR 17-APR-2001; 2001US-0284555P.

XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.

XX
PI (UYCA-) UNIV CASE WESTERN RESERVE.

XX
PI Mack DH, Markowitz SD;

XX
DR WPI; 2002-698677/75.

XX
DR N-PSDB; AB081560.

XX
PT New genes that are up- or down-regulated in colorectal cancer, useful for
XX
diagnosing colorectal cancer in a subject, or for identifying modulators
XX
of colorectal cancer-associated proteins and genes for treating
XX
colorectal cancer.
XX
PS Claim 8; Page 255; 260pp; English.
XX

CC The present sequence is the protein sequence of a human polypeptide
CC encoded by a gene that exhibits decreased expression in colon cancer-
CC derived metastases compared to normal colon tissue. It is an example of
CC claimed polypeptides that are encoded by genes which are differentially
CC expressed in metastatic colorectal cancer cells. Such polypeptides are
CC useful in diagnostic and prognostic assays, for raising antibodies useful
CC e.g. in immunotherapy, and in screening for modulator compounds of
CC therapeutic value

XX
SQ

Query Match 100.0%; Score 283; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQMGAGCSQNEYPDSLHACIPQRLCSSNTPPLTCORYNASVTVSKG 51
Db 1 MLQMGAGCSQNEYPDSLHACIPQRLCSSNTPPLTCORYNASVTVSKG 51

RESULT 10

AAE28961
ID AAE28961 standard; protein; 184 AA.

XX
AC
XX
AAE28961;

DT 27-JAN-2003 (first entry)

XX
DE Human B-cell maturation antigen (BCMA).

XX
KW Human; tumour; B-cell maturation antigen; transmembrane activator;

XX
KW calcium-modulator; cyclophilin ligand-interactor; TACI; gene therapy;

XX
KW neoplasm; chronic lymphocytic leukaemia; lymphoproliferative disease;

XX
KW non-Hodgkin's lymphoma; light chain gammopathy; inflammation; asthma;

XX
KW BCMA; multiple myeloma.

XX
OS
XX
Homo sapiens.

XX
XX
Key Location/Qualifiers

FT 1..54 /note= "Antigenic epitope"

FT 1..48 /note= "Extracellular domain"

FT 8..41 /note= "Cysteine rich region"

XX
PN WO200266516-A2.

XX
PD 29-AUG-2002.

XX
PF 06-FEB-2002; 2002WO-US003500.

XX
PR 20-FEB-2001; 2001US-0270274P.

XX
PR 12-APR-2001; 2001US-0283447P.

XX
PA (ZYMO) ZYMOGENETICS INC.

XX
PI Kindsvogel W;

XX
DR WPI; 2002-723183/78.

XX
DR N-PSDB; AAD46410.

XX
PT B-cell maturation antigen and transmembrane activator and calcium-
XX
modulator and cyclophilin ligand-interactor, useful for treating
XX
disorders e.g. inflammation or lymphoma.
XX
PS Disclosure; Page 63; 67pp; English.

XX
XX
The invention relates to the manufacture of a composition for inhibiting
XX
the proliferation of tumour cells. The method involves using an antibody
XX
component that binds both the B-cell maturation antigen (BCMA) and the
XX
transmembrane activator and calcium-modulator and cyclophilin ligand-
XX
interactor (TACI). BCMA and TACI binding antibody compositions are useful

CC for inhibiting proliferation of tumour cells, particularly inhibiting
CC ZTNF4 activity in a mammal associated with increased endogenous antibody
CC production or a disorder consisting of neoplasm, chronic lymphocytic
CC leukaemia, multiple myeloma, non-Hodgkin's lymphoma, post-transplantation
CC lymphoproliferative disease or light chain gammopathy or inflammation
CC e.g. asthma. The invention is also useful in gene therapy. The present is
CC human BCMA protein
XX
SQ Sequence 184 AA:
Query Match 100.0%; Score 283; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLOMAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORXCNASVTNSVKG 51
1 MLOMAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORXCNASVTNSVKG 51
DB 1 MLOMAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORXCNASVTNSVKG 51
RESULT 11
AAE35216 standard; protein; 184 AA.
XX
AC AAE35216;
XX
DT 28-MAY-2003 (first entry)
XX
DE Human B-cell maturation receptor (BCMA) protein.
XX
KW Transmembrane activator; calcium modulator; nephrotoxic; antibacterial;
KW TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;
KW anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive;
KW glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;
KW dermatological; neuroprotective; cyclophilin ligand-interactor; human;
KW autoimmune disease; systemic lupus erythematosus; multiple sclerosis;
KW diabetes mellitus; rheumatoid arthritis; renal disease; inflammation;
KW B-cell maturation receptor; BCMA; receptor.
XX
OS Homo sapiens.
XX
PN MO200294852-A2.
XX
PD 28-NOV-2002.
XX
PF 20-MAY-2002; 2002WO-US015910.
XX
PR 24-MAY-2001; 2001US-0293343P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Rixon MW, Gross JA;
XX
DR MPI; 2003-148455/14.
XX
N-PSDB; AAD53754.
XX
PT Transmembrane activator and calcium modulator and cyclophilin ligand-
PT interactor (TACI)-immunoglobulin fusion protein, for treating cancer or
PT diabetes, comprises a TACI receptor group and an immunoglobulin group.
XX
PS Disclosure; Col 100; 71pp; English.
XX
XX The invention relates to fusion proteins comprising transmembrane
CC activator and calcium modulator and cyclophilin ligand-interactor (TACI)
CC receptor group that binds tumour necrosis factor-like protein (ZTNF2 or
CC ZTNF4; and an immunoglobulin group comprising a constant region of an
CC immunoglobulin. The invention is used to manufacture a medicament for
CC inhibiting the proliferation of tumour cells in a mammalian subject. The
CC composition comprising the fusion protein may also be used in treating
CC autoimmune diseases (e.g. systemic lupus erythematosus, multiple
CC sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal
CC diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft
CC rejection, anaemia and septic shock. The fusion proteins are also used in
CC gene therapy. The present sequence is human B-cell maturation receptor

CC (BCMA) protein used in the invention
XX
SQ Sequence 184 AA;
Query Match 100.0%; Score 283; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLOMAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORXCNASVTNSVKG 51
1 MLOMAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORXCNASVTNSVKG 51
DB 1 MLOMAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORXCNASVTNSVKG 51
RESULT 12
ADA49361 standard; protein; 184 AA.
XX
AC ADA49361;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human BCMA protein.
XX
KW human; TALI-1; antagonist; immunosuppressive; antineumatic;
KW antiinflammatory; antiarthritic; dermatological; antidiabetic;
KW neuroprotective; antihypertic; antipyretic; nephrotoxic; vasotropic;
KW vaccine; autoimmune disease; rheumatoid arthritis;
KW systemic lupus erythematosus; insulin dependent diabetes mellitus;
KW multiple sclerosis; myasthenia gravis; Grave's disease;
KW autoimmune hemolytic anaemia; autoimmune thrombocytopenic purpura;
KW Goodpasture's syndrome; pemphigus vulgaris; acute rheumatic fever;
KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA.
XX
OS Homo sapiens.
XX
PN WO2003035846-A2.
XX
PD 01-MAY-2003.
XX
PF 24-OCT-2002; 2002WO-US034376.
XX
PR 24-OCT-2001; 2001US-0345106P.
XX
PR 14-JAN-2002; 2002US-034862P.
XX
PR 07-FEB-2002; 2002US-0354966P.
XX
PR 13-AUG-2002; 2002US-0403364P.
XX
PA (NAJBE-) NAT JEWISH MEDICAL & RES CENT.
XX
PI Zhang G, Shu H, Liu Y, Xu L;
XX
DR N-PSDB; ADA49360.
XX
PT Novel TALI-1 antagonist protein useful for inhibiting TALI-1 biological
PT activity in mammal, has a modification in the region connecting beta
PT strands D and E that reduces the biological activity of TALI-1
PT antagonist.
XX
PS Claim 62; Page 613; 618pp; English.
XX
XX The invention relates to a novel TALI-1 antagonist protein, comprising a
CC sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID
CC NO:2, by at least one modification in the region connecting abgr; strands
CC D and E that reduces the biological activity of the TALI-1 antagonist as
CC compared to wild-type TALI-1. A protein of the invention has
CC immunosuppressive, antineumatic, antiinflammatory, antiarthritic,
CC dermatological, antidiabetic, neuroprotective, antihypertic, antipyretic,
CC nephrotoxic, and vasotropic activity. A TALI-1 antagonist may be used in
CC a vaccine. A protein of the invention is useful for inhibiting TALI-1
CC biological activity in a mammal. TC is useful for treating autoimmune
CC diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin
CC dependent diabetes mellitus, multiple sclerosis, myasthenia gravis,
CC Grave's disease, autoimmune hemolytic anaemia, autoimmune

CC thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris,
CC acute rheumatic fever, post-streptococcal glomerulonephritis and
CC polyarteritis nodosa. The present sequence represents human BCMA.
XX
SQ Sequence 184 AA;
Query Match 100.0%; Score 283; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MLQWAGQCSQNEYFDSLHACIPQRLRCSSNTPPLTCORYCNASVTNSVGK 51
DB 1 MLQWAGQCSQNEYFDSLHACIPQRLRCSSNTPPLTCORYCNASVTNSVGK 51
RESULT 13
ABP60552
ID ABP60552 standard; protein; 184 AA.
XX
AC ABP60552;
XX
DE 28-MAR-2003 (first entry)
XX
DE Human tumour necrosis factor BCMA.
XX
APRIL; scFv; immunospecific; tumour necrosis factor delta; TNF-delta;
XX dermatological; immunosuppressive; antiinflammatory; antirheumatic;
XX antitachyarrhythmic; cytoskeletal; antianemic; antiallergic; antidiabetic;
XX neuroprotective; ophthalmological; tuberculosic; antidiabetic;
XX antipsoriatic; anti-HIV; antiatherosclerotic; vasotropic; thymimetic;
XX haemostatic; cancer; autoimmune disease; graft versus host disease; GVHD;
XX inflammatory disorder; proliferative disorder; single chain antibody;
XX antibody; human; BCMA; tumour necrosis factor.
XX
OS Homo sapiens.
XX
PN WO200294192-A2.
XX
PD 28-NOV-2002.
XX
PF 22-MAY-2002; 2002WO-US016106.
XX
PR 24-MAY-2001; 2001US-0293100P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM;
XX
DR WPI; 2003-156740/15.
XX
PT Novel isolated antibody that immunospecifically binds tumor necrosis
XX factor delta, useful for treating, preventing or ameliorating Non-
XX Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's
XX syndrome.
XX
PS Disclosure; Page 222; 225pp; English.
XX
XX The invention relates to a novel antibody or its fragment, which
XX immunospecifically binds tumour necrosis factor Delta (TNF-delta/APRIL).
XX The antibody of the invention has dermatological, immunosuppressive,
XX antiinflammatory, antirheumatic, antitachyarrhythmic, antidiabetic,
XX antiallergic, antiaesthetic, neuroprotective, cytoskeletal, antianemic,
XX tuberculosic, antidiabetic, antipsoriatic, ophthalmological,
XX antiatherosclerotic, vasotropic, thymimetic, and haemostatic activity.
XX The antibody or its fragment are useful for treating, preventing or
XX ameliorating cancer such as Non-Hodgkin's lymphoma or multiple myeloma in
XX human, disease or disorder such as autoimmune disease, and graft versus
XX host disease (GVHD). The autoimmune disease is systemic lupus
XX erythematosus, rheumatoid arthritis or Sjogren's syndrome. The antibody
XX is useful for detecting, diagnosing, prognosing, treating, preventing or
XX ameliorating a disease or disorder associated with aberrant APRIL or
XX APRIL receptor expression or aberrant function of APRIL or APRIL
XX receptor. The disease or disorders includes autoimmune and inflammatory

CC disorders such as autoimmune neutropenia, haemolytic anaemia, dermatitis,
CC asthma, allergic encephalomyelitis, myocarditis, multiple sclerosis,
CC uveitis, tuberculosis, diabetes mellitus, psoriasis, cancer of the immune
CC system, particularly B cell cancers, immune disorders such as myasthenia
CC gravis, Hashimoto's disease, immunodeficiency syndrome, Bruton's disease,
CC infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS)), and
CC proliferative disorders (e.g. leukemia). The present sequence represents
CC the tumour necrosis factor BCMA
XX
SQ Sequence 184 AA;
Query Match 100.0%; Score 283; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MLQWAGQCSQNEYFDSLHACIPQRLRCSSNTPPLTCORYCNASVTNSVGK 51
DB 1 MLQWAGQCSQNEYFDSLHACIPQRLRCSSNTPPLTCORYCNASVTNSVGK 51
RESULT 14
ABP97717
ID ABP97717 standard; protein; 184 AA.
XX
AC ABP97717;
XX
DE 28-MAY-2003 (first entry)
XX
DE Amino acid sequence of human BCMA receptor.
XX
XX Human; TACI; BR3; receptor; tumour necrosis factor ligand; TNF ligand;
XX TALL-1; APRIL; systemic lupus erythematosus; BCMA.
XX
OS Homo sapiens.
XX
PN WO2003014294-A2.
XX
PD 20-FEB-2003.
XX
PF 24-JUL-2002; 2002WO-US023487.
XX
PR 03-AUG-2001; 2001US-0310114P.
XX
PR 30-APR-2002; 2002US-0377171P.
XX
PA (GETH) GENENTECH INC.
XX
PI Dixit V, Grewal I, Ridgway J, Yan M;
XX
DR WPI; 2003-256560/25.
XX
DR N-PSDB; AB268871.
XX
PT New nucleic acid encoding a TACIs or BR3 polypeptide, useful for
XX preparing a composition for treating systemic lupus erythematosus.
XX
PS Disclosure; Fig 2; 153pp; English.
XX
XX The present sequence represents a human BCMA polypeptide. The
XX specification also describes TACI and BR3 polypeptides. TACI and BR3 are
XX receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and APRIL
XX bind to the TACI receptor, while TNF family ligands TALL-1 also binds to
XX BR3 receptor. The TACI and BR3 receptor nucleic acid is useful for
XX preparing a composition for treating systemic lupus erythematosus
XX
SQ Sequence 184 AA;
Query Match 100.0%; Score 283; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MLQWAGQCSQNEYFDSLHACIPQRLRCSSNTPPLTCORYCNASVTNSVGK 51
DB 1 MLQWAGQCSQNEYFDSLHACIPQRLRCSSNTPPLTCORYCNASVTNSVGK 51

RESULT 15

ADD67527
ID ADD67527 standard; protein; 184 AA.

AC ADD67527;

DT 15-JAN-2004 (first entry)

DE Human Ly1732P protein SEQ ID NO:4.

haematological malignancy; immunconjugate; cytostatic; immunostimulant;
vaccine; immunotherapy; cancer; multiple myeloma cell;
chronic lymphocytic leukaemia; B cell leukaemia; lymphoma; anti-cancer;
human.

OS Homo sapiens.

PN WO2003062401-A2.

PD 31-JUL-2003.

PF 22-JAN-2003; 2003WO-US002353.

PR 22-JAN-2002; 2002US-00057475.

PA (CORI-) CORIXA CORP.

PI Gaiger A, Algate PA, Mannion J, Clapper JD, Wang A, Ordonez N;
PI Carter L, McNeill PD,

DR WPI; 2003-598749/56.

DR N-PSDB; ADD67526.

New hematological malignancy-related genes and polypeptides, useful for
screening anti-cancer agents, and generating antibodies or
immunconjugates for treating e.g. multiple myeloma cell or chronic
lymphocytic leukemia.

PT Claim 9; SEQ ID NO 4; 307pp; English.

The present invention describes an isolated polynucleotide (1), which is
overexpressed in haematological malignancies, and which encodes a
polypeptide or an immunogenic fragment of the polypeptide. Also
described: (1) an isolated polypeptide; (2) an expression vector
comprising (1) operably linked to an expression control sequence; (3) a
host cell comprising an expression vector; (4) an isolated antibody that
specifically binds to the polypeptide or its immunogenic fragment; and
(5) immunconjugates comprising the antibody above, or an antibody that
specifically binds to a polypeptide, or its immunogenic fragment, encoded
by (1). (1) has cytostatic and immunostimulant activities, and can be
used in vaccines and immunotherapy. The immunconjugates are useful in
the manufacture of a medicament, particularly as active ingredients in a
composition for treating cancer, e.g. multiple myeloma cell, chronic
lymphocytic leukaemia, B cell leukaemias, or lymphomas in humans, sheep,
primates, goats, bovines, equines, porcines, lupines, canines or felines.
The polynucleotide (1) or polypeptide can be used for screening anti-
cancer agents, and generating antibodies or immunconjugates for treating
or preventing the above-mentioned diseases. The polynucleotide,
polypeptide or antibody can be used for detecting, diagnosing or
prognosticating the haematological malignancies described above. The
present sequence is used in the exemplification of the present invention.

CC Sequence 184 AA;

Query Match 100.0%; Score 283; DB 7; Length 184;

Best Local Similarity 100.0%; Pred. No. 1.5e-25; Mismatches 0; Indels 0; Gaps 0;

1 MLQMAQGSQNEYPDSLHACIPQRLRCSSNTPPLTCRCRYCNASTVNSVK 51
1 MLQMAQGSQNEYPDSLHACIPQRLRCSSNTPPLTCRCRYCNASTVNSVK 51

RESULT 16

ADG43715
ID ADG43715 standard; protein; 184 AA.

AC ADG43715;

DT 26-FEB-2004 (first entry)

DE Human B-cell maturation antigen SEQ ID NO:1.

human; neurodegenerative immunological disorder; demyelination;
Central Nervous System; CNS; inflammation; B-cell maturation antigen;
BCMA; multiple sclerosis; neuroprotective; nootropic; antiinflammatory;
gene therapy.

OS Homo sapiens.

PN WO2003072713-A2.

PD 04-SEP-2003.

PF 21-FEB-2003; 2003WO-US005147.

PR 21-FEB-2002; 2002US-0358427P.

PA (BIOD) BIOGEN INC.

PI Kalled SL, Reid H;

DR WPI; 2003-721758/68.

DR N-PSDB; ADG43716.

Treating a neurodegenerative immunological disorder, e.g. demyelination
or inflammation in a mammal comprises administering a B-cell maturation
antigen (BCMA), an antibody against BCMA or a BCMA ligand.

PT Claim 8; Page 68-69; 72pp; English.

The invention relates to a novel method for treating a neurodegenerative
immunological disorder, demyelination or Central Nervous System (CNS)
inflammation in a mammal. The method comprises administering B-cell
maturation antigen (BCMA), or an antibody against BCMA or a BCMA ligand
(the mammal has or is at risk of developing multiple sclerosis). The
method of the invention has neuroprotective, nootropic, and
antiinflammatory activity, and may have a use in gene therapy. The
CC methods, BCMA, and antibodies are useful for treating a neurodegenerative
immunological disorder such as multiple sclerosis, demyelination or CNS
inflammation. The present sequence represents human BCMA.

CC Sequence 184 AA;

Query Match 100.0%; Score 283; DB 7; Length 184;

Best Local Similarity 100.0%; Pred. No. 1.5e-25; Mismatches 0; Indels 0; Gaps 0;

1 MLQMAQGSQNEYPDSLHACIPQRLRCSSNTPPLTCRCRYCNASTVNSVK 51
1 MLQMAQGSQNEYPDSLHACIPQRLRCSSNTPPLTCRCRYCNASTVNSVK 51

RESULT 17

ADK00756
ID ADK00756 standard; protein; 184 AA.

AC ADK00756;

DT 06-MAY-2004 (first entry)

DE Native human BCMA.

CAM1, interactor receptor; TAC1; Cytostatic; Antiinflammatory;
Dermatological; Immunosuppressive; Antirheumatic; Antiarthritic;

| | |
|-----------|---|
| KW | Antiidiabetic; Neuroprotective; Antiasthmatic; Anti-allergic; Anti-HIV; |
| KM | Antibacterial; antiparasitic; systemic lupus erythematosus; |
| KW | diabetes mellitus; AIDS; BCMA. |
| OS | |
| XX | Homo sapiens. |
| PN | MO2004011611-A2. |
| XX | |
| PD | 05-FEB-2004. |
| XX | |
| PF | 25-JUL-2003; 2003WO-US023421. |
| XX | |
| PR | 25-JUL-2002; 2002US-0398530P. |
| XX | |
| PA | (GETH) GENENTECH INC. |
| XX | |
| PI | Chuntharapai A, Grewal I, Kim KJ, Yan M; |
| DR | WPI, 2004-143841/14. |
| XX | |
| DR | N-PSDB; ADR00755. |
| PT | New anti-TACI receptor monoclonal antibody, useful for diagnosing and |
| XX | treating pathological conditions associated with tumor necrosis factor, |
| PT | e.g. cancer or immune-related disease, such as Rheumatoid arthritis or |
| XX | psoriasis. |
| PS | |
| XX | Disclosure; SEQ ID NO 6; 110pp; English. |
| CC | |
| CC | The present invention relates to an isolated monoclonal antibody which |
| CC | binds to a transmembrane activator of and CML interactor (TRAC1) |
| CC | receptor. The TRAC1 antibodies are useful for modulating TALL-1 or TRAC1 |
| CC | polypeptide biological activity in mammalian cells, or for diagnosing and |
| CC | treating pathological conditions associated with TNF and TNF receptor- |
| CC | related molecules, e.g. cancer or immune-related disease, such as |
| CC | systemic lupus erythematosus, rheumatoid arthritis, Sjogren's syndrome, |
| CC | systemic vasculitis, diabetes mellitus, Crohn's disease, |
| CC | glomerulonephritis, multiple sclerosis, psoriasis, asthma, urticaria or |
| CC | infectious diseases including AIDS, hepatitis infection, bacterial |
| CC | infection, fungal infection, protozoal infection and parasitic infection. |
| CC | The present sequence represents native human BCMA. |
| XX | |
| XX | Sequence 184 AA; |
| SO | |
| | Query Match 100.0%; Score 283; DB 8; Length 184; |
| | Best Local Similarity 100.0%; Pred. NO. 1.5e-25; |
| | Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0. |
| QY | 1 M:OMAGGCGSNGEFPDSLTHACIPCCOLRGSSNPPILTCORRYCNASVTVSKG 51 |
| | |
| DB | 1 M:OMAGGCGSNGEFPDSLTHACIPCCOLRGSSNPPILTCORRYCNASVTVSKG 51 |
| | |
| RESULT 18 | |
| ADQ94442 | |
| ID | ADQ94442 standard; protein; 184 AA. |
| XX | |
| AC | ADQ94442; |
| XX | |
| DT | 07-OCT-2004 (first entry) |
| DE | |
| XX | Neutrokin-alpha, BCMA. |
| KW | neutrokin-alpha; chelator; B-lymphocyte stimulator; BlyS; TALL-1; THANK; |
| KM | BAF; neutrokin-alpha receptor; complex; metal ion; radiotherapy; |
| KW | B-cell mediated disease; non-Hodgkin's lymphoma; |
| KM | chronic lymphocytic leukaemia; multiple myeloma; |
| KW | systemic lupus erythematosus; rheumatoid arthritis; multiple sclerosis; |
| KM | Crohn's disease; diabetes; Wegener's granulomatosis; myasthenia gravis; |
| KW | asthma; cancer; Sjogren's syndrome; diagnostic imaging; lymphocyte; |
| KM | B cell; cancerous cell; metastasis; lymphatic system. |
| OS | |
| XX | Homo sapiens. |

| | | |
|-----------|--|---|
| XX | NX | MOZ004058309-AI. |
| XX | PD | 15-JUL-2004. |
| XX | PF | 22-DEC-2003; 2003WO-USO40979. |
| XX | PR | 23-DEC-2002; 2002US-O435262P. |
| XX | PR | 02-MAY-2003; 2003US-O467198P. |
| XX | PA | (HUMA-) HUMAN GENOME SCI INC. |
| XX | P1 | Parmelee D, Yeh R, Galperina O, Hilbert D, Rosen CA; |
| XX | DR | WPI; 2004-553134/53. |
| XX | DR | N-PSDB; ADO94441. |
| XX | DR | GEMBAK; NM_001192. |
| XX | PT | Neutrokin-alpha conjugate useful for targeting complexed metal ion to |
| XX | PT | cells expressing receptor (predominantly lymphoid) for radiotherapy |
| XX | PT | treatment of, for example, non-Hodgkin's lymphoma comprises neutrokin- |
| XX | PT | alpha protein and chelator. |
| XX | PS | Disclosure: SEQ ID NO 9; 228bp; English. |
| XX | CC | This sequence represents neutrokin-alpha, BCMA, which may be used in the |
| XX | CC | protein conjugate of the invention. The neutrokin-alpha protein |
| XX | CC | conjugate comprises neutrokin-alpha protein and chelator, where the |
| XX | CC | neutrokin-alpha protein (also known as B-lymphocyte stimulator (BLyS), |
| XX | CC | TALL-1, THANK and BAFF) is capable of binding neutrokin-alpha receptor |
| XX | CC | and is selected from full length or mature neutrokin-alpha protein. The |
| XX | CC | protein conjugate of the invention is useful in a complex with a metal |
| XX | CC | ion associated with the chelator which is useful for administering |
| XX | CC | radiotherapy to a subject such as human who is in need of radiotherapy, |
| XX | CC | which involves administering the complex to the subject, where it is |
| XX | CC | administered as an injectable solution, and the subject has a B-cell |
| XX | CC | mediated disease. The subject has a condition chosen from non-Hodgkin's |
| XX | CC | lymphoma, chronic lymphocytic leukaemia, multiple myeloma, systemic lupus |
| XX | CC | erythematosus, rheumatoid arthritis, multiple sclerosis, Crohn's disease, |
| XX | CC | diabetes, Wegner's granulomatosis, myasthenia gravis and asthma, |
| XX | CC | preferably non-Hodgkin's lymphoma. The complex is useful for treating |
| XX | CC | cancer, which involves administering it to a subject having cancer, where |
| XX | CC | a cell of the cancer expresses a neutrokin-alpha receptor on its |
| XX | CC | surface. The cancer is a B cell cancer, which is chosen from non- |
| XX | CC | Hodgkin's lymphoma, multiple myeloma and chronic lymphocytic leukaemia. |
| XX | CC | The complex is also useful for treating an autoimmune disease or |
| XX | CC | disorder, chosen from systemic lupus erythematosus, rheumatoid arthritis |
| XX | CC | and Sjogren's syndrome. The complex may also be used for diagnostic |
| XX | CC | imaging. A composition comprising the protein conjugate or the complex is |
| XX | CC | useful for killing a cell chosen from a cell bearing a neutrokin-alpha |
| XX | CC | receptor, and a cell in close proximity to a cell bearing neutrokin- |
| XX | CC | alpha receptor, which involves contacting the cell with the composition |
| XX | CC | to kill the cell. The cell is lymphocyte, B cell or cancerous cell that |
| XX | CC | has metastasised into the lymphatic system. |
| XX | SO | Sequence 184 AA; |
| XX | Query_Match | 100.0%; Score 283; DB 8; Length 184; |
| XX | Best Local Similarity | 100.0%; Pred.No.1.5e-25; |
| XX | Matches 51; Conservative | 100.0%; Mismatches 0; Indels 0; Gaps 0; |
| OY | 1 MLQMGAGCSQNEYPDSLHACIPCOLRCSSTPPLTCORNCNASVTNSVKG 51 | |
| Db | 1 MLQMGAGCSQNEYPDSLHACIPCOLRCSSTPPLTCORNCNASVTNSVKG 51 | |
| RESULT 19 | | |
| ID | ADP56014 | |
| XX | ADP56014 standard; protein; 184 AA. | |
| DT | 18-NOV-2004 (first entry) | |

DE Human PRO protein sequence SEQ ID NO:1990.
 XX human; PRO; immune related disease; inflammatory immune response;
 KW immune response stimulation; antiallergic; antihaemic; antiarthritic;
 KW antisthmatic; antidiabetic; antiinflammatory; antipsoiatic;
 KW antineumatic; antithyroid; CNS; dermatological; gastrointestinal;
 KW haemostatic; hepatotropic; immunosuppressive; muscular;
 KW nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;
 KW varicide; gene therapy.
 XX Homo sapiens.
 OS
 XX WO2004039956-A2.
 PN
 XX 13-MAY-2004.
 PD
 XX 28-OCT-2003; 2003WO-US034381.
 PF
 XX 29-OCT-2002; 2002US-0422472P.
 PR
 XX (GETH) GENENTECH INC.
 PA
 XX Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM;
 PI Wood WI, Wu TP;
 DR MPI; 2004-376182/35.
 N-PSDB; ADP56013.
 XX
 PT New PRO polynucleotides and polypeptides, useful in useful in diagnosing
 PT and treating an immune related disease, e.g. systemic lupus
 PT erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in
 PT stimulating an immune response.
 PT
 XX Claim 1; SEQ ID NO 1990; 3009pp; English.
 PS
 XX
 CC The present invention describes an isolated PRO nucleic acid (1). Also
 CC described: (1) a vector comprising (1); (2) a host cell comprising the
 CC vector of (1); (3) a process for producing a PRO polypeptide; (4) an
 CC isolated PRO polypeptide; (5) a chimeric molecule comprising the
 CC polypeptide of (4) fused to a heterologous amino acid sequence; (6) an
 CC antibody which specifically binds to a polypeptide of (4); (7) a
 CC composition of matter comprising a polypeptide of (4), an agonist or
 CC antagonist of the polypeptide or an antibody that binds to the
 CC polypeptide in combination with a carrier; (8) an article of manufacture
 CC comprising a container, a label on the container and a composition of
 CC matter of (7); (9) a method of treating an immune related disease in a
 CC mammal; (10) a method for determining the presence of a PRO polypeptide
 CC in a sample suspected of having the polypeptide; (11) a method of
 CC diagnosing an immune related disease or an inflammatory immune response
 CC in mammal; (12) a method of identifying a compound that inhibits or
 CC mimics the activity of or expression of a gene encoding a PRO polypeptide
 CC; and (13) a method of stimulating the immune response in a mammal. The
 CC PRO sequences have antiallergic, antihaemic, antiarthritic, the
 CC antisthmatic, antidiabetic, antiinflammatory, antipsoiatic,
 CC antineumatic, antithyroid, CNS, dermatological, gastrointestinal,
 CC hepatotropic, hepatotropic, immunosuppressive, muscular,
 CC nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and
 CC virocidic activities, and can be used in gene therapy. The nucleic acid
 CC (1) and the encoded polypeptides, compositions, kits and methods are
 CC useful in diagnosing and treating an immune related disease and in
 CC stimulating an immune response. The present sequence represents a human
 CC PRO protein from the present invention.
 CC
 SQ Sequence 184 AA;
 XX
 QY Query Match 100.0%; Score 283; DB 8; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.5e-25;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 MLQMAQCQSQNEFYDLSLHACIPQQLRCSSNTPLTCORYCNASVTNSVGK 51
 1 MLQMAQCQSQNEFYDLSLHACIPQQLRCSSNTPLTCORYCNASVTNSVGK 51

RESULT 20
 ADW03432
 ID ADW03432 standard; protein; 184 AA.
 XX
 AC ADW03432;
 XX
 DT 24-MAR-2005 (first entry)
 XX
 DE Human BCMA protein amino acid sequence.
 XX
 KW B-lymphocyte; b-cell lymphoma; autoimmune disease; immunosuppressive;
 KW non-hodgkin lymphoma; hodgkins disease; cytostatic;
 KW chronic lymphocytic leukemia; hairy cell leukemia; rheumatoid arthritis;
 KW antiarthritic; antineumatic; systemic lupus erythematosus;
 KW Wegener granulomatosis; antiallergic; antiinflammatory; vasotropic;
 KW inflammatory bowel disease; gastrointestinal-gen.;
 KW idiopathic thrombocytopenic purpura; hemostatic; multiple sclerosis;
 KW asthma; antisthmatic; psoriasis; antipsoiatic; myasthenia gravis;
 KW muscular-gen.; neuroprotective; vasculitis; diabetes; antidiabetic;
 KW glomerulonephritis; nephrotropic; BCMA.
 XX
 OS Homo sapiens.
 XX
 PN WO2005000351-A2.
 XX
 PD 06-JAN-2005.
 XX
 PF 04-JUN-2004; 2004WO-US017693.
 PR 05-JUN-2003; 2003US-0476414P.
 PR 05-JUN-2003; 2003US-0476481P.
 PR 06-JUN-2003; 2003US-0476531P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Chan A, Gong Q, Martin F;
 DR MPI; 2005-058069/06.
 N-PSDB; ADW03431.
 XX
 PT Depleting B cells from a mixed population of cells by contacting the
 PT cells with a Blys antagonist and a CD20 binding antibody, useful for
 PT treating B cell malignancies and autoimmune disorders.
 XX
 PS Disclosure; Fig 2; 114pp; English.
 CC The invention comprises a method of depleting B cells from a mixed
 CC population of cells, the method involves contacting the mixed population
 CC of cells with Blys antagonist (e.g. an immunoadhesin) and a CD20 binding
 CC antibody (e.g. hu2H7.v16). The method of the invention is useful for
 CC treating B cell malignancies and autoimmune disorders, such as: non-
 CC Hodgkin's lymphoma, Hodgkin's disease, follicular center cell lymphomas,
 CC lymphocytic leukemia, hairy cell leukemia, rheumatoid arthritis, systemic
 CC lupus erythematosus, Wegener's disease, inflammatory bowel disease,
 CC idiopathic thrombocytopenic purpura, multiple sclerosis, asthma,
 CC psoriasis, Iga nephropathy, myasthenia gravis, vasculitis, diabetes and
 CC glomerulonephritis. The present amino acid sequence represents a human
 CC BCMA protein.
 CC
 SQ Sequence 184 AA;
 XX
 QY Query Match 100.0%; Score 283; DB 9; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.5e-25;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 MLQMAQCQSQNEFYDLSLHACIPQQLRCSSNTPLTCORYCNASVTNSVGK 51
 1 MLQMAQCQSQNEFYDLSLHACIPQQLRCSSNTPLTCORYCNASVTNSVGK 51
 RESULT 21
 AD267760

```
ID AD267760 standard; protein; 184 AA.
XX
XX AD267760;
AC
XX 14-JUL-2005 (first entry)
DT
XX Human tumor necrosis factor receptor BCMA.
DE
XX Tumor necrosis factor receptor BCMA.
XX cytostatic.
KM
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH Domain 6..45
FT /note= "Cys-rich domain"
FT
XX WO2005037865-A2.
XX
XX 28-APR-2005.
XX
XX 18-OCT-2004; 2004WO-US034375.
XX
XX 16-OCT-2003; 2003US-0511698P.
XX
XX 18-OCT-2004; 2004US-0619552P.
XX
XX (Zymo ) ZYMOGENETICS INC.
XX
XX Fox BA, Holloway JL, Sheppard PO, Dillon SR;
XX
XX WPI; 2005-315682/32.
XX
XX New tumor necrosis factor receptor (TNFR) polypeptides, useful as
XX detecting ligands, and for modulating tumor growth, metastasis and
XX immunity, such as separating resting from stimulated immune cells.
XX
XX Disclosure; SEQ ID NO 8; 133pp; English.
XX
XX The invention provides novel tumor necrosis factor receptor ztnfr14
XX polynucleotides AD267753 and polypeptides AD267754, expression vectors
XX and antibodies. Ztnfr14 polynucleotides are used in claimed methods for
XX detecting a genetic abnormality in a patient and for detecting a cancer
XX in a patient. Recombinant ztnfr14 polypeptide, optionally conjugated to a
XX toxin, is used in a claimed method of killing cancer cells. Ztnfr14
XX polypeptides can be used to detect ligands, agonists and antagonists. The
XX polypeptides, polynucleotides and antibodies may also be used in methods
XX that modulate tumor growth, metastasis, and immunity such as separating
XX resting from stimulated immune cells. The present sequence is that of
XX human TNFR BCMA. This sequence was compared with that of ztnfr14 in the
XX identification of ztnfr14 as a member of the TNFR family.
XX
XX Sequence 184 AA:
SQ
XX
XX Query Match 100.0%; Score 283; DB 9; Length 184;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-25;
XX Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MLOMAGGCSQNEYPFDSLHACIPCOLRCSNTPTTCORYCNASTVNSVGK 51
DB 1 MLOMAGGCSQNEYPFDSLHACIPCOLRCSNTPTTCORYCNASTVNSVGK 51
XX
XX
XX RESULT 22
XX AEA23348
XX ID AEA23348 standard; protein; 184 AA.
XX
XX AEA23348;
AC
XX 11-AUG-2005 (first entry)
DT
XX Tumor antigen of hematopoietic origin TAO23.
XX
XX cytostatic; gene therapy; therapy; cell growth; protein purification;
XX
```

```
KM DNA purification; hyperproliferation; neoplasm;
XX tumor antigen of hematopoietic origin; TAO23.
XX
XX Homo sapiens.
OS
XX WO2005049075-A2.
XX
XX 02-JUN-2005.
XX
XX 16-NOV-2004; 2004WO-US038262.
XX
XX 17-NOV-2003; 2003US-0520842P.
XX
XX 24-DEC-2003; 2003US-0532426P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Crowley C, Desauvage FJ, Eaton DL, Ebens A, Polson A, Smith V;
XX
XX WPI; 2005-405198/41.
XX
XX N-PSDB; AEA23347.
XX
XX Inhibiting the growth of a cell that expresses a protein by contacting
XX the cell with anti-tumor antigens of hematopoietic origin (TAO23)
XX polypeptide, antibody or organic molecule, useful for treating
XX hematopoietic and malignant tumors.
XX
XX Disclosure; SEQ ID NO 46; 367pp; English.
XX
XX The invention describes a method of inhibiting the growth of a cell that
XX expresses a protein comprising contacting the cell with an antibody,
XX oligopeptide or organic molecule that binds to the protein, the binding
XX of the antibody, oligopeptide or organic molecule to the protein and
XX causing an inhibition of growth of the cell. Also described is a method
XX for treating or preventing a cell proliferative disorder associated with
XX increased expression or activity of a protein having at least 80 % amino
XX acid sequence identity to: a polypeptide having any of SEQ ID NO: 2, 8,
XX 10, 12, 16, 20, 22, 49 and 51; a polypeptide having the amino acid
XX sequence of (a), lacking its associated signal peptide; an extracellular
XX domain of the polypeptide having the amino acid sequence of (a), with or
XX without its associated signal peptide; a polypeptide encoded by any of
XX SEQ ID NO: 1, 7, 9, 11, 15, 19, 21, 48 and 50; or a polypeptide encoded
XX by the full-length coding region of the nucleotide sequence of (d),
XX comprising administering to a subject in need of such treatment an
XX antagonist of the protein, and effectively treating or preventing the
XX cell proliferative disorder. Also disclosed are anti-tumor antigens of
XX hematopoietic origin (TAO23) polypeptides, encoding nucleic acids,
XX oligopeptides, vectors, host cells and antibodies used in the methods of
XX the invention. The methods and compositions of the present invention are
XX useful for treating hematopoietic and malignant tumors in mammals. This
XX is the amino acid sequence of tumor antigen of hematopoietic origin
XX TAO23.
XX
XX Sequence 184 AA:
SQ
XX
XX Query Match 100.0%; Score 283; DB 9; Length 184;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-25;
XX Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MLOMAGGCSQNEYPFDSLHACIPCOLRCSNTPTTCORYCNASTVNSVGK 51
DB 1 MLOMAGGCSQNEYPFDSLHACIPCOLRCSNTPTTCORYCNASTVNSVGK 51
XX
XX
XX RESULT 23
XX AEC02031
XX ID AEC02031 standard; protein; 184 AA.
XX
XX AEC02031;
AC
XX 20-OCT-2005 (first entry)
DT
XX Amin acid sequence of a BCMA protein.
XX
XX
```

KM APRIL; BAFf; immune disorder; immunomodulator; antiinflammatory; cancer;
 KW cytostatic; neoplasm; immunosuppressive; therapeutic; BCMA;
 KM B-cell maturation antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO2005075511-A1.
 XX
 PD 18-AUG-2005.
 XX
 PF 04-AUG-2004; 2004WO-US025247.
 XX
 PR 29-JAN-2004; 2004US-0540271P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Kelley RF, Patel D;
 XX
 DR WPI; 2005-555932/56.
 XX
 PT New polypeptides that inhibit APRIL and/or BAFf binding to BCMA, useful
 PT for treating immune-related disease, cancer or T-cell mediated disease
 PT such as graft rejection, graft versus host disease (GVHD) and
 PT inflammation.
 XX
 PS Disclosure; SEQ ID NO 20; 140pp; English.
 XX
 CC The specification describes polypeptides that bind April or BAFf. The
 CC polypeptides inhibit APRIL or BAFf binding to B-cell maturation antigen
 CC (BCMA). APRIL and BAFf are tumor necrosis family (TNF) members. The
 CC polypeptides of the invention are useful for treating immune-related
 CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
 CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
 CC scleroma; or T-cell mediated disease such as graft rejection, graft
 CC versus host disease (GVHD) and inflammation. The present sequence
 CC represents a BCMA protein.
 XX
 SQ Sequence 184 AA;
 XX
 Query Match 100.0%; Score 283; DB 9; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.5e-25;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MCGMAGCGSQNEYPFSLHACIPCOLRCSSNPPLTCQRCYCNASTNSVKG 51
 DB 1 MCGMAGCGSQNEYPFSLHACIPCOLRCSSNPPLTCQRCYCNASTNSVKG 51
 RESULT 24
 ID AAB60699 standard; protein; 302 AA.
 XX
 AC AAB60699;
 XX
 DT 11-SEP-2003 (revised)
 DT 22-MAY-2001 (first entry)
 XX
 DE Mouse IgG signal/human BAFf-R/human IgG Fc fusion protein, BAFf-R-Fc.
 XX
 KM Human BAFf-R; BAFf receptor; TNF family; immunoregulatory agent;
 KM immune-related disorder; B-cell growth inhibitor;
 KM B-cell maturation inhibitor; immunoglobulin production inhibitor;
 KM autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
 KM renal disorder; immunosuppressive disorder; HIV infection;
 KM organ transplantation; antiinflammatory; systemic lupus erythematosus;
 KM autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
 KM B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
 KM lymphoma; gene therapy; cancer; tumour; IgG Fc; fusion construct.
 XX
 OS Homo sapiens.
 OS Mus sp.
 OS Chimeric.
 XX

PN WO200112812-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 16-AUG-2000; 2000WO-US022507.
 XX
 PR 17-AUG-1999; 99US-0149378P.
 PR 11-FEB-2000; 2000US-0181684P.
 PR 18-FEB-2000; 2000US-01893536P.
 XX
 PA (BIOL) BIOGEN INC.
 PA (APOT-) APOTEC R & D SA.
 XX
 PI Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;
 XX Thompson J;
 XX
 DR WPI; 2001-202866/20.
 DR N-PSDB; AAF59999.
 XX
 PT Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
 PT lympho-proliferative disorder by administering BAFf-receptor polypeptide,
 PT chimeric molecule comprising receptor or anti-BAFf-R antibody homolog.
 XX
 PS Example 4; Fig 2; 59pp; English.
 XX
 CC The invention relates to the use of a BAFf receptor (BAFf-R, also known
 CC as BCMA) protein, or a BAFf-R fusion protein as an agent for the
 CC treatment of a variety of immune-related disorders. BAFf-R is a member of
 CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory
 CC agent, and also plays a role in the development of hypertension and
 CC related disorders. BAFf-R, fusion proteins containing it, and BAFf-R-
 CC specific antibodies can be used for inhibiting B-cell growth, dendritic
 CC cell-induced B-cell growth and maturation, and immunoglobulin production,
 CC and in the treatment of autoimmune disorders. B-cell lymphoproliferative
 CC disorders, hypertension and renal disorders. The BAFf-R proteins may also
 CC be used in the treatment of immunosuppressive disorders and HIV
 CC infection, and in patients undergoing organ transplantation. The BAFf-R
 CC proteins or BAFf-R specific antibodies may be used for treating,
 CC suppressing or altering an immune response involving a signalling pathway
 CC between BAFf-R and BAFf, thereby inhibiting inflammation. Since BAFf-R
 CC inhibits B-cell growth and maturation it is useful for treating diseases
 CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
 CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
 CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
 CC human BAFf-R may be used in gene therapy to treat tumours, lymphomas,
 CC autoimmune disorders and inherited B-cell-associated disorders. The
 CC present sequence represents the BAFf-R fusion protein BAFf-R-Fc,
 CC comprising a mouse IgG-kappa signal sequence, residues 1-153 of human
 CC BAFf-R and a human IgG Fc sequence. (Updated on 11-SEP-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 302 AA;
 XX
 Query Match 100.0%; Score 283; DB 4; Length 302;
 Best Local Similarity 100.0%; Pred. No. 2.5e-25;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MCGMAGCGSQNEYPFSLHACIPCOLRCSSNPPLTCQRCYCNASTNSVKG 51
 DB 24 MCGMAGCGSQNEYPFSLHACIPCOLRCSSNPPLTCQRCYCNASTNSVKG 74
 RESULT 25
 ID AAE00507 standard; protein; 302 AA.
 XX
 AC AAE00507;
 XX
 DT 11-SEP-2003 (revised)
 DT 31-JUL-2001 (first entry)
 XX
 DE Human BCMA-Immunoglobulin G Fc region fusion construct.
 XX

Human: A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic; gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease; carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension; systemic lupus erythematosus; SLE; inflammation; cardiovascular disease; B-cell lympho-proliferative disorder; BCM; immunosuppressive disease; organ transplantation; HIV; human immunodeficiency virus; TNF; murine; tumour necrosis factor; B cell maturation protein; BCMa; fusion protein; immunoglobulin G; IgG; Fc region.

XX Homo sapiens.
OS Mus sp.
OS Chimeric.

XX Key
FH Location/Qualifiers
FT 1..22
FT /label= Signal peptide
FT /note= "Derived from murine Ig kappa sequence"
FT 23..302
FT /label= Mature_human_BcMa_IgG_Fc_fusion_protein
FT 23..302
FT /note= "Derived from human BCMa protein"
FT 24..302
FT /label= Cysteine-rich domain
FT /note= "Derived from human BCMa"
FT 76..302
FT /note= "Derived from human IgG Fc region"

XX Region
XX WO200124811-A1.
XX 12-APR-2001.
XX 05-OCT-2000; 2000WO-US027579.
XX PF 06-OCT-1999; 99US-0157933P.
XX PR 11-FEB-2000; 2000US-0181807P.
XX PR 30-JUN-2000; 2000US-0215688P.
XX (BIOJ) BIOGEN INC.
XX (APOT-) APOTEC R & D SA.
XX PI Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;
XX WPI, 2001-266242/27.
XX DR N-PSDB; AAD03847.
XX PT Treating a mammal for a condition associated with undesired cell
XX PT proliferation such as cancer or carcinoma, comprises administering a
XX PT composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R)
XX PT antagonist.
XX Example 1; Fig 3B; 85pp; English.
XX The invention relates to a method of treating a mammal for a condition
XX associated with undesired cell proliferation such as cancer or carcinoma.
XX The method involves administering a composition comprising A
XX Proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell
XX maturation protein (BCM or BCMa) antagonist that antagonises the
XX interaction between APRIL and its cognate receptor(s). This method is
XX useful for treating undesired cell proliferation such as cancer or
XX carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
XX prostate carcinoma, and other carcinomas whose proliferation is modulated
XX by APRIL. It is also useful for treating autoimmune diseases (Grave's
XX disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular
XX diseases, renal disorders, B-cell lympho-proliferative disorders,
XX immunosuppressive diseases, organ transplantation, inflammation and human
XX immunodeficiency virus (HIV), and for treating, suppressing or altering
XX an immune response involving a signalling pathway between APRIL-R and its
XX ligand. APRIL-R DNA is also useful in gene therapy. The present sequence
XX is a fusion construct containing human APRIL-R also referred as BCMa or
XX BCM protein, Fc region of human immunoglobulin G (IgG) and a signal
XX sequence from murine Ig kappa cDNA. (Updated on 11-SEP-2003 to
XX standardise OS field)

XX SQ Sequence 302 AA;
XX Query Match 100.0%; Score 283; DB 4; Length 302;
XX Best Local Similarity 100.0%; Pred. No. 2.5e-25;
XX Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MLQWAGCQNEYPDSLHACIPCOLRCSNTPTTCORYCNASVTNSVK 51
XX |||||||
XX 24 MLQWAGCQNEYPDSLHACIPCOLRCSNTPTTCORYCNASVTNSVK 74
XX
XX RESULT 26
XX ADG43717
XX ID ADG43717 standard; protein; 302 AA.
XX AC ADG43717;
XX DT 26-FEB-2004 (first entry)
XX XX
XX DE Human B-cell maturation antigen-Fc SEQ ID NO:3.
XX
XX human; neurodegenerative immunological disorder; demyelination;
XX Central Nervous System; CNS; inflammation; B-cell maturation antigen;
XX BCMa; multiple sclerosis; neuroprotective; nootropic; antiinflammatory;
XX gene therapy; mouse.
XX
XX OS Chimeric.
XX OS Homo sapiens.
XX OS Mus sp.
XX
XX Key
FH Location/Qualifiers
FT 1..23
FT /note= "Murine Igkappa signal sequence"
FT 24..74
FT /note= "Human BCMa extracellular domain"
FT 75..302
FT Region
FT /note= "Human Ig heavy chain Fc region"

XX WO2003072713-A2.
XX PN
XX PD 04-SEP-2003.
XX PF 21-FEB-2003; 2003WO-US005147.
XX PR 21-FEB-2002; 2002US-0358427P.
XX (BIOJ) BIOGEN INC.
XX Kalled SL, Reid H;
XX WPI, 2003-721758/68.
XX DR N-PSDB; ADG43718.
XX PT Treating a neurodegenerative immunological disorder, e.g. demyelination
XX PT or inflammation in a mammal comprises administering a B-cell maturation
XX PT antigen (BCM), an antibody against BCMa or a BCMa ligand.
XX Claim 12; Page 70-71; 72pp; English.
XX The invention relates to a novel method for treating a neurodegenerative
XX immunological disorder, demyelination or Central Nervous System (CNS)
XX inflammation in a mammal. The method comprises administering B-cell
XX maturation antigen (BCM), or an antibody against BCMa or a BCMa ligand
XX (the mammal has or is at risk of developing multiple sclerosis). The
XX method of the invention has neuroprotective, nootropic, and
XX antiinflammatory activity, and may have a use in gene therapy. The
XX methods, BCMa, and antibodies are useful for treating a neurodegenerative
XX immunological disorder such as multiple sclerosis, demyelination or CNS
XX inflammation. The present sequence is used in the exemplification of the
XX invention.
XX Sequence 302 AA;

Query Match 100.0%; Score 283; DB 7; Length 302;
Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLCMAQCQCCQNEYPFDSLHACIPQCLRCSSNTPPLTCQRCXCNASVYNSVKG 51
DB 24 MLCMAQCQCCQNEYPFDSLHACIPQCLRCSSNTPPLTCQRCXCNASVYNSVKG 74

RESULT 27

ABR40082
ID ABR40082 standard; protein; 184 AA.

XX ABR40082;

DT 27-JUN-2003 (first entry)

XX Human Genoxit.

XX Human; genoxit; anorectic; antilipemic; antiarteriosclerotic; cardi-
antidiabetic; hypotensive; ophthalmological; neuroprotective;
XX nephrotropic; obesity; Tumour Necrosis Factor Receptor Super Family;
XX Type III transmembrane protein; insulin resistance; atherosclerosis;
XX atheromatous disease; heart disease; hypertension; stroke; syndrome X;
XX diabetes mellitus; hyperlipidaemia; hyperuricaemia.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Domain 1..54 /label= Extracellular_domain

FT Misc-difference 3 /label= Gln, Lys

FT Domain 55..77 /label= Transmembrane_domain

FT Domain 78..184 /label= Intracellular_domain

XX MO2003013582-A1.

XX 20-FEB-2003.

XX 05-AUG-2002; 2002WO-1B003498.

XX 06-AUG-2001; 2001US-0310754P.

XX (GEST) GENSET SA.

XX Lucas J, Dialynas D, Briggs K;

XX WPI; 2003-268160/26.

XX N-PSDB; ACC00340.

XX New use of agonist or antagonist of Genoxit activity for preventing or
PT treating obesity-related diseases or disorders, e.g. hyperlipidemia and
PT atherosclerosis.

XX PS Disclosure; Page 32; 35pp; English.

XX The present invention relates to the use of an agonist or antagonist of
XX Genoxit activity for preventing or treating obesity. Genoxit is a member
XX of the Tumour Necrosis Factor Receptor Super Family and is a Type III
XX transmembrane protein. The agonists or antagonists of the invention are
XX useful for treating or preventing obesity-related diseases or disorders,
XX e.g. obesity, insulin resistance, atherosclerosis, atheromatous disease,
XX heart disease (e.g. cardiac insufficiency, coronary insufficiency, high
XX blood pressure), hypertension, stroke, syndrome X, diabetes mellitus
XX (type I and II), hyperlipidaemia and hyperuricaemia, also diabetic
XX complications, e.g. microangiopathic lesions, ocular lesions,
XX retinopathy, neuropathy and renal lesions

XX Sequence 184 AA;

Query Match 97.9%; Score 277; DB 6; Length 184;
Best Local Similarity 98.0%; Pred. No. 7.7e-25;
Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLCMAQCQCCQNEYPFDSLHACIPQCLRCSSNTPPLTCQRCXCNASVYNSVKG 51
DB 1 MLCMAQCQCCQNEYPFDSLHACIPQCLRCSSNTPPLTCQRCXCNASVYNSVKG 51

RESULT 28

ABG95060
ID ABG95060 standard; protein; 288 AA.

XX ABG95060;

DT 04-DEC-2002 (first entry)

XX Human translocation (4; 16)(q26; p13) protein.

XX Chromosome aberration; oncogenic fusion protein; cancer;
XX Proliferative disease; cellular protein isoform; heat shock protein 90;
XX HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
XX T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
XX acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
XX acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
XX papillary thyroid carcinoma; Ewing's sarcoma; liposarcoma;
XX rhabdomyosarcoma; synovial sarcoma; viral infection.

OS Homo sapiens.

XX MO200269900-A2.

XX 12-SEP-2002.

XX 01-MAR-2002; 2002WO-US006518.

XX 01-MAR-2001; 2001US-0272751P.

XX (CONF-) CONFORMA THERAPEUTICS CORP.

XX Fritz LC, Burrows FT;

XX WPI; 2002-698710/75.

XX N-PSDB; ABS73235.

XX Treating genetically-defined disease associated with chromosomal
PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
PT diseases, involves administering an inhibitor of heat shock protein 90.

XX PS Disclosure; Page 189-190; 389pp; English.

XX The invention describes a method of treating genetically-defined disease
XX associated with chromosomal aberrations yielding oncogenic fusion
XX proteins (I), treating cancerous cells containing (I) in a heterogeneous
XX cell population, treating proliferative diseases associated with mutant
XX protein or cellular protein isoforms (II) dependent on heat shock protein
XX (HSP)-90, or selectively treating cells expressing (II) involving
XX administering HSP90-inhibitor. The method is useful for treating
XX genetically-defined disease with chromosomal aberration yielding
XX oncogenic fusion protein, treating cancerous cells containing fusion
XX protein in heterogeneous cell population, treating proliferative disease
XX (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
XX cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
XX p53), or selectively treating cells expressing mutant protein or cellular
XX protein isoform in a patient heterozygous for (II). The method is useful
XX for treating a disease e.g. haematopoietic disorder such as T or B cell
XX lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,
XX or a disease characterised by a solid tumour such as papillary thyroid
XX carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
XX synovial sarcoma. The method is also useful for treating viral
XX infections. This represents a protein encoded by the DNA sequence of a
XX chromosome aberration

SQ Sequence 288 AA; Query Match 96.8%; Score 274; DB 5; Length 288; Best Local Similarity 98.0%; Pred. No. 2.8e-24; Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LOMAGCCSNEYFDSLHACIPCOLRCSNTPTLCORRCNASVTNSVKG 51
106 LKMAQCCGQNEFYFDSLHACIPCOLRCSNTPTLCORRCNASVTNSVKG 155

Db

RESULT 29
AAE15485
ID AAE15485 standard; peptide; 51 AA.
AC AAE15485;
XX
XX
DT 12-MAR-2002 (first entry)
XX
XX
DE Human B-cell maturation (BCMA) protein extracellular domain.
XX
KW Human; transmembrane activator and intracellular CAML interactor; TACI; cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis.
XX
OS Homo sapiens.
XX
PN WO200187979-A2.
XX
PD 22-NOV-2001.
XX
PF 14-MAY-2001; 2001WO-US015567.
XX
PR 12-MAY-2000; 2000US-0204039P.
XX 27-JUN-2000; 2000US-0214591P.
PR 14-MAY-2001; 2001US-00214591.
XX
PA (AMGE-) AMGEN INC.
XX
PI Theell LE, Yu G;
XX
DR WPI; 2002-066686/09.
XX
PT Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family ligand.
PT
PS Claim 1, Fig 10A; 94pp; English.
XX
XX The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF family ligand), having the consensus region of TACI, BCMA, or the TACI/BCMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence

CC is human BCMA protein extracellular domain
XX
SQ Sequence 51 AA; Query Match 95.1%; Score 269; DB 5; Length 51; Best Local Similarity 100.0%; Pred. No. 1.8e-24; Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MAGCCSNEYFDSLHACIPCOLRCSNTPTLCORRCNASVTNSVKG 51
1 MAGCCSNEYFDSLHACIPCOLRCSNTPTLCORRCNASVTNSVKG 48

Db

RESULT 30
AAE15484
ID AAE15484 standard; protein; 181 AA.
AC AAE15484;
XX
XX
DT 12-MAR-2002 (first entry)
XX
XX
DE Human B-cell maturation (BCMA) protein.
XX
KW Human; transmembrane activator and intracellular CAML interactor; TACI; cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis.
XX
OS Homo sapiens.
XX
PN WO200187979-A2.
XX
PD 22-NOV-2001.
XX
PF 14-MAY-2001; 2001WO-US015567.
XX
PR 12-MAY-2000; 2000US-0204039P.
XX 27-JUN-2000; 2000US-0214591P.
PR 14-MAY-2001; 2001US-00214591.
XX
PA (AMGE-) AMGEN INC.
XX
PI Theell LE, Yu G;
XX
DR WPI; 2002-066686/09.
XX
PT Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family ligand.
PT
PS Disclosure; Fig 10A; 94pp; English.
XX
XX The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF family ligand), having the consensus region of TACI, BCMA, or the TACI/BCMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for treating B-cell or T-cell

CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human BCMA protein
CC
SQ Sequence 181 AA;

Query Match 95.1%; Score 269; DB 5; Length 181;
Best Local Similarity 100.0%; Pred. No. 6.8e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MAGGCSQNEYFDSLHACIPCOLRCSNTPPLTCORNCASVTNSYKG 51
Db 1 MAGGCSQNEYFDSLHACIPCOLRCSNTPPLTCORNCASVTNSYKG 48
|||||

RESULT 31
AAE15488
ID AAE15488 standard; protein; 283 AA.
AC AAE15488;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human BCMA-immunoglobulin Fc region fusion protein.
XX
KW Human: transmembrane activator and intracellular CAML interactor; TACI;
KW lymphostatic; B cell maturation protein; BCMA; tumor necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis; fusion protein.
XX
OS Homo sapiens.
XX
PN WO200187979-A2.
XX
PD 22-NOV-2001.
XX
PF 14-MAY-2001; 2001WO-US015567.
XX
PR 12-MAY-2000; 2000US-0204039P.
PR 27-JUN-2000; 2000US-0214591P.
PR 14-MAY-2001; 2001US-00214591.
XX
PA (AMGE-) AMGEN INC.
XX
PI Theil LE, Yu G;
XX
DR WPI, 2002-066686/09.
XX
PT Inhibiting activity of B cell maturation protein and/or transmembrane
XX PT activator and intracellular cyclophilin ligand interactor, by
XX PT administering a binding partner for APRIL, a tumor necrosis factor family
XX PT ligand.
XX
PS Disclosure; Fig 10B; 94pp; English.
XX
CC The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering a
CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region

CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human BCMA protein-immunoglobulin Fc region fusion protein
CC
SQ Sequence 283 AA;

Query Match 95.1%; Score 269; DB 5; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.1e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MAGGCSQNEYFDSLHACIPCOLRCSNTPPLTCORNCASVTNSYKG 51
Db 1 MAGGCSQNEYFDSLHACIPCOLRCSNTPPLTCORNCASVTNSYKG 48
|||||

RESULT 32
AEC02042
ID AEC02042 standard; protein; 296 AA.
AC AEC02042;
XX
DT 20-OCT-2005 (first entry)
XX
DE Amino acid sequence of a BCMA-Fc fusion protein.
XX
KW APRIL; BAF; immune disorder; immunomodulator; antiinflammatory; cancer;
KW lymphostatic; neoplasm; immunosuppressive; therapeutic; BCMA;
KW B-cell maturation antigen; Fc.
XX
OS Homo sapiens.
XX
PN WO2005075511-A1.
XX
PD 18-AUG-2005.
XX
PF 04-AUG-2004; 2004WO-US025247.
XX
PR 29-JAN-2004; 2004US-0540271P.
XX
PA (GETH) GENENTECH INC.
XX
PI Kelley RF, Patel D;
XX
DR WPI, 2005-555932/56.
XX
PT New polypeptides that inhibit APRIL and/or BAF binding to BCMA, useful
XX PT for treating immune-related disease, cancer or T-cell mediated disease
XX PT such as graft rejection, graft versus host disease (GVHD) and
XX PT inflammation.
XX
PS Example 6; SEQ ID NO 31; 140pp; English.
XX
CC The specification describes polypeptides that bind APRIL or BAF. The
CC polypeptides inhibit APRIL or BAF binding to B-cell maturation antigen
CC (BCMA). APRIL and BAF are tumor necrosis factor (TNF) members. The
CC polypeptides of the invention are useful for treating immune-related
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
CC sclerosis; or T-cell mediated disease such as graft rejection, graft
CC versus host disease (GVHD) and inflammation. The present sequence
CC represents a BCMA-Fc fusion protein, where 122 of BCMA is changed to Iys.

SQ Sequence 296 AA;
Query Match 90.8%; Score 257; DB 9; Length 296;
Best Local Similarity 97.9%; Pred. No. 3.1e-22;
Matches 46; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 5 AGCGSNEYFDSLHACIPQQLRCSNTPPLTCORYCNASVTSYKVG 51
DB 18 AGCGSNEYFDSLHACIPQQLRCSNTPPLTCORYCNASVTSYKVG 64
RESULT 33
ID AAE15501 standard; peptide; 58 AA.
XX AAE15501;
AC AAE15501;
XX 12-MAR-2002 (first entry)
XX
XX
XX Human B cell maturation protein cysteine rich extracellular region.
DE
XX Human; transmembrane activator and intracellular CML interactor; TACI;
XX cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
XX lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
XX prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
XX drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
XX Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
XX human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
XX rheumatoid arthritis; atherosclerosis.
XX Homo sapiens.
OS
XX WO200187979-A2.
XX
XX
XX 22-NOV-2001.
XX
XX 14-MAY-2001; 2001WO-US015567.
XX
XX 12-MAY-2000; 2000US-0204039P.
XX 27-JUN-2000; 2000US-0214591P.
XX 14-MAY-2001; 2001US-00214591.
XX
XX (AMGEN-) AMGEN INC.
PA
XX Theell LE, Yu G;
PI
XX WPI; 2002-066686/09.
XX
XX Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor; by
PT administering a binding partner for APRIL, a tumor necrosis factor family
PT ligand.
XX
XX Disclosure; Fig 13; 94pp; English.
XX
XX The invention relates to a method for inhibiting TACI (transmembrane
XX activator and intracellular CML interactor) and/or B cell maturation
XX protein (BCMA) activity in a mammal. The method comprises administering a
XX specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
XX family ligand), having the consensus region of TACI, BCMA, or the TACI/
XX BCMA extracellular consensus sequence, but not the extracellular region
XX of TACI or BCMA. The method is useful for inhibiting activity of TACI
XX and/or BCMA in a mammal which is useful for treating B-cell or T-cell
XX lymphoproliferative disorders, one or more solid tumours such as lung,
XX gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
XX antagonists are useful for treating inflammation and immune function
XX diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
XX dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
XX disease), drug and insect sting allergy, inflammatory bowel disease
XX (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
XX sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
XX bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
XX with leucocyte infiltration of the skin or organs. The present sequence

CC is human BCMA cysteine-rich extracellular region
XX
XX SQ Sequence 58 AA;
Query Match 88.0%; Score 249; DB 5; Length 58;
Best Local Similarity 100.0%; Pred. No. 5e-22;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 8 CSONEYFDSLHACIPQQLRCSNTPPLTCORYCNASVTSYKVG 51
DB 1 CSONEYFDSLHACIPQQLRCSNTPPLTCORYCNASVTSYKVG 44
RESULT 34
ID AD267761
XX AD267761 standard; protein; 40 AA.
XX
XX AD267761;
AC
XX
XX 14-JUL-2005 (first entry)
XX
XX
XX Human tumor necrosis factor receptor BCMA Cys-rich domain.
DE
XX Tumor necrosis factor receptor; BCMA; cancer; neoplasm; diagnosis;
XX cytosolic.
XX
XX Homo sapiens.
OS
XX WO2005037865-A2.
XX
XX 28-APR-2005.
XX
XX 18-OCT-2004; 2004WO-US034375.
XX
XX 16-OCT-2003; 2003US-0511698P.
XX 18-OCT-2004; 2004US-0619552P.
XX
XX (ZYMO) ZYMOGENETICS INC.
PA
XX Fox BA, Holloway JL, Sheppard PO, Dillon SR;
PI
XX WPI; 2005-315682/32.
XX
XX New tumor necrosis factor receptor (TNFR) polypeptides, useful as
PT detecting ligands, and for modulating tumor growth, metastasis and
PT immunity, such as separating resting from stimulated immune cells.
XX
XX Disclosure; SEQ ID NO 9; 132pp; English.
XX
XX The invention provides novel tumor necrosis factor receptor ztnfr14
XX polynucleotides AD267753 and polypeptides AD267754, expression vectors
XX and antibodies. Ztnfr14 polynucleotides are used in claimed methods for
XX detecting a genetic abnormality in a patient and for detecting a cancer
XX in a patient. Recombinant ztnfr14 polypeptide, optionally conjugated to a
XX toxin, is used in a claimed method of killing cancer cells. Ztnfr14
XX polypeptides can be used to detect ligands, agonists and antagonists. The
XX polypeptides, polynucleotides and antibodies may also be used in methods
XX that modulate tumor growth, metastasis, and immunity such as separating
XX resting from stimulated immune cells. The present sequence is that of the
XX Cys-rich domain of human TNFR BCMA AD267760. This sequence was compared
XX with that of ztnfr14 in the identification of ztnfr14 as a member of the
XX TNFR family.
XX
XX SQ Sequence 40 AA;
Query Match 81.3%; Score 230; DB 9; Length 40;
Best Local Similarity 100.0%; Pred. No. 6.2e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 6 GCGSNEYFDSLHACIPQQLRCSNTPPLTCORYCNASV 45
DB 1 GCGSNEYFDSLHACIPQQLRCSNTPPLTCORYCNASV 40

RESULT 35
ID AEC02033 standard; peptide; 38 AA.
AC AEC02033;
XX
XX
DT 20-OCT-2005 (first entry)
XX
XX
DE Amino acid sequence of an extracellular domain of BCMA.
XX
XX
KW APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;
KW cytostatic; neoplasm; immunosuppressive; therapeutic;
KW B-cell maturation antigen; BCMA.
XX
XX
OS Synthetic.
XX
XX
PN WO2005075511-A1.
XX
XX
PD 18-AUG-2005.
XX
XX
PF 04-AUG-2004; 2004WO-US025247.
XX
XX
PR 29-JAN-2004; 2004US-0540271P.
XX
XX
PA (GETH) GENENTECH INC.
XX
XX
PI Kelley RF, Patel D;
XX
XX
DR WPI; 2005-555932/56.
XX
XX
PT New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful
PT for treating immune-related disease, cancer or T-cell mediated disease
PT such as graft rejection, graft versus host disease (GVHD) and
PT inflammation.
XX
XX
PS Disclosure; SEQ ID NO 22; 140pp; English.
XX
XX
XX The specification describes polypeptides that bind APRIL or BAFF. The
XX polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen
XX (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The
XX polypeptides of the invention are useful for treating immune-related
XX diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
XX lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
XX scleroma; or T-cell mediated disease such as graft rejection, graft
XX versus host disease (GVHD) and inflammation. The present sequence
XX represents an extracellular domain of BCMA.
XX
XX
SQ Sequence 38 AA;
XX
XX
Query Match 76.0%; Score 215; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 3.6e-18;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
QY 9 SONEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVT 46
DB 1 SONEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVT 38
XX
XX
RESULT 36
ID AAB60700 standard; protein; 157 AA.
XX
XX
AC AAB60700;
XX
XX
DT 22-MAY-2001 (first entry)
XX
XX
DE Human BAFF receptor (BAFF-R) sequence encoded by A plasmid pUST535.
XX
XX
KW Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
KW immune-related disorder; B-cell growth inhibitor; BCMA;
KW B-cell maturation inhibitor; immunoglobulin production inhibitor;
KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
KW

XX renal disorder; immunosuppressive disorder; HIV infection;
KW organ transplantation; antiinflammatory; systemic lupus erythematosus;
KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
KW lymphoma; gene therapy; cancer; tumour; plasmid pUST535.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200112812-A2.
XX
XX
PD 22-FEB-2001.
XX
XX
PF 16-AUG-2000; 2000WO-US022507.
XX
XX
PR 17-AUG-1999; 99US-0149378P.
XX
PR 11-FEB-2000; 2000US-0181684P.
XX
PR 18-FEB-2000; 2000US-0183536P.
XX
XX
PA (BIOJ) BIOGEN INC.
XX
XX
PA (APOT-) APOTEC R & D SA.
XX
XX
PI Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;
PI Thompson J;
XX
XX
DR WPI; 2001-202866/20.
XX
XX
DR N-PSDB; AAF60000.
XX
XX
PT Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
PT lympho-proliferative disorder by administering BAFF-receptor polypeptide,
PT chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.
XX
XX
PS Example 1; Fig 3; 59pp; English.
XX
XX
XX The invention relates to the use of a BAFF receptor (BAFF-R, also known
XX as BCMA) protein, or a BAFF-R fusion protein as an agent for the
XX treatment of a variety of immune-related disorders. BAFF-R is a member of
XX the TNF (tumour necrosis factor) family, acting as an immunoregulatory
XX agent, and also plays a role in the development of hypertension and
XX related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-
XX specific antibodies can be used for inhibiting B-cell growth, dendritic
XX cell-induced B-cell growth and maturation, and immunoglobulin production,
XX and in the treatment of autoimmune disorders. B-cell lymphoproliferative
XX disorders, hypertension and renal disorders. The BAFF-R proteins may also
XX be used in the treatment of immunosuppressive disorders and HIV
XX infection, and in patients undergoing organ transplantation. The BAFF-R
XX proteins or BAFF-R specific antibodies may be used for treating,
XX suppressing or altering an immune response involving a signalling pathway
XX between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R
XX inhibits B-cell growth and maturation it is useful for treating diseases
XX such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
XX Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
XX progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
XX human BAFF-R may be used in gene therapy to treat tumours, lymphomas,
XX autoimmune disorders and inherited B-cell-associated disorders. The
XX present sequence represents a human BAFF-R protein sequence as encoded by
XX plasmid pUST535. However, this BAFF-R protein sequence is 27 amino acids
XX shorter than that given in AAB60698
XX
XX
SQ Sequence 157 AA;
XX
XX
Query Match 72.8%; Score 206; DB 4; Length 157;
Best Local Similarity 87.2%; Pred. No. 1.9e-16;
Matches 41; Conservative 0; Mismatches 0; Indels 6; Gaps 2;
XX
XX
QY 1 MLQMGAGCSONEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTN 47
DB 1 MLQMGAG---QNEYFDSLHACIPCOLR---NTPPLTCORYCNASVTN 41
XX
XX
RESULT 37
ID AAE15486 standard; peptide; 34 AA.
XX

AC AAE15486;
XX
XX 12-MAR-2002 (first entry)
DE Human B-cell maturation (BCMA) protein cysteine-rich consensus region.
XX
XX Human; transmembrane activator and intracellular CAML interactor; TACI;
KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis.
XX
XX Homo sapiens.
OS
XX WO200187979-A2.
PN
XX
XX 22-NOV-2001.
PD
XX
XX 14-MAY-2001; 2001WO-US015567.
PE
XX
XX 12-MAY-2000; 2000US-0204039P.
PR
XX 27-JUN-2000; 2000US-0214591P.
PR 14-MAY-2001; 2001US-00214591.
XX
XX (AMGE-) AMGEN INC.
PA
XX
XX Theell LE, Yu G;
PI
XX
XX WPI; 2002-066686/09.
DR
XX
XX Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor family
PT ligand.
XX
XX
XX Claim 1; Fig 10A; 94pp; English.
PS
XX
XX The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering a
CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human BCMA protein cysteine-rich consensus region
XX
XX
XX Sequence 34 AA;
SQ

Query Match 71.0%; Score 201; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 41
DB 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34

ID ADA49366 standard; peptide; 34 AA.
XX
XX
AC ADA49366;
XX
XX 20-NOV-2003 (first entry)
DE Human BCMA cysteine rich domain.
XX
XX
XX TALL-1, antagonist; immunosuppressive; antirheumatic; antiinflammatory;
KW antiarthritic; dermatological; antidiabetic; neuroprotective;
KW antihypertoid; antipyretic; nephrotoxic; vasotropic; vaccine;
KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
KW insulin dependent diabetes mellitus; multiple sclerosis;
KW myasthenia gravis; Grave's disease; autoimmune hemolytic anaemia;
KW autoimmune thrombocytopenic purpura; Goodpasture's syndrome;
KW pemphigus vulgaris; acute rheumatic fever;
KW post-streptococcal glomerulonephritis; polyarthritis nodosa; BCMA; CRD;
KW cysteine rich domain.
XX
XX
XX Homo sapiens.
OS
XX
XX WO2003035846-A2.
PN
XX
XX 01-MAY-2003.
PD
XX
XX 24-OCT-2002; 2002WO-US034376.
PE
XX
XX 24-OCT-2001; 2001US-0345106P.
PR 14-JAN-2002; 2002US-0348962P.
PR 07-FEB-2002; 2002US-0354966P.
PR 13-AUG-2002; 2002US-0403364P.
XX
XX
XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.
PA
XX
XX Zhang G, Shu H, Liu Y, Xu L;
PI
XX
XX WPI; 2003-403345/38.
DR
XX
XX Novel TALL-1 antagonist protein useful for inhibiting TALL-1 biological
PT activity in mammal, has a modification in the region connecting beta
PT strands D and E that reduces the biological activity of TALL-1
PT antagonist.
XX
XX
XX Disclosure; Page 616; 618pp; English.
PS
XX
XX The invention relates to a novel TALL-1 antagonist protein, comprising a
CC sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID
CC NO:2, by at least one modification in the region connecting Ebgrr; strands
CC D and E that reduces the biological activity of the TALL-1 antagonist as
CC compared to wild-type TALL-1. A protein of the invention has
CC immunosuppressive, antirheumatic, antiinflammatory, antiarthritic,
CC dermatological, antidiabetic, neuroprotective, antihypertoid, antipyretic,
CC nephrotoxic, and vasotropic activity. A TALL-1 antagonist may be used in
CC a vaccine. A protein of the invention is useful for inhibiting TALL-1
CC biological activity in a mammal. TC is useful for treating autoimmune
CC diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin
CC dependent diabetes mellitus, multiple sclerosis, myasthenia gravis,
CC Grave's disease, autoimmune hemolytic anaemia, autoimmune
CC thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris,
CC acute rheumatic fever, post-streptococcal glomerulonephritis and
CC polyarthritis nodosa. The present sequence represents a cysteine rich
CC domain (CRD) module of human BCMA.
XX
XX
XX Sequence 34 AA;
SQ

Query Match 71.0%; Score 201; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 41
DB 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34

PT New polypeptides that inhibit APRIL and/or BAFf binding to BCMA, useful
PT for treating immune-related disease, cancer or T-cell mediated disease
PT such as graft rejection, graft versus host disease (GVHD) and
PT inflammation.

PS Claim 13; SEQ ID NO 17; 140bp; English.

XX The specification describes polypeptides that bind APRIL or BAFf. The
XX polypeptides inhibit APRIL or BAFf binding to B-cell maturation antigen
XX (BCMA). APRIL and BAFf are tumor necrosis family (TNF) members. The
CC polypeptides of the invention are useful for treating immune-related
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
CC scleroma; or T-cell mediated disease such as graft rejection, graft
CC versus host disease (GVHD) and inflammation. The present sequence
CC represents a polypeptide of the invention, derived from formula II (see
CC AEC02017), that that bind BAFf.

XX Sequence 34 AA;

Query Match 68.6%; Score 194; DB 9; Length 34;
Best Local Similarity 97.1%; Pred. No. 1e-15;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 41
Db 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 34

RESULT 42
AEC02017
ID AEC02017 standard; peptide; 34 AA.
AC AEC02017;
XX 20-OCT-2005 (first entry)
DT
XX Formula I derived polypeptide F that binds APRIL.
DE
XX APRIL; BAFf; immune disorder; immunomodulator; antiinflammatory; cancer;
XX cytostatic; neoplasm; immunosuppressive; therapeutic.
XX
XX Synthetic.
OS
XX WO2005075511-A1.
PN
XX 18-AUG-2005.
PD
XX 04-AUG-2004; 2004WO-US025247.
PF
XX 29-JAN-2004; 2004US-0540271P.
PR
XX (GETH) GENENTECH INC.
PA
XX Kelley RF, Patel D;
XX
XX WPI; 2005-555932/56.
DR
XX New polypeptides that inhibit APRIL and/or BAFf binding to BCMA, useful
PT for treating immune-related disease, cancer or T-cell mediated disease
PT such as graft rejection, graft versus host disease (GVHD) and
PT inflammation.

XX Claim 7; SEQ ID NO 6; 140bp; English.

XX The specification describes polypeptides that bind APRIL or BAFf. The
XX polypeptides inhibit APRIL or BAFf binding to B-cell maturation antigen
XX (BCMA). APRIL and BAFf are tumor necrosis family (TNF) members. The
CC polypeptides of the invention are useful for treating immune-related
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
CC scleroma; or T-cell mediated disease such as graft rejection, graft
CC versus host disease (GVHD) and inflammation. The present sequence

CC represents polypeptide of the invention that binds APRIL, derived from
CC AEC02012.
XX
XX Sequence 34 AA;

Query Match 68.6%; Score 194; DB 9; Length 34;
Best Local Similarity 97.1%; Pred. No. 1e-15;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 41
Db 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 34

RESULT 43
AEC02025
ID AEC02025 standard; peptide; 34 AA.
AC AEC02025;
XX 20-OCT-2005 (first entry)
DT
XX Formula II derived polypeptide D that binds BAFf.
DE
XX APRIL; BAFf; immune disorder; immunomodulator; antiinflammatory; cancer;
XX cytostatic; neoplasm; immunosuppressive; therapeutic.
XX
XX Synthetic.
OS
XX WO2005075511-A1.
PN
XX 18-AUG-2005.
PD
XX 04-AUG-2004; 2004WO-US025247.
PF
XX 29-JAN-2004; 2004US-0540271P.
PR
XX (GETH) GENENTECH INC.
PA
XX Kelley RF, Patel D;
XX
XX WPI; 2005-555932/56.
DR
XX New polypeptides that inhibit APRIL and/or BAFf binding to BCMA, useful
PT for treating immune-related disease, cancer or T-cell mediated disease
PT such as graft rejection, graft versus host disease (GVHD) and
PT inflammation.

XX Claim 13; SEQ ID NO 14; 140bp; English.

XX The specification describes polypeptides that bind APRIL or BAFf. The
XX polypeptides inhibit APRIL or BAFf binding to B-cell maturation antigen
XX (BCMA). APRIL and BAFf are tumor necrosis family (TNF) members. The
CC polypeptides of the invention are useful for treating immune-related
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
CC scleroma; or T-cell mediated disease such as graft rejection, graft
CC versus host disease (GVHD) and inflammation. The present sequence
CC represents a polypeptide of the invention, derived from formula II (see
CC AEC02017), that that bind BAFf.

XX Sequence 34 AA;

Query Match 67.8%; Score 192; DB 9; Length 34;
Best Local Similarity 97.1%; Pred. No. 1.8e-15;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 41
Db 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 34

RESULT 44


```

AEC02024
ID AEC02024 standard; peptide; 34 AA.
XX
AC AEC02024;
XX
DT 20-OCT-2005 (first entry)
XX
DE Formula II derived polypeptide C that binds BAPF.
XX
KM APRIL; BAPF; immune disorder; immunomodulator; antiinflammatory; cancer;
XX cytostatic; neoplasm; immunosuppressive; therapeutic.
XX
OS Synthetic.
XX
PN WO2005075511-A1.
XX
PD 18-AUG-2005.
XX
PF 04-AUG-2004; 2004WO-US025247.
XX
PR 29-JAN-2004; 2004US-0540271P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Kelley RF, Patel D;
XX
PI Kelley RF, Patel D;
XX
DR WPI; 2005-555932/56.
XX
XX
PT New polypeptides that inhibit APRIL and/or BAPF binding to BCMA, useful
PT for treating immune-related disease, cancer or T-cell mediated disease
PT such as graft rejection, graft versus host disease (GVHD) and
PT inflammation.
XX
PS Claim 13; SEQ ID NO 13; 140pp; English.
XX
CC The specification describes polypeptides that bind APRIL or BAPF. The
CC polypeptides inhibit APRIL or BAPF binding to B-cell maturation antigen
CC (BCMA). APRIL and BAPF are tumor necrosis family (TNF) members. The
CC polypeptides of the invention are useful for treating immune-related
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
CC sclerosis; or T-cell mediated disease such as graft rejection, graft
CC versus host disease (GVHD) and inflammation. The present sequence
CC represents a polypeptide of the invention, derived from formula II (see
CC AEC02021), that that bind BAPF.
XX
SQ Sequence 34 AA;
XX
Query Match 67.8%; Score 192; DB 9; Length 34;
Best Local Similarity 97.1%; Pred. No. 1.8e-15;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 8 CSONEFDSLVAHACIPQQLRCSSNTPTLCQRYC 41
DB 1 CSONEFDSLVAHACIPQQLRCSSNTPTLCQRYC 34
XX
RESULT 45
AEC02020
ID AEC02020 standard; peptide; 34 AA.
XX
AC AEC02020;
XX
DT 20-OCT-2005 (first entry)
XX
DE Formula I derived polypeptide I that binds APRIL.
XX
KM APRIL; BAPF; immune disorder; immunomodulator; antiinflammatory; cancer;
XX cytostatic; neoplasm; immunosuppressive; therapeutic.
XX
OS Synthetic.
XX
PN WO2005075511-A1.
XX

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XX
PD 18-AUG-2005.
XX
PF 04-AUG-2004; 2004WO-US025247.
XX
PR 29-JAN-2004; 2004US-0540271P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Kelley RF, Patel D;
XX
PI Kelley RF, Patel D;
XX
DR WPI; 2005-555932/56.
XX
XX
PT New polypeptides that inhibit APRIL and/or BAPF binding to BCMA, useful
PT for treating immune-related disease, cancer or T-cell mediated disease
PT such as graft rejection, graft versus host disease (GVHD) and
PT inflammation.
XX
PS Claim 7; SEQ ID NO 9; 140pp; English.
XX
CC The specification describes polypeptides that bind APRIL or BAPF. The
CC polypeptides inhibit APRIL or BAPF binding to B-cell maturation antigen
CC (BCMA). APRIL and BAPF are tumor necrosis family (TNF) members. The
CC polypeptides of the invention are useful for treating immune-related
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
CC sclerosis; or T-cell mediated disease such as graft rejection, graft
CC versus host disease (GVHD) and inflammation. The present sequence
CC represents a polypeptide of the invention that binds APRIL, derived from
CC AEC02012.
XX
SQ Sequence 34 AA;
XX
Query Match 67.5%; Score 191; DB 9; Length 34;
Best Local Similarity 94.1%; Pred. No. 2.3e-15;
Matches 32; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
QY 8 CSONEFDSLVAHACIPQQLRCSSNTPTLCQRYC 41
DB 1 CSONEFDSLVAHACIPQQLRCSSNTPTLCQRYC 34
XX
RESULT 46
AEC02018
ID AEC02018 standard; peptide; 34 AA.
XX
AC AEC02018;
XX
DT 20-OCT-2005 (first entry)
XX
DE Formula I derived polypeptide G that binds APRIL.
XX
KM APRIL; BAPF; immune disorder; immunomodulator; antiinflammatory; cancer;
XX cytostatic; neoplasm; immunosuppressive; therapeutic.
XX
OS Synthetic.
XX
PN WO2005075511-A1.
XX
PD 18-AUG-2005.
XX
PF 04-AUG-2004; 2004WO-US025247.
XX
PR 29-JAN-2004; 2004US-0540271P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Kelley RF, Patel D;
XX
PI Kelley RF, Patel D;
XX
DR WPI; 2005-555932/56.
XX
XX
PT New polypeptides that inhibit APRIL and/or BAPF binding to BCMA, useful
PT for treating immune-related disease, cancer or T-cell mediated disease

```

PT such as graft rejection, graft versus host disease (GVHD) and
PT inflammation.
XX
XX Claim 7; SEQ ID NO 7; 140bp; English.
XX
CC The specification describes polypeptides that bind APRIL or BAF. The
CC polypeptides inhibit APRIL or BAF binding to B-cell maturation antigen
CC (BCMA). APRIL and BAF are tumor necrosis family (TNF) members. The
CC polypeptides of the invention are useful for treating immune-related
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
CC sclerosis; or T-cell mediated disease such as graft rejection, graft
CC versus host disease (GVHD) and inflammation. The present sequence
CC represents polypeptide of the invention that binds APRIL, derived from
CC AEC02012.
XX
SQ Sequence 34 AA;
XX
Query Match 66.8%; Score 189; DB 9; Length 34;
Best Local Similarity 94.1%; Pred. No. 4e-15;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 8 CSQNEYPDSLHACIPCOLRCSNTPTTCQRYC 41
Db 1 CSQNEYPDSLHACKPCDLRCSNTPTTCQRYC 34
XX
RESULT 47
AEC02029
ID AEC02029 standard; peptide; 34 AA.
XX
AC AEC02029;
XX
DT 20-OCT-2005 (first entry)
XX
DE Formula II derived polypeptide H that binds BAF.
XX
XX APRIL; BAF; immune disorder; immunomodulator; antiinflammatory; cancer;
XX cytostatic; neoplasm; immunosuppressive; therapeutic.
XX
OS Synthetic.
XX
XX WO2005075511-A1.
XX
PD 18-AUG-2005.
XX
PF 04-AUG-2004; 2004WO-US025247.
XX
PR 29-JAN-2004; 2004US-0540271P.
XX
PA (GETH) GENENTECH INC.
XX
PI Kelley RF, Patel D;
XX
PI WPI; 2005-555932/56.
XX
DR New polypeptides that inhibit APRIL and/or BAF binding to BCMA, useful
PT for treating immune-related disease, cancer or T-cell mediated disease
PT such as graft rejection, graft versus host disease (GVHD) and
PT inflammation.
XX
PS Claim 13; SEQ ID NO 18; 140bp; English.
XX
CC The specification describes polypeptides that bind APRIL or BAF. The
CC polypeptides inhibit APRIL or BAF binding to B-cell maturation antigen
CC (BCMA). APRIL and BAF are tumor necrosis family (TNF) members. The
CC polypeptides of the invention are useful for treating immune-related
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
CC sclerosis; or T-cell mediated disease such as graft rejection, graft
CC versus host disease (GVHD) and inflammation. The present sequence
CC represents a polypeptide of the invention, derived from formula II (see
CC AEC02021), that that bind BAF.

XX
SQ Sequence 34 AA;
XX
Query Match 66.8%; Score 189; DB 9; Length 34;
Best Local Similarity 94.1%; Pred. No. 4e-15;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 8 CSQNEYPDSLHACIPCOLRCSNTPTTCQRYC 41
Db 1 CSQNEYPDSLHACKPCDLRCSNTPTTCQRYC 34
XX
RESULT 48
AEC02019
ID AEC02019 standard; peptide; 34 AA.
XX
AC AEC02019;
XX
DT 20-OCT-2005 (first entry)
XX
DE Formula I derived polypeptide H that binds APRIL.
XX
XX APRIL; BAF; immune disorder; immunomodulator; antiinflammatory; cancer;
XX cytostatic; neoplasm; immunosuppressive; therapeutic.
XX
OS Synthetic.
XX
XX WO2005075511-A1.
XX
PD 18-AUG-2005.
XX
PF 04-AUG-2004; 2004WO-US025247.
XX
PR 29-JAN-2004; 2004US-0540271P.
XX
PA (GETH) GENENTECH INC.
XX
PI Kelley RF, Patel D;
XX
PI WPI; 2005-555932/56.
XX
DR New polypeptides that inhibit APRIL and/or BAF binding to BCMA, useful
PT for treating immune-related disease, cancer or T-cell mediated disease
PT such as graft rejection, graft versus host disease (GVHD) and
PT inflammation.
XX
PS Claim 7; SEQ ID NO 8; 140bp; English.
XX
CC The specification describes polypeptides that bind APRIL or BAF. The
CC polypeptides inhibit APRIL or BAF binding to B-cell maturation antigen
CC (BCMA). APRIL and BAF are tumor necrosis family (TNF) members. The
CC polypeptides of the invention are useful for treating immune-related
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
CC sclerosis; or T-cell mediated disease such as graft rejection, graft
CC versus host disease (GVHD) and inflammation. The present sequence
CC represents polypeptide of the invention that binds APRIL, derived from
CC AEC02012.
XX
SQ Sequence 34 AA;
XX
Query Match 64.3%; Score 182; DB 9; Length 34;
Best Local Similarity 91.2%; Pred. No. 2.7e-14;
Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 8 CSQNEYPDSLHACIPCOLRCSNTPTTCQRYC 41
Db 1 CSQNEYPDSLHACKPCDLRCSNTPTTCQRYC 34
XX
RESULT 49
AAB08844
ID AAB08844 standard; peptide; 185 AA.

DB Mouse B cell maturation (BCMA) protein.
XX
KW Mouse; transmembrane activator and intracellular CAML interactor; TACI;
KW cyrostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis.
XX
OS Mus sp.
XX
PN WO200187979-A2.
XX
XX 22-NOV-2001.
XX
PD 14-MAY-2001; 2001WO-US015567.
XX
PF 12-MAY-2000; 2000US-0204039P.
XX PR 27-JUN-2000; 2000US-0214591P.
XX PR 14-MAY-2001; 2001US-00214591.
XX
PA (AMGEN) AMGEN INC.
XX
PI Theell LE, Yu G;
XX
XX WPI, 2002-066686/09.
DR
XX
PT Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor. By
PT administering a binding partner for APRIL, a tumor necrosis factor family
PT ligand.
XX
PS Disclosure; Fig 11; 94pp; English.
XX
XX The invention relates to a method for inhibiting TACI (transmembrane
XX activator and intracellular CAML interactor) and/or B cell maturation
XX protein (BCMA) activity in a mammal. The method comprises administering a
XX specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
XX family ligand), having the consensus region of TACI, BCMA, or the TACI/
XX BCMA extracellular consensus sequence, but not the extracellular region
XX of TACI or BCMA. The method is useful for inhibiting activity of TACI
XX and/or BCMA in a mammal which is useful for treating B-cell or T-cell
XX lymphoproliferative disorders, one or more solid tumours such as lung,
XX gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
XX antagonists are useful for treating inflammation and immune function
XX diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
XX dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
XX disease), drug and insect sting allergy, inflammatory bowel disease
XX (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
XX sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
XX bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
XX with leucocyte infiltration of the skin or organs. The present sequence
XX is mouse BCMA protein
XX
SQ Sequence 185 AA;
XX
Query Match 64.0%; Score 181; DB 5; Length 185;
Best Local Similarity 70.8%; Pred. No. 2.1e-13;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

DT 14-JUL-2005 (first entry)
XX
DE Mouse tumor necrosis factor receptor BCMA.
XX
KW Tumor necrosis factor receptor; BCMA; cancer; neoplasm; diagnosis;
KW cyrostatic.
XX
XX Mus musculus.
OS
XX
XX WO2005037865-A2.
XX
PN 28-APR-2005.
XX
XX 18-OCT-2004; 2004WO-US034375.
XX
XX 16-OCT-2003; 2003US-0511698P.
XX PR 18-OCT-2004; 2004US-0619552P.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
PA
XX
XX Fox BA, Holloway JL, Sheppard PO, Dillon SR;
XX
XX WPI, 2005-315682/32.
DR
XX
XX New tumor necrosis factor receptor (TNFR) polypeptides, useful as
XX detecting ligands, and for modulating tumor growth, metastasis and
XX immunity, such as separating resting from stimulated immune cells.
XX
PS Disclosure; SEQ ID NO 10; 132pp; English.
XX
XX The invention provides novel tumor necrosis factor receptor ztnfr14
XX polynucleotides AD267753 and polypeptides AD267754, expression vectors
XX and antibodies. Human ztnfr14 polynucleotides are used in claimed methods
XX for detecting a genetic abnormality in a patient and for detecting a
XX cancer in a patient. Recombinant ztnfr14 polypeptide, optionally
XX conjugated to a toxin, is used in a claimed method of killing cancer
XX cells. Ztnfr14 polypeptides can be used to detect ligands, agonists and
XX antagonists. The polypeptides, polynucleotides and antibodies may also be
XX used in methods that modulate tumor growth, metastasis, and immunity such
XX as separating resting from stimulated immune cells. The present sequence
XX is that of murine TNFR BCMA. This sequence was compared with that of
XX the murine ztnfr14 AD267756 in the identification of ztnfr14 as a member of
XX the TNFR family.
XX
SQ Sequence 185 AA;
XX
Query Match 64.0%; Score 181; DB 9; Length 185;
Best Local Similarity 70.8%; Pred. No. 2.1e-13;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

DT 29-AUG-2003 (revised)
DT 12-MAR-2002 (first entry)
XX
XX
DE Mouse BCMA-human immunoglobulin Fc region fusion protein.
XX
KW Human; transmembrane activator and intracellular CAML interactor; TACI;
KW cyrostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW

| Query Match | Best Local Similarity | Score | DB | Length |
|--|-----------------------|--------|---------------------------------|--------|
| Matches 34; Conservative | 64.0%; | 70.8%; | DB 5; | 281; |
| | | | Pred. No. 3,3e-13; | |
| | | | Mismatches 8; Indels 2; Gaps 1, | |
| 4 MAGGCSONEHYFDSLHACIPQLRCSSNTPPLTCORYCNASTNTSVKG 51 | | | | |
| 1 MAOOCFHSYFDSLHACKPCHLRCSN--PPATCPYCDPSVTSSVKG 46 | | | | |

RESULT 54

ABJ38417

ABJ38417 standard; protein; 42 AA.

ABJ38417;

12-JUN-2003 (first entry)

TALL-1 related protein SEQ ID No 197.

TALL-1-binding protein; TALL-1, B-cell-mediated autoimmune disease; systemic lupus erythematosus; B-cell-mediated cancer; lymphoma;

| | | |
|-----------|---|---|
| KM | | inflammation; rheumatoid arthritis; acute pancreatitis; atherosclerosis; |
| KW | | Alzheimer's disease; asthma; cachexia; cirrhosis; diabetes; osteoporosis; |
| KM | | glomerulonephritis; Hashimoto's thyroiditis; ischaemic injury; psoriasis; |
| KW | | multiple myeloma; multiple sclerosis; Parkinson's disease; vasculitis; |
| KM | | gene therapy. |
| XX | | |
| OS | Homo sapiens. | |
| XX | | |
| PN | WO200292620-A2. | |
| XX | | |
| PD | 21-NOV-2002. | |
| XX | | |
| PF | 13-MAY-2002; 2002WO-US015273. | |
| XX | | |
| PR | 11-MAY-2001; 2001US-0290196P. | |
| XX | | |
| PA | (AMGEN-) AMGEN INC. | |
| XX | | |
| PI | Min H, Hsu H; | |
| DR | WPI; 2003-156719/15. | |
| XX | | |
| PT | New TALL-1-binding polypeptide, useful for modulating the activity of | |
| PT | TALL-1 and in treating, preventing or diagnosing a B-cell-mediated | |
| PT | autoimmune diseases; cancers or lymphomas. | |
| XX | | |
| PS | Disclosure; Page 26; 236pp; English. | |
| XX | | |
| CC | The invention relates to a novel TALL-1-binding polypeptide comprising a | |
| CC | defined sequence in the specification. The composition is useful in | |
| CC | modulating the activity of TALL-1, and in treating, preventing, | |
| CC | ameliorating, diagnosing or prophylaxising a B-cell-mediated autoimmune | |
| CC | disease (e.g. systemic lupus erythematosus) or B-cell-mediated cancer or | |
| CC | lymphoma. The composition may also be used in treating inflammations | |
| CC | (e.g. rheumatoid arthritis), acute pancreatitis, Alzheimer's disease, | |
| CC | asthma, atherosclerosis, cachexia, cirrhosis, diabetes, | |
| CC | glomerulonephritis, Hashimoto's thyroiditis, ischaemic injury, multiple | |
| CC | myeloma, multiple sclerosis, osteoporosis, Parkinson's disease, psoriasis | |
| CC | and vasculitis. Disorders may be treated with the novel composition using | |
| CC | gene therapy. This sequence represents a TALL-1 related protein of the | |
| CC | invention | |
| XX | | |
| CC | | |
| SQ | Sequence 42 AA; | |
| | | |
| | Query Match | 55.8%; Score 158; DB 6; Length 42; |
| | Best Local Similarity | 100.0%; Pred. No. 2.5e-11; |
| | Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | |
| OY | 1 MLQMAAGCSONEYFDSLHACIPQLNC 28 | |
| | | |
| DB | 15 MLQMAAGCSONEYFDSLHACIPQLNC 42 | |
| | | |
| RESULT 55 | | |
| ID | ADIS3060 | |
| ADIS3060 | ADIS3060 standard; peptide; 26 AA. | |
| XX | | |
| AC | ADIS3060; | |
| XX | | |
| DT | 22-APR-2004 (first entry) | |
| XX | | |
| DE | Human BCMA receptor binding site. | |
| XX | | |
| KM | protein co-ordinate data; cytosolic; anti-allergic; immunosuppressive; | |
| KW | anti-rheumatic; anti-arthritis; neuroprotective; anti-inflammatory; | |
| KM | antidiabetic; dermatological; antiasmatic; neurokinine-alpha; | |
| KW | crystallography; cancer; allergic disorder; autoimmune disease; | |
| KW | rheumatoid arthritis; multiple sclerosis; Crohn's disease; diabetes; | |
| KM | systemic lupus erythematosus; asthma; receptor. | |
| XX | | |
| OS | Homo sapiens. | |
| XX | | |
| PN | WO2003050134-A2. | |

```
XX 19-JUN-2003.
PD
XX
XX 07-NOV-2002; 2002MO-US035661.
PR
XX 07-NOV-2001; 2001US-0331049P.
PR
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Li Y, Oren DE, Arnold E, Volovik Y;
PI
XX WPI; 2003-532895/50.
DR
XX
XX New crystalline Neutrokin-alpha protein, useful for designing compounds
PT that bind, inhibit or mimic a Neutrokin-alpha protein or enhance the
PT activity of a Neutrokin-alpha protein for treating e.g. cancer or
PT allergic disorders.
XX
XX Disclosure; Fig 4; 362pp; English.
PS
XX
XX The invention relates to a neutrokin-alpha protein in crystalline form.
CC The crystalline neutrokin-alpha protein is useful for designing
CC molecules that have biological activity or compounds that bind, inhibit
CC or mimic a neutrokin-alpha protein and/or enhance the activity of a
CC neutrokin-alpha protein. The three-dimensional structure of a neutrokin
CC -alpha protein is useful in determining the three-dimensional of other
CC neutrokin-alpha proteins and their homologs. The compounds that mimic,
CC prevent or inhibit the activity of the protein are useful for treating
CC cancer, allergic disorders, or autoimmune diseases such as rheumatoid
CC arthritis, multiple sclerosis, Crohn's disease, diabetes, systemic lupus
CC erythematosus or asthma. This sequence represents the residues in the
CC receptor for binding a cytokine ligand.
XX
XX Sequence 26 AA;
SQ
XX
XX Query Match 53.4%; Score 151; DB 7; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 12 EYFDSLHACIPQRCSSNTPTPLTC 37
Db 1 EYFDSLHACIPQRCSSNTPTPLTC 26
XX
XX RESULT 56
AAE15491
ID AAE15491 standard; protein; 117 AA.
XX
XX AAE15491;
AC
XX 29-AUG-2003 (revised)
DT 12-MAR-2002 (first entry)
XX
XX Human-murine B cell maturation protein (BCMA) consensus sequence.
DE
XX Human; transmembrane activator and intracellular CAML interactor; TACI;
KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis; mouse.
XX
XX Homo sapiens.
OS Mus sp.
XX Chimeric.
XX WO200187979-A2.
XX
XX 22-NOV-2001.
PD
XX 14-MAY-2001; 2001MO-US015567.
.PF
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XX 12-MAY-2000; 2000US-0204039P.
PR
XX 27-JUN-2000; 2000US-0214591P.
PR
XX 14-MAY-2001; 2001US-00214591.
XX
XX (AMGE-) AMGEN INC.
PA
XX
XX The11 LE, Yu G;
PI
XX
XX WPI; 2002-066686/09.
DR
XX
XX Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor family
PT ligand.
XX
XX Disclosure; Fig 11; 94pp; English.
PS
XX
XX The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering a
CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human-murine B cell maturation protein (BCMA) consensus sequence.
XX
XX (Updated on 29-AUG-2003 to standardise OS field)
XX
XX Sequence 117 AA;
SQ
XX
XX Query Match 36.7%; Score 104; DB 5; Length 117;
Best Local Similarity 69.8%; Pred. No. 0.0002;
Matches 30; Conservative 1; Mismatches 2; Indels 10; Gaps 6;
XX
XX 9 SQNEYFDSLHACIPQRCSSNTPTPLTCORYCNASVTNSYVG 51
Db 2 AQCEYFDSLHAC-PC-IRCS----PPTCQ-YC--SVI-SYVG 34
XX
XX RESULT 57
AAE15492
ID AAE15492 standard; peptide; 24 AA.
XX
XX AAE15492;
AC
XX 29-AUG-2003 (revised)
DT 12-MAR-2002 (first entry)
XX
XX Human-murine BCMA consensus sequence cysteine rich region.
DE
XX Human; transmembrane activator and intracellular CAML interactor; TACI;
KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis; mouse.
XX
XX Homo sapiens.
OS Mus sp.
XX Chimeric.
XX
```

XX
PN WO200187979-A2.
XX
PD 22-NOV-2001.
XX
PF 14-MAY-2001; 2001WO-US015567.
XX
PR 12-MAY-2000; 2000US-0204039P.
XX
PR 27-JUN-2000; 2000US-0214591P.
XX
PR 14-MAY-2001; 2001US-00214591.
XX
PA (AMGEN) AMGEN INC.
XX
PI Theell LE, Yu G;
XX
XX MPI; 2002-066686/09.
DR
XX
XX Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor family
PT ligand.
XX
XX Disclosure; Fig 11; 94pp; English.
XX
XX The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering a
CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human-murine B cell maturation protein (BCMA) consensus sequence
CC cysteine rich region. (Updated on 29-AUG-2003 to standardise OS field)
XX
XX SQ Sequence 24 AA;
Query Match 32.0%; Score 90.5; DB 5; Length 24;
Best Local Similarity 73.3%; Pred. No. 0.0015;
Matches 22; Conservative 0; Mismatches 1; Indels 7; Gaps 4;
QY 12 EYFDSLHACIPQALRSSNTPLTCORC 41
DB 2 EYFDSLHAC-PC-LKCS---PTCQ-YC 24
RESULT 58
AAAY94006
ID AAAY94006 standard; protein; 249 AA.
XX
XX AAAY94006;
AC
XX
XX 20-OCT-2000 (first entry)
DT
XX
XX A murine znrf4, a tumour necrosis factor ligand.
DE
XX
XX Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
XX transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
XX znrf4 activity; antibody production; autoimmune disease; amyloidosis;
XX systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
XX rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
XX end stage renal failure; glomerulonephritis; vasculitis; nephritis;
XX renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy;
XX

XX
XX Immune response; immunosuppression; graft rejection; joint pain;
XX graft versus host disease; inflammation; swelling; anaemia; septic shock;
XX insulin dependent diabetes mellitus; Crohn's disease; hypertension;
XX renal artery stenosis; occlusion; cholesterol; renal emboli.
XX
XX Mus musculus.
XX
XX OS
XX PN WO200040716-A2.
XX
XX PD 13-JUL-2000.
XX
XX PF 07-JAN-2000; 2000WO-US000396.
XX
XX PR 07-JAN-1999; 99US-00226533.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Gross JA, Xu W, Madden K, Yee DP;
XX MPI; 2000-452538/39.
XX
XX N-PSDB; AAA58566.
DR
XX
XX Inhibiting znrf4 activity in a mammal, to treat autoimmune diseases,
PT renal disease, graft versus host disease, and inflammation, comprises
PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide.
XX
XX
XX Disclosure; Page 163; 175pp; English.
XX
XX The present sequence represents murine znrf4, a tumour necrosis factor
CC ligand. The extracellular domains of BR43x2 (an isoform of the
CC transmembrane activator and CAML-interactor (TACI) receptor), TACI or
CC BCMA (a related B cell protein) contain a cysteine rich domain, and are
CC used for inhibiting znrf4 activity. They may also be used for inhibiting
CC BR43x2, TACI or BCMA receptor-ligand engagement associated with activated
CC or resting B lymphocytes, effector T-cells, or with antibody production.
CC The antibody production is associated with an autoimmune disease selected
CC from systemic lupus erythematosus, myasthenia gravis, multiple sclerosis
CC and rheumatoid arthritis. The znrf4 activity and BR43x2, TACI or BCMA
CC receptor-ligand engagement is associated with asthma, bronchitis,
CC emphysema, end stage renal failure, glomerulonephritis, vasculitis,
CC nephritis, pyelonephritis, renal neoplasms, multiple myelomas, lymphomas,
CC light chain neuropathy, amyloidosis, moderating immune response,
CC immunosuppression, graft rejection, graft versus host disease,
CC inflammation, insulin dependent diabetes mellitus, Crohn's disease, joint
CC pain, swelling, anaemia, or septic shock. BR43x2, TACI, and BCMA
CC polypeptides, fusions, antibodies, agonists or antagonists can be used to
CC treat hypertension, renal artery stenosis, or occlusion, and cholesterol
CC or renal emboli
XX
XX SQ Sequence 249 AA;
Query Match 25.3%; Score 71.5; DB 3; Length 249;
Best Local Similarity 35.3%; Pred. No. 3.3;
Matches 12; Conservative 8; Mismatches 13; Indels 1; Gaps 1;
QY 8 CSQNEFYDSLHACIPQALRSSNTPLTCORC 41
DB 6 CPKXDYWDSSRSKSCVSCALTCQGRS-QRTCTDFC 38
RESULT 59
ABM85744
ID ABM85744 standard; protein; 249 AA.
XX
XX ABM85744;
AC
XX
XX 18-NOV-2004 (first entry)
DT
XX
XX Mouse protein sequence mCP1369.
DE
XX
XX Cytostatic; carcinoma; lymphoma; cancer; murine.
XX
XX Mus musculus.
OS

PN WO2003073826-A2.
 XX
 XX 12-SEP-2003.
 PD
 XX 28-FEB-2003; 2003WO-US006235.
 PF
 XX 01-MAR-2002; 2002US-00087192.
 XX
 PA (SAGR-) SAGRES DISCOVERY.
 P1
 P1 Morris DW;
 XX
 XX WPI; 2003-328604/31.
 DR
 XX
 PT Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
 PT comprises a nucleotide sequence.
 PS
 XX
 PS Claim 5; SEQ ID NO 1647; OPD; English.
 XX
 CC The present invention relates to novel DNA and protein sequences which
 CC are associated with carcinomas. The sequences are useful for: (i) for
 CC screening drug candidates; (ii) for screening of bioactive agent capable
 CC of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
 CC a bioactive agent capable of modulating the activity of CAP; (iv) for
 CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
 CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
 CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
 CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
 CC determining Carcinoma Associated (CA) gene copy number. In addition, the
 CC CA genes are useful as DNA vaccines and the CAP are useful as markers of
 CC carcinoma including lymphoma. The present sequence is one such CAP. Note:
 CC This patent is an equivalent to basic patent US2002182586A1, for which no
 CC sequence data was published
 XX
 XX Sequence 249 AA;
 QQ

Query Match Score 71.5; DB 7; Length 249;
Best Local Similarity 35.3%; Pred. No. 3.3;
Matches 12; Conservative 8; Mismatches 13; Indels 1; Gaps 1

Dd 8 CSONEYFDSLHACIPCOLRCSSNTPEPLTCORVC 41
 |:::|||::|||::|||::||
6 CPKQGYWDSRKSVCVSCALTCGQR-GRCTCTFC 38

RESULT 60
ADZ67773
ID ADZ67773 standard; protein; 249 AA.
XX
XX ADZ67773;
XX
XX DT 14-JUL-2005 (first entry)
XX
DE Mouse tumor necrosis factor receptor TACI.
XX
XX DE Tumor necrosis factor receptor; TACI; cancer; neoplasm; diagnosis;
KW cyrostatic.
XX
XX Mus musculus.
OS
XX MO2005037865-A2.
PN
XX 28-APR-2005.
PD
XX 18-OCT-2004; 2004MO-USO34375.
XX
PF 16-OCT-2003; 2003US-0511698P.
XX
PR 18-OCT-2004; 2004US-0619552P.
XX
XX (ZYMO) ZYMOGENETICS INC.
PA
XX
XX Fox BA, Holloway JL, Sheppard PO, Dillon SR;

| | | | |
|---------|---------------------------------------|---|------------|
| DR | | WPI; 2005-315682/32. | |
| XX | | | |
| XX | | New tumor necrosis factor receptor (TNFR) polypeptides, useful as | |
| PT | | detecting ligands, and for modulating tumor growth, metastasis and | |
| PT | | immunity, such as separating resting from stimulated immune cells. | |
| XX | | | |
| PS | | Disclosure; SEQ ID NO 21; 132bp; English. | |
| XX | | | |
| CC | | The invention provides novel tumor necrosis factor receptor (TNFR) | |
| CC | | ztnfr14 polynucleotides ADZ67753 and polypeptides ADZ67754, expression | |
| CC | | vectors and antibodies. Human ztnfr14 polynucleotides are used in claimed | |
| CC | | methods for detecting a genetic abnormality in a patient and for | |
| CC | | detecting a cancer in a patient. Recombinant ztnfr14 polypeptide, | |
| CC | | optionally conjugated to a toxin, is used in a claimed method of killing | |
| CC | | cancer cells. Ztnfr14 polypeptides can be used to detect ligands, and | |
| CC | | agonists and antagonists. The polypeptides, polynucleotides and | |
| CC | | antibodies may also be used in methods that modulate tumor growth, | |
| CC | | metastasis, and immunity such as separating resting from stimulated | |
| CC | | immune cells. The present sequence is that of murine TNFR TACI. This | |
| CC | | sequence was compared with that of murine ztnfr14 ADZ67756 in the | |
| CC | | identification of ztnfr14 as a member of the TNFR family. | |
| XX | | | |
| SQ | Sequence 249 AA; | | |
| | | | |
| | Query Match | 25.3%; Score 71.5; DB 9; Length 249; | |
| | Best Local Similarity | 35.3%; Pred. No. 3.3; | |
| Matches | 12; Conservative | 8; Mismatches | 13; Indels |
| Oy | 8 CSONEFYDLSLHACTIPQLRGSSNPPFLTCQRXC | 41 | |
| | ::::: ::: | | |
| Db | 6 CPDDQYWDSSRSKSCVSCALTCGQRS-QRTCTDFC | 38 | |

| | | |
|----|----|---|
| CC | XX | RESULT 61 |
| CC | XX | AEA55078 |
| CC | XX | ID AEA55078 standard; protein; 249 AA. |
| CC | XX | AEA55078; |
| CC | XX | 11-AUG-2005 (first entry) |
| CC | XX | Tumor necrosis factor receptor superfamily member 13b protein, SEQ: 54. |
| CC | XX | Plasma membrane; diagnosis; therapeutic; cancer; cytostatic; neoplasm; |
| CC | XX | tumor necrosis factor receptor. |
| CC | XX | Mus musculus. |
| CC | XX | WO2005052182-A2. |
| CC | XX | 09-JUN-2005. |
| CC | XX | 25-NOV-2004; 2004WO-IL001085. |
| CC | XX | 26-NOV-2003; 2003US-0524885F. |
| CC | XX | (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM. |
| CC | XX | Linial M, Imberg A, Bledi Y; |
| CC | XX | WPI; 2005-418017/42. |
| CC | XX | DR REFSQ; NP_067324. |
| CC | XX | Characterizing proteins present in a plasma membrane of a cell, useful in |
| CC | XX | identifying diagnostic markers and potential drugs, comprises subjecting |
| CC | XX | a cell to a protease treatment. |
| CC | XX | Claim 25; SEQ ID NO 54; 196pp; English. |
| CC | XX | The present invention relates to a method of characterizing proteins |
| CC | XX | present in the plasma membrane (PM) of live cells. The proteins of the |
| CC | XX | invention are useful in identifying diagnostic markers and potential |

CC drugs. The invention is useful for identifying drugs for diagnosing and
 CC treating disorders such as cancer which are associated with abnormal
 CC representation of cell surface proteins. The present sequence is mouse
 CC tumor necrosis factor receptor superfamily member 13b protein.

XX Sequence 249 AA;

Query Match 25.3%; Score 71.5; DB 9; Length 249;
 Best Local Similarity 35.3%; Pred. No. 3.3;
 Matches 12; Conservative 8; Mismatches 13; Indels 1; Gaps 1;

QY 8 CSQNEYPDSLHACIPCOLRCSNTPTPTCQRYC 41
 Db 6 CPKQYWDSSRKSCVSCALTCISQRS-QRTCTDFC 38

RESULT 62
 ADC71568
 ID ADC71568 standard; protein; 1548 AA.
 XX
 AC ADC71568;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Mouse subtilisin-like protein convertase 6 (SPC6).
 XX
 KM neuroleptic; subtilisin-like protein convertase 6 agonist;
 KM subtilisin-like protein convertase 6 antagonist; transgenic;
 KM subtilisin-like protein convertase 6; SPC6; schizophrenia.
 XX
 OS Mus sp.
 XX
 PN US2003093824-A1.
 XX
 PD 15-MAY-2003.
 XX
 PF 25-JUN-2002; 2002US-00180903.
 XX
 PR 26-JUN-2001; 2001US-0300978P.
 PR 24-SEP-2001; 2001US-0324820P.
 XX
 PA (ALIE/) ALLEN K D.
 XX
 PI Allen KD;
 XX
 DR WPI: 2003-777261/73.
 DR N-PSDB; ADC71567.
 XX
 PT New transgenic mouse useful in methods for identifying potential
 PT therapeutic agents for treating a variety of diseases, including
 PT schizophrenia, comprises a disruption in a subtilisin-like protein
 PT convertase 6 (SPC6) gene.
 XX
 PS Disclosure; SEQ ID NO 2; 349P; English.
 XX
 CC The invention describes a transgenic mouse (1) comprising a disruption in
 CC an subtilisin-like protein convertase (SPC6) gene, where there is no
 CC native expression of an endogenous SPC6 gene. The therapeutic agent is
 CC administered by inhalation or insufflation or oral, buccal, parenteral,
 CC topical, subcutaneous, intraperitoneal, intravenous, intrapleural,
 CC intraocular, intraarterial, or rectal route. The transgenic mouse and
 CC associated methods are useful for identifying potential therapeutic
 CC agents (e.g. SPC6 agonists and antagonists) for treating conditions
 CC associated with SPC6. The identified agents are potentially useful for
 CC treating diseases such as schizophrenia. The mouse is useful for
 CC investigating the biological roles of SPC6. This is the amino acid
 CC sequence of mouse SPC6.
 XX
 SQ Sequence 1548 AA;

Query Match 24.9%; Score 70.5; DB 7; Length 1548;
 Best Local Similarity 34.7%; Pred. No. 30;
 Matches 17; Conservative 5; Mismatches 22; Indels 5; Gaps 1;

QY 7 OCSQNEYPDSLHACIPCOLRCSNTPTPTCQRYC 50
 Db 1151 ECAAYEYWEHSGHRQCPCHKKSCSGSPEDQCYTCRPTPLNTTCVK 1199

RESULT 63
 ABB80243
 ID ABB80243 standard; protein; 1877 AA.
 XX
 AC ABB80243;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Murine subtilase.
 XX
 KM Subtilase; chromosome 9q21.13; EST; expressed sequence tag; kidney;
 KM renal cell; head; neck; heart; multiple sclerosis; lesion; cervix;
 KM pooled germ cell; tumour; uterus; adenocarcinoma; retina II; stomach;
 KM proprotein convertase subtilisin; furin-like repeat; Alzheimer's disease;
 KM Parkinson's disease; pain; colon; pelvic pain; pre-oesophageal dysphagia;
 KM gastritis; ulcers; urinary incontinence; lupus nephritis;
 KM renal transplant rejection; myocardial infarction; erectile dysfunction;
 KM ovary; lung; thyroid; carcinoma; lymphoma; Kaposi's sarcoma;
 KM congestive heart failure; ischaemia; hypertensive vascular disease.
 XX
 OS Mus musculus.
 XX
 PN MO2003060109-A2.
 XX
 PD 24-JUL-2003.
 XX
 PF 14-JAN-2003; 2003WO-EP000253.
 XX
 PR 15-JAN-2002; 2002US-0347876P.
 PR 29-JUL-2002; 2002US-0398734P.
 XX
 PA (FARB) BAYER AG.
 XX
 PI Koehler RH;
 XX
 DR WPI: 2003-608065/57.
 XX
 PT New subtilase-encoding polynucleotide and its encoded protein, useful for
 PT identifying modulators of subtilase activity, and in gene therapy for
 PT treating e.g. Alzheimer's disease, cancers, congestive heart failure or
 PT ischemia.
 XX
 PS Disclosure; Page 122-26; 135P; English.
 XX
 CC This sequence shows a murine subtilase. The homologous human subtilase
 CC coding sequence is located on chromosome 9q21.13. Related EST's are
 CC expressed in kidney (renal cell adenocarcinoma), head and neck tissue,
 CC heart, multiple sclerosis lesions, cervix, pooled germ cell tumours,
 CC uterus tumour, adenocarcinoma, retina II and stomach. The subtilisin
 CC protein is a long membrane bound protein which shows 96% identity to
 CC human proprotein convertase subtilisin. There are two blocks of 11 furin-
 CC like repeats in the C-terminal portion of the protein. It has one
 CC transmembrane domain, also in the C-terminal portion, suggesting that the
 CC protein is localised on the outside of the membrane. The subtilase
 CC polynucleotide and polypeptide are useful for identifying test compounds,
 CC which may act as agonists or antagonists at the receptor site and which
 CC can be regulated to provide therapeutic effects. Vectors comprising the
 CC polynucleotide are useful for modulating the activity of subtilase in a
 CC disease, e.g. a central nervous system disorder, a gastrointestinal
 CC disorder, cancer, a cardiovascular disorder, a genitourinary disorder, or
 CC diabetes. In particular, these diseases are Alzheimer's disease,
 CC Parkinson's disease, pain, colon tumour, pre-oesophageal dysphagia,
 CC gastritis, ulcers, urinary incontinence, lupus nephritis, renal
 CC transplant rejection, pelvic pain, erectile dysfunction, ovary tumour,
 CC lung tumour, thyroid tumour, carcinoma, lymphoma, Kaposi's sarcoma,
 CC congestive heart failure, myocardial infarction, ischaemia, hypertensive
 CC vascular diseases, etc. These are also useful for preventing or

DB 1179 CSODEYFDHEBGVCVPCM-----PPTTPQ 1202

RESULT 66

ID ADR18914 standard; protein; 2240 AA.

XX ADR18914;

XX 04-NOV-2004 (first entry)

DE Mature Human mucin-like protein, SCS0004, variant SEQ ID 4.

XX Antibacterial; Virucide; Antiallergic; Antiasthmatic; Antiinflammatory;

KW Ophthalmological; Auditory; Vulnerary; Gastrointestinal; Cytostatic;

KW Gene Therapy; Mucin-like protein; human; mucin; bacterial infection;

KW allergic asthma; inflammation; viral infection; allergic conjunctivitis;

KW otitis; tissue injury; epithelial wounding; inflammatory bowel disease;

KW Crohn's disease; small adenocarcinoma of the lung; lung cancer;

XX gastric intestinal metaplasia; chronic cholecystitis; skin cancer.

OS Homo sapiens.

XX MO2004069136-A2.

PN 19-AUG-2004.

PD 04-FEB-2004; 2004MO-EP050082.

PF 05-FEB-2003; 2003US-0445217P.

PR (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.

PI Bienkowska J, Mcallister G;

XX MPI; 2004-604324/58.

DR New isolated mucin-like polypeptides, useful for diagnosing or treating,

XX e.g. bacterial infections, allergic asthma, inflammation, allergic

PT conjunctivitis, otitis, inflammatory bowel disease, Crohn's disease, lung

PT cancer, or skin cancer.

PS Claim 2; SEQ ID NO 4; 170bp; English.

XX The present invention relates to novel mucin-like proteins (I) and their

CC coding sequences. The present sequence is one such human mucin-like

CC protein. The mucin-like proteins and coding sequences are useful in the

CC therapy or in the prevention of a disease when the increase in the mucin-

CC like activity of a polypeptide is needed e.g. bacterial infections,

CC allergic asthma, inflammation, respiratory syncytial virus (RSV)-induced

CC disease, allergic conjunctivitis, otitis, tissue injury, epithelial

CC wounding, inflammatory bowel disease, Crohn's disease, small

CC adenocarcinoma of the lung, lung cancer, gastric intestinal metaplasia,

CC chronic cholecystitis, or skin cancer.

XX

SQ Sequence 2240 AA;

Query Match 24.2%; Score 68.5; DB 8; Length 2240;

Best Local Similarity 45.2%; Pred. No. 76;

Matches 14; Conservative 2; Mismatches 8; Indels 7; Gaps 1;

OY 8 CSQNEFYDSLHACIPCOLRCSSNTPPLTCQ 38

DB 1161 CSQDEYFDHEBGVCVPCM-----PPTTPQ 1184

RESULT 67

ID ADR18913 standard; protein; 2258 AA.

XX ADR18913;

XX 04-NOV-2004 (first entry)

XX Human mucin-like protein, SCS0004, variant SEQ ID 3.

DE

XX Antibacterial; Virucide; Antiallergic; Antiasthmatic; Antiinflammatory;

KW Ophthalmological; Auditory; Vulnerary; Gastrointestinal; Cytostatic;

KW Gene Therapy; Mucin-like protein; human; mucin; bacterial infection;

KW allergic asthma; inflammation; viral infection; allergic conjunctivitis;

KW otitis; tissue injury; epithelial wounding; inflammatory bowel disease;

KW Crohn's disease; small adenocarcinoma of the lung; lung cancer;

XX gastric intestinal metaplasia; chronic cholecystitis; skin cancer.

OS Homo sapiens.

XX

XX Key Location/Qualifiers

XX Peptide 1..18

FT /label= Signal_peptide

FT Protein 19..2258

FT /label= Mature_protein

XX MO2004069136-A2.

PN 19-AUG-2004.

PD 04-FEB-2004; 2004MO-EP050082.

PF 05-FEB-2003; 2003US-0445217P.

PR (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.

PI Bienkowska J, Mcallister G;

XX MPI; 2004-604324/58.

DR New isolated mucin-like polypeptides, useful for diagnosing or treating,

XX e.g. bacterial infections, allergic asthma, inflammation, allergic

PT conjunctivitis, otitis, inflammatory bowel disease, Crohn's disease, lung

PT cancer, or skin cancer.

PS Claim 2; SEQ ID NO 3; 170bp; English.

XX The present invention relates to novel mucin-like proteins (I) and their

CC coding sequences. The present sequence is one such human mucin-like

CC protein. The mucin-like proteins and coding sequences are useful in the

CC therapy or in the prevention of a disease when the increase in the mucin-

CC like activity of a polypeptide is needed e.g. bacterial infections,

CC allergic asthma, inflammation, respiratory syncytial virus (RSV)-induced

CC disease, allergic conjunctivitis, otitis, tissue injury, epithelial

CC wounding, inflammatory bowel disease, Crohn's disease, small

CC adenocarcinoma of the lung, lung cancer, gastric intestinal metaplasia,

CC chronic cholecystitis, or skin cancer.

XX

SQ Sequence 2258 AA;

Query Match 24.2%; Score 68.5; DB 8; Length 2258;

Best Local Similarity 45.2%; Pred. No. 77;

Matches 14; Conservative 2; Mismatches 8; Indels 7; Gaps 1;

OY 8 CSQNEFYDSLHACIPCOLRCSSNTPPLTCQ 38

DB 1179 CSQDEYFDHEBGVCVPCM-----PPTTPQ 1202

RESULT 68

ID ADR18915 standard; protein; 2264 AA.

XX ADR18915;

XX 04-NOV-2004 (first entry)

DE His-tagged Human mucin-like protein, SCS0004, variant SEQ ID 5.

XX Antibacterial; Virucide; Antiallergic; Antiasthmatic; Antiinflammatory;

| | |
|-----------|--|
| KV | Ophthalmological; Auditory; Vulvureary; Gastrointestinal; Cystostatic; |
| KW | Gene Therapy; Mucin-like protein; human; mucin; mucinobacterial infection; |
| KM | allergic asthma; inflammation; viral infection; allergic conjunctivitis; |
| KN | otitis; tissue injury; epithelial wounding; inflammatory bowel disease; |
| KX | Crohn's disease; small adenocarcinoma of the lung; lung cancer; |
| XX | gastric intestinal metaplasia; chronic cholecystitis; skin cancer. |
| OS | Homo sapiens. |
| PN | WO2004069136-A2. |
| XX | |
| PD | 19-AUG-2004. |
| XX | |
| PF | 04-FEB-2004; 2004WO-BP050082. |
| PR | 05-FEB-2003; 2003US-0445217P. |
| XX | |
| PA | (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV. |
| XX | |
| PI | Bienkowska J, McAllister G; |
| DR | WPI; 2004-604324/58. |
| XX | |
| PT | New isolated mucin-like polypeptides, useful for diagnosing or treating, |
| PT | e.g. bacterial infections, allergic asthma, inflammation, allergic |
| PT | conjunctivitis, otitis, inflammatory bowel disease, Crohn's disease, lung |
| PT | cancer, or skin cancer. |
| PS | |
| XX | Claim 2; SEQ ID NO 5; 170pp; English. |
| CC | |
| CC | The present invention relates to novel mucin-like proteins (I) and their |
| CC | coding sequences. The present sequence is one such human mucin-like |
| CC | protein. The muchn-like proteins and coding sequences are useful in the |
| CC | therapy or in the prevention of a disease when the increase in the mucin- |
| CC | like activity of a polypeptide is needed e.g. bacterial infections, |
| CC | allergic asthma, inflammation, respiratory syncytial virus (RSV)-induced |
| CC | disease, allergic conjunctivitis, otitis, tissue injury, epithelial |
| CC | wounding, inflammatory bowel disease, Crohn's disease, small |
| CC | adenocarcinoma of the lung, lung cancer, gastric intestinal metaplasia, |
| CC | chronic cholecystitis, or skin cancer. |
| XX | |
| SQ | Sequence 2264 AA: |
| | |
| | Query Match 24.2%; Score 68.5; DB 8; Length 2264; |
| | Best Local Similarity 45.2%; Pred. No. 77; |
| | Matches 14; Conservative 2; Mismatches 8; Indels 7; Gaps 1 |
| OY | 8 CSQNEVPDLSLHACIPQLQRCSNPPLTLCQ 38 : : - |
| DB | 1179 CSQDEYFDHEBGVCVPCM-----PPTTPQ 1202 |
| RESULT 69 | |
| AAU10951 | ID AAU10951 standard; protein; 37 AA. |
| XX | |
| AC | AAU10951; |
| XX | |
| DT | 12-MAR-2002 (first entry) |
| XX | |
| DE | Human AGP-3 receptor cysteine rich repeat region #1. |
| XX | |
| KM | Human; AGP-3; antiinflammatory; antiarthritic; immunosuppressive; |
| KN | dermatological; neuroprotective; nootropic; immunomodulator; metabolic; |
| KX | antidiabetic; analgesic; nephrotropic; osteopathic; cyostatic; fever; |
| KW | antiParkinsonian; antispasmodic; vasotropic; antibacterial; asthma; |
| KV | AGP-3 receptor; tumor necrosis factor ligand family; AGP-3 receptor; |
| KX | mesenteric lymph node; AGP-3R; inflammatory disease; immune disorder; |
| KM | rheumatoid arthritis; graft-versus-host disease; Crohn's disease; |
| KN | pneurctitis; amyotrophic lateral sclerosis; ALS; Alzheimer's disease; |
| KX | diabetes; glomerulonephritis; inflammatory bowel disease; ischaemia; |
| KV | multiple sclerosis; Parkinson's disease; transgenic animal. |
| XX | |

| | |
|-----------|--|
| XX | Homo sapiens. |
| XX | MOZ00185782-A2. |
| PX | |
| PD | 15-NOV-2001. |
| XX | |
| PF | 12-FEB-2001; 2001WO-US004568. |
| PR | 11-FEB-2000; 2000US-0181800P. |
| XX | |
| PA | (AMGE-) AMGEN INC. |
| P1 | Boyle WJ, Hsu H; |
| XX | |
| DR | WPI; 2002-049441/06. |
| XX | |
| PT | Composition useful for identifying modulator of receptor for treating |
| PT | asthma and glomerulonephritis, comprises AGP-3 (tumor necrosis factor |
| PT | ligand family member) receptor and encoding nucleic acids. |
| XX | |
| PS | Claim 1; Fig 18; 124pp; English. |
| XX | |
| CC | The invention relates to a composition (I) comprising AGP-3 receptor |
| CC | (tumour necrosis factor ligand family member) related protein (II) |
| CC | attached to a vehicle protein. (I) is useful for modulating AGP-3-related |
| CC | activity in mesenteric lymph nodes (MLN) of a mammal. (II) is useful in |
| CC | assays to identify cells and tissues that express AGP-3R or proteins |
| CC | related to AGP-3R-related protein and for identifying compounds (agonists |
| CC | or antagonists) that interact with AGP-3R proteins. (II) is also useful |
| CC | for identifying intracellular proteins that interact with the respective |
| CC | cryoplastic domains by yeast two-hybrid screening process. (II) is |
| CC | involved in B cell growth, survival and activation particularly in lymph |
| CC | node, spleen, and Peyer's patches. AGP-3R agonists and antagonists |
| CC | identified using (II) are used for modulating B cell response and are |
| CC | used to treat diseases characterised by inflammatory processes or |
| CC | deregulated immune response such as rheumatoid arthritis, graft-versus- |
| CC | host disease, Crohn's disease, lupus, etc. (II) is also useful in the |
| CC | production of hybridoma cells which are derived from B cells, which |
| CC | involves treating the hybridoma cells with (II). (II) is useful in the |
| CC | treatment of inflammatory conditions of joints, e.g., rheumatoid |
| CC | arthritis, osteoarthritis, etc. (II), its agonists or antagonists are |
| CC | useful for treating acute pancreatitis, amyotrophic lateral sclerosis |
| CC | (ALS), Alzheimer's disease, asthma, atherosclerosis, cachexia/anorexia, |
| CC | diabetes, fever, glomerulonephritis, inflammatory bowel disease, |
| CC | ischemic injury including cerebral ischaemia, multiple myeloma, multiple |
| CC | sclerosis, osteoporosis, Parkinson's disease, pain, reperfusion injury, |
| CC | septic shock, etc. The nucleic acids are also useful for developing |
| CC | transgenic animals expressing (II), which are useful for producing the |
| CC | polypeptides and for the study of in vivo biological activity. The |
| CC | present sequence represents the amino acid sequence of human AGP-3 |
| CC | cysteine-rich repeat region #1 |
| XX | |
| SQ | Sequence 37 AA; |
| | |
| | Query Match 23.9%; Score 67.5; DB 5; Length 37. |
| | Best Local Similarity 30.6%; Pred. No. 1.3; |
| Matches | 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1; |
| OY | 8 CSQNEYFDSLHACIPCOLRCSSNTPLTCORYNA 43 : : : : : : : : Db 2 CPBEQYMDPLLGTCTMCSKTCICNHQS -ORTCAAFCS 36 |
| RESULT 70 | |
| ADZ67772 | |
| ID | ADZ67772 standard; protein; 48 AA. |
| XX | |
| AC | ADZ67772; |
| XX | |
| DT | 14-JUL-2005 (first entry) |
| XX | |
| DE | Human tumor necrosis factor receptor TACI Cys-rich domain. |

KW Tumor necrosis factor receptor; TACI; cancer; neoplasm; diagnosis;
KM cytosolic.
XX
OS Homo sapiens.
XX
FN WO2005037865-A2.
XX
PD 28-APR-2005.
XX
PF 18-OCT-2004; 2004WO-US034375.
XX
PR 16-OCT-2003; 2003US-0511699P.
XX
PR 18-OCT-2004; 2004US-0619552P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Fox BA, Holloway JL, Sheppard PO, Dillon SR;
XX
DR WPI; 2005-315682/32.
XX
XX New tumor necrosis factor receptor (TNFR) polypeptides, useful as
PT detecting ligands, and for modulating tumor growth, metastasis and
PT immunity, such as separating resting from stimulated immune cells.
XX
XX Disclosure; SEQ ID NO 20; 132pp; English.
XX
PS The invention provides novel tumor necrosis factor receptor (TNFR)
XX ztnfr14 polynucleotides AD267753 and polypeptides AD267754, expression
CC vectors and antibodies. Ztnfr14 polynucleotides are used in claimed
CC methods for detecting a genetic abnormality in a patient and for
CC detecting a cancer in a patient. Recombinant ztnfr14 polypeptide,
CC optionally conjugated to a toxin, is used in a claimed method of killing
CC cancer cells. Ztnfr14 polypeptides can be used to detect ligands,
CC agonists and antagonists. The polypeptides, polynucleotides and
CC antibodies may also be used in methods that modulate tumor growth,
CC metastasis, and immunity such as separating resting from stimulated
CC immune cells. The present sequence is that of the Cys-rich domain of
CC human TNFR TACI AD267771. This sequence was compared with that of ztnfr14
CC in the identification of ztnfr14 as a member of the TNFR family.
XX
SQ Sequence 48 AA;
XX
XX Query Match 23.9%; Score 67.5; DB 9; Length 48;
XX Best Local Similarity 30.6%; Pred. No. 1.7;
XX Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
OY 8 GSONEYFDSLHACTIPQRLRSSNTPLTCQRYCNA 43
DB 13 CPBEQYWDPLLTGTCWSCSKTICNHQS-QRTCAAFCRS 47
XX
XX RESULT 71
XX ID AAE15500 standard; peptide; 59 AA.
XX
XX AAE15500;
XX
XX 12-MAR-2002 (first entry)
XX
XX Human TACI cysteine rich extracellular region.
XX
XX Human; transmembrane activator and intracellular CAML interactor; TACI;
KM cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KM lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KM prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KM drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KM Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KM human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KM rheumatoid arthritis; atherosclerosis.
XX
XX Homo sapiens.
XX
XX WO200187979-A2.
XX
XX

XX
PD 22-NOV-2001.
XX
PF 14-MAY-2001; 2001WO-US015567.
XX
XX
XX 12-MAY-2000; 2000US-0204039P.
XX
PR 27-JUN-2000; 2000US-0214591P.
XX
PR 14-MAY-2001; 2001US-00214591.
XX
XX
XX (AMGE-) AMGEN INC.
XX
XX Theell LE, Yu G;
XX
XX WPI; 2002-066686/09.
XX
XX Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor family
PT ligand.
XX
XX Disclosure; Fig 13; 94pp; English.
XX
XX The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering a
CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour, APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human TACI cysteine-rich extracellular region
XX
XX Sequence 59 AA;
XX
XX Query Match 23.9%; Score 67.5; DB 5; Length 59;
XX Best Local Similarity 30.6%; Pred. No. 2.2;
XX Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
OY 8 GSONEYFDSLHACTIPQRLRSSNTPLTCQRYCNA 43
DB 1 CPBEQYWDPLLTGTCWSCSKTICNHQS-QRTCAAFCRS 35
XX
XX RESULT 72
XX ID AAW75785 standard; protein; 166 AA.
XX
XX AAW75785;
XX
XX 18-JUN-1999 (first entry)
XX
XX Human lymphocyte surface receptor extracellular domain.
XX
XX TACI; transmembrane activator and CAML-interactor;
KM calcium signal-modulating cyclophilin ligand; human;
KM lymphocyte surface receptor; human; B-cell; B lymphocyte; infection;
KM cancer; rheumatoid arthritis; autoimmune disease; glomerulonephritis;
KM immunosuppressive; graft versus host disease; transplant rejection;
KM therapy; signal transduction.
XX
XX Homo sapiens.
XX
XX WO9839361-A1.
XX
XX

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XX PD 11-SEP-1998.
XX XX
XX PF 03-MAR-1998; 98WO-US004270.
XX XX
XX PR 03-MAR-1997; 97US-00810572.
XX XX
XX PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX PI
XX PI Bram RJ, Von Bulow G;
XX XX
XX DR WPI; 1998-506346/43.
XX DR N-PSDB; AAV57330.
XX XX
XX PT New isolated transmembrane activator protein - used to develop products
XX PT for treating e.g. infections, cancers, autoimmune and inflammatory
XX PT conditions, transplant rejection or graft-versus-host disease.
XX XX
XX PS Claim 8; Page 73; 89pp; English.
XX XX
XX CC This is the amino acid sequence of the N-terminal, i.e. the
XX CC extracellular, domain of novel human transmembrane activator and CAML-
XX CC interactor (TACI) protein (see AAW5783). TACI is a lymphocyte receptor
XX CC protein that is involved in the calcium activation pathway. It is
XX CC normally present in B-lymphocytes, and to a much lesser extent in
XX CC immature T-lymphocytes, and can therefore be targeted to specifically
XX CC regulate B cell responses without affecting T cell activity. The
XX CC extracellular domain of TACI functions as a binding site for a ligand
XX CC that stimulates the activation of the cell by inducing the binding of the
XX CC C-terminal portion (see AAW5784) of TACI to the N-terminal domain of
XX CC CAML. A recombinant form of the extracellular portion of TACI acts as a
XX CC dominant-negative or blocking agent and acts to suppress the immune
XX CC system. It can be used to treat or prevent autoimmune disease, graft
XX CC rejection or graft versus host disease. The extracellular region is also
XX CC used in a claimed method for identifying a ligand for TACI, in which
XX CC binding of a candidate molecule is determined by detecting cellular
XX CC activation of the AP-1, CAMP or NF-KB pathway, of NF-AT transcription
XX CC factor, or of NF-AT dependent transcription
XX XX
XX SQ Sequence 166 AA;
XX XX
XX Query Match 23.9%; Score 67.5; DB 2; Length 166;
XX Best Local Similarity 30.6%; Pred. No. 6.5;
XX Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
XX XX
OY 8 CSQNEYPDSLHACTPCQLRCSSNTPPLTCGRYCNA 43
DB 34 CPEEQYWDPLLTGTCWCKTICNHQS-QRTCAAFCS 68
XX XX
XX RESULT 73
XX AAE15494
XX ID AAE15494 standard; protein; 166 AA.
XX AC AAE15494;
XX XX
XX DT 12-MAR-2002 (first entry)
XX XX
XX DE Human TACI extracellular domain.
XX XX
XX KW Human; transmembrane activator and intracellular CAML interactor; TACI;
XX KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
XX KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
XX KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
XX KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
XX KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
XX KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
XX KW rheumatoid arthritis; atherosclerosis.
XX KW
XX OS Homo sapiens.
XX XX
XX PN WO200187979-A2.
XX XX
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XX PD 22-NOV-2001.
XX XX
XX PF 14-MAY-2001; 2001WO-US015567.
XX XX
XX PR 12-MAY-2000; 2000US-0204039P.
XX PR 27-JUN-2000; 2000US-0214591P.
XX PR 14-MAY-2001; 2001US-00214591.
XX XX
XX PA (AMGE-) AMGEN INC.
XX XX
XX PI Theill LE, Yu G;
XX XX
XX DR WPI; 2002-066686/09.
XX XX
XX PT Inhibiting activity of B cell maturation protein and/or transmembrane
XX PT activator and intracellular cyclophilin ligand interactor, by
XX PT administering a binding partner for APRIL, a tumor necrosis factor family
XX PT ligand.
XX XX
XX PS Claim 1; Fig 12A; 94pp; English.
XX XX
XX CC The invention relates to a method for inhibiting TACI (transmembrane
XX CC activator and intracellular CAML interactor) and/or B cell maturation
XX CC protein (BCMA) activity in a mammal. The method comprises administering a
XX CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
XX CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
XX CC BCMA extracellular consensus sequence, but not the extracellular region
XX CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
XX CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
XX CC lymphoproliferative disorders, one or more solid tumours such as lung,
XX CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
XX CC antagonists are useful for treating inflammation and immune function
XX CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
XX CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
XX CC disease), drug and insect sting allergy, inflammatory bowel disease
XX CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
XX CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
XX CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
XX CC with leucocyte infiltration of the skin or organs. The present sequence
XX CC is human TACI protein extracellular domain
XX XX
XX SQ Sequence 166 AA;
XX XX
XX Query Match 23.9%; Score 67.5; DB 5; Length 166;
XX Best Local Similarity 30.6%; Pred. No. 6.5;
XX Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
XX XX
OY 8 CSQNEYPDSLHACTPCQLRCSSNTPPLTCGRYCNA 43
DB 34 CPEEQYWDPLLTGTCWCKTICNHQS-QRTCAAFCS 68
XX XX
XX RESULT 74
XX ADN03188
XX ID ADN03188 standard; protein; 171 AA.
XX AC ADN03188;
XX XX
XX DT 15-JUL-2004 (first entry)
XX XX
XX DE Human TACI-HSHP fragment SEQ ID NO:18.
XX XX
XX KW transmembrane activator and CAML interactor; TACI; extracellular domain;
XX KW trimerising polypeptide; homotrimeric protein complex; antiinflammatory;
XX KW antirheumatic; antirheumatic; immunosuppressive; antiatherosclerotic;
XX KW cytosolic; gene therapy; inflammatory disease; rheumatoid arthritis;
XX KW inflammatory bowel disease; autoimmune disease; atherosclerosis;
XX KW osteoporosis; allograft rejection; cancer; human;
XX KW heat shock binding protein; HSBP; fusion protein.
XX KW
XX OS Homo sapiens.
XX XX
XX OS Synthetic.
XX XX
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PN WO2004033486-A2.

XX 22-APR-2004.

PD 10-OCT-2003; 2003WO-US032878.

XX 11-OCT-2002; 2002US-0417801P.

XX (ZYMO) ZYMOGENETICS INC.

XX West JW, Brandt CS, Jaspers SR;

PI WPJ; 2004-364855/34.

DR N-PSDB; ADN03187.

XX

PT New polypeptide comprising an extracellular domain of the transmembrane

PT activator and calcium-signal modulating cyclophilin ligand (CAML)

PT Interactor (TACI), and a trimerizing polypeptide, useful for treating

PT inflammatory diseases.

XX

PS Example 4; SEQ ID NO 18; 36Pp; English.

XX

CC The present invention describes an isolated polypeptide comprising an

CC extracellular domain of the transmembrane activator and calcium-signal

CC modulating cyclophilin ligand (CAML) interactor (TACI), and a trimerizing

CC polypeptide. Also described: (1) a homotrimeric protein complex

CC comprising the polypeptide; (2) an expression vector comprising the

CC following operably linked elements, a transcription promoter, the nucleic

CC acid sequence encoding the polypeptide, and a transcription terminator;

CC (3) a cultured cell into which has been introduced the expression vector,

CC where the cell expresses the polypeptide; (4) producing a homotrimeric

CC protein complex by culturing the cell, and recovering the homotrimeric

CC B cell proliferation by exposing the B cells to the homotrimeric protein

CC complex. The polypeptide has antiinflammatory, antiarthritic,

CC antirheumatic, immunosuppressive, antiartherosclerotic and cytostatic

CC activities, and can be used in gene therapy. The polypeptides are useful

CC for treating and controlling inflammatory diseases, e.g. Rheumatoid

CC arthritis or inflammatory bowel disease, autoimmune disease,

CC atherosclerosis, osteoporosis, allograft rejection and cancer. The

CC present sequence represents a human TACI and heat shock binding protein

CC (HSBP) fusion protein fragment, which is used in the exemplification of

CC the present invention.

XX

SQ Sequence 171 AA;

XX

Query Match 23.9%; Score 67.5; DB 8; Length 171;

Best local Similarity 30.6%; Pred. No. 6.7;

Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 11

QY 8 CSQNEFDSLHACIPQLRCSSNTPPLTCORYCNA 43

DB 6 CPSEQYMDPLIGTCWMSCKTICNHOS-QRTCAFCRS 40

AAE09244

ID AAE09244 standard; protein; 265 AA.

XX AAE09244;

XX 19-NOV-2001 (first entry)

DT

XX Human TACI splice variant protein.

DE Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;

XX TACI; BCGM; therapy; cancer; leukemia; myeloma; lymphoma;

KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.

XX Homo sapiens.

OS

XX WO200160397-A1.

PN

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PD 23-AUG-2001.
PF 28-NOV-2000; 2000MO-US032378.
PR 16-FEB-2000; 2000US-0182938P.
PR 22-AUG-2000; 2000US-0226986P.
PA (GETH ) GENENTECH INC.
PI Ashkenazi AJ, Dodge KM, Grewal I, Kim KJ, Marsters SA, Pletti RM;
PI Yan M;
DR WPI; 2001-541628/60.
PT Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
PT activity, for treating autoimmune disorders and cancer, comprises
PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
PT antagonists.
XX
XX Example 1; Fig 6; 160pp; English.
XX
XX The invention relates to methods of using one or more agonists or
XX antagonists to modulate the activity of the members of TNF (tumour
XX necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g.
XX TACI or BcMA. The method is useful for treating pathological conditions
XX or diseases associated with increased TALL-1 and APRIL expression or
XX activity. TALL-1 and APRIL antagonists are used to block the interaction
XX between APRIL and TALL-1 with TACI or BcMA. They are useful for treating
XX a mammal suffering from cancer such as leukaemia, lymphoma, myeloma,
XX cancers of lung and colon and autoimmune diseases e.g. rheumatoid
XX arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The
XX present sequence is human TACI splice variant protein
XX
XX Sequence 265 AA:
SQ
Query Match 23.8%; Score 67.5; DB 4; Length 265;
Best Local Similarity 30.6%; Pred. No. 11,
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
QY 8 CSQNEVFDLSLHACIPCOLRCSSNTPELFCORYCNA 43
| : : | | | : : : | : : | :
Db 34 CPREGVMDPLLGTCMCKTICNQS-QRTCAAFCS 68
RESULT 76
ABP97723
ID ABP97723 standard; protein; 266 AA.
XX
XX ABP97723;
XX AC
XX DT 28-MAY-2003 (first entry)
XX
XX Amino acid sequence of an alternatively spliced human TACI receptor.
XX DE
XX KW Human; TNCI; BR3; receptor; tumour necrosis factor ligand; TNF ligand;
XX TALL-1; April; systemic lupus erythematosus.
XX
XX Homo sapiens.
XX OS
XX PN MO2003014294-A2.
XX
XX 20-FEB-2003.
XX
XX 24-JUL-2002; 2002MO-US023487.
XX
XX 03-AUG-2001; 2001US-0310114P.
XX PR 30-APR-2002; 2002US-0377171P.
XX
XX (GETH ) GENENTECH INC.
XX PA
XX Dixit V, Grewal I, Ridgway J, Yan M;
XX WPI; 2003-256560/25.
XX

```


XX New nucleic acid encoding a TACIs or BR3 polypeptide, useful for
PT preparing a composition for treating systemic lupus erythematosus.
XX
XX Disclosure; Fig 8; 153pp; English.
XX
XX The present sequence represents an alternatively spliced human TACI
CC polypeptide. The specification also describes BR3 polypeptides. TACI and
CC BR3 are receptors. Tumour necrosis factor (TNF) family ligands. TACI-1 and
CC April bind to the TACI receptor, while TNF family ligands TACI-1 also
CC binds to BR3 receptor. The TACI and BR3 receptor nucleic acid is useful
CC for preparing a composition for treating systemic lupus erythematosus
XX
XX Sequence 266 AA;
SQ
Query Match 23.9%; Score 67.5; DB 6; Length 266;
Best Local Similarity 30.6%; Pred. No. 11;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
OY 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNA 43
DB 34 CPEEQYWDPLGTCTCWSCKTICNHQS-QRTCAAFCRS 68
RESULT 77
ADM03442
ID ADM03442 standard; protein; 266 AA.
XX
XX ADM03442;
AC
XX
XX 24-MAR-2005 (first entry)
DT
XX
XX Human TACI protein amino acid sequence #3.
DE
XX
XX B-lymphocyte; b-cell lymphoma; autoimmune disease; immunosuppressive;
KM non-hodgkin lymphoma; hodgkins disease; cytostatic;
KM chronic lymphocytic leukemia; hairy cell leukemia; rheumatoid arthritis;
KM antirheumatic; antineumatic; systemic lupus erythematosus;
KM Wegener granulomatosis; antiallergic; antiinflammatory; vasotropic;
KM inflammatory bowel disease; gastrointestinal-gen.;
KM idiopathic thrombocytopenic purpura; hemostatic; multiple sclerosis;
KM asthma; antiaesthetic; psoriasis; antipsoriatic; myasthenia gravis;
KM muscular-gen.; neuroprotective; vasculitis; diabetes; antidiabetic;
KM glomerulonephritis; nephrotropic; TACI.
XX
XX Homo sapiens.
OS
XX
XX WO2005000351-A2.
PN
XX
XX 06-JAN-2005.
PD
XX
XX 04-JUN-2004; 2004WO-US017693.
PF
XX
XX 05-JUN-2003; 2003US-0476414P.
PR 05-JUN-2003; 2003US-0476414P.
PR 06-JUN-2003; 2003US-0476531P.
XX
XX (GETH) GENENTECH INC.
PA
XX
XX Chan A, Gong Q, Martin F;
PI
XX
XX WPI; 2005-058069/06.
DR
XX
XX
XX Depleting B cells from a mixed population of cells by contacting the
PT cells with a Blys antagonist and a CD20 binding antibody, useful for
PT treating B cell malignancies and autoimmune disorders.
XX
XX Disclosure; Fig 8; 114pp; English.
XX
XX The invention comprises a method of depleting B cells from a mixed
CC population of cells, the method involves contacting the mixed population
CC of cells with Blys antagonist (e.g. an immunoadhesin) and a CD20 binding
CC antibody (e.g. hu2H7.v16). The method of the invention is useful for

CC treating B cell malignancies and autoimmune disorders, such as: non-
CC Hodgkin's lymphoma, Hodgkin's disease, follicular center cell lymphomas,
CC lymphocytic leukemia, hairy cell leukemia, rheumatoid arthritis, systemic
CC lupus erythematosus, Wegener's disease, inflammatory bowel disease,
CC idiopathic thrombocytopenic purpura, multiple sclerosis, asthma,
CC psoriasis, IGA nephropathy, myasthenia gravis, vasculitis, diabetes and
CC glomerulonephritis. The present amino acid sequence represents a human
CC TACI protein.
XX
XX Sequence 266 AA;
SQ
Query Match 23.9%; Score 67.5; DB 9; Length 266;
Best Local Similarity 30.6%; Pred. No. 11;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
OY 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNA 43
DB 34 CPEEQYWDPLGTCTCWSCKTICNHQS-QRTCAAFCRS 68
RESULT 78
AAU10949
ID AAU10949 standard; protein; 291 AA.
XX
XX AAU10949;
AC
XX
XX 12-MAR-2002 (first entry)
DT
XX
XX Human AGP-3 receptor extracellular domain.
DE
XX
XX Human; AGP-3; antiinflammatory; antiarthritic; immunosuppressive;
KM dermatological; neuroprotective; nootropic; immunomodulator; metabolic;
KM antidiabetic; analgesic; nephrotropic; osteopathic; cytostatic; fever;
KM antiparkinsonian; antipsoriatic; vasotropic; antibacterial; asthma;
KM AGP-3 receptor; tumour necrosis factor ligand family; AGP-3 receptor;
KM mesenteric lymph node; AGP-3R; inflammatory disease; immune disorder;
KM rheumatoid arthritis; graft-versus-host disease; Crohn's disease;
KM pancreatitis; amyotrophic lateral sclerosis; ALS; Alzheimer's disease;
KM diabetes; glomerulonephritis; inflammatory bowel disease; ischaemia;
KM multiple sclerosis; Parkinson's disease; transgenic animal.
XX
XX Homo sapiens.
OS
XX
XX WO200185782-A2.
PN
XX
XX 15-NOV-2001.
PD
XX
XX 12-FEB-2001; 2001WO-US004568.
PF
XX
XX 11-FEB-2000; 2000US-0181800P.
PR
XX
XX (AMGE-) AMGEN INC.
PA
XX
XX Boyle WJ, Hsu H;
PI
XX
XX WPI; 2002-049441/06.
DR
XX
XX
XX Composition, useful for identifying modulator of receptor for treating
PT asthma and glomerulonephritis, comprises AGP-3 (tumour necrosis factor
PT ligand family member) receptor and encoding nucleic acids.
XX
XX Claim 1; Fig 18; 124pp; English.
PS
XX
XX The invention relates to a composition (I) comprising AGP-3 receptor
CC (tumour necrosis factor ligand family member) related protein (II)
CC attached to a vehicle protein. (I) is useful for modulating AGP-3-related
CC activity in mesenteric lymph nodes (MLN) of a mammal. (II) is useful in
CC assays to identify cells and tissues that express AGP-3R or proteins
CC related to AGP-3R-related protein and for identifying compounds (agonists
CC or antagonists) that interact with AGP-3R proteins. (II) is also useful
CC for identifying intracellular proteins that interact with the respective
CC cytoplasmic domains by yeast two-hybrid screening process. (II) is
CC involved in B cell growth, survival and activation particularly in lymph

CC node, spleen, and Peyer's patches. AGP-3R agonists and antagonists
CC identified using (II) are used for modulating B cell responses and are
CC used to treat diseases characterised by inflammatory processes or
CC deregulated immune responses such as rheumatoid arthritis, graft-versus-
CC host disease, Crohn's disease, lupus, etc. (II) is also useful in the
CC production of hybridoma cells which are derived from B cells, which
CC involves treating the hybridoma cells with (II). (II) is useful in the
CC treatment of inflammatory conditions of joints, e.g., rheumatoid
CC arthritis, osteoarthritis, etc. (II), its agonists or antagonists are
CC useful for treating acute pancreatitis, amyotrophic lateral sclerosis
CC (ALS), Alzheimer's disease, asthma, atherosclerosis, cachexia/anorexia,
CC diabetes, fever, glomerulonephritis, inflammatory bowel disease,
CC ischaemic injury including cerebral ischaemia, multiple myeloma, multiple
CC sclerosis, osteoporosis, Parkinson's disease, pain, repetitive injury,
CC septic shock, etc. The nucleic acids are also useful for developing
CC transgenic animals expressing (II), which are useful for producing the
CC polypeptides and for the study of *in vivo* biological activity. The
CC present sequence represents the amino acid sequence of human AGP-3
CC extracellular domain
XX
XQ Sequence 291 AA;

| | | | | |
|--------------------------|-------|---------------|----------|-----------|
| Query March | 23.9% | Score 67.5 | DB 5 | Length 21 |
| Best Local Similarity | 30.6% | Pred. No. 12 | | |
| Matches 11, Conservative | 9 | Mismatches 15 | Indels 1 | Gaps 1 |

QY 8 CSQNEYFDLSLHACIPQLRCSSTNPPLTTCQRYCNA 43
| : : | | : : : | : : :
Db 34 CPBEQYMDPLIGTCSCKTICNHQS-QRTCAAFCRS 68

| | |
|----------|------------------------------------|
| RESULT | 79 |
| ADZ67771 | |
| ID | ADZ67771 standard; protein; 292 AA |

DT 14-JUL-2005 (first entry)

Human tumor necrosis factor receptor TACI.

KW Tumor necrosis factor receptor; TNF; cancer; neoplasm; diagnosis;
KW cytostatic.

OS Homo sapiens.

| | | |
|----|--------|--------------------------|
| FH | Key | Location/Qualifiers |
| FT | Domain | 22. .43 |
| FT | | /note= "Cys-rich domain" |

PN WO2005037865-A2

PD 28-APR-2005

PF 18-OCT-2004; 2004WO-US034375.

PR 16-OCT-2003; 2003US-0511698P

XX (ENNO) EMMOCCHIAIENTE C C +NO

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844
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847
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850
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DR WPI; 2005-315682/32.

PT New tumor necrosis factor receptor (TNFR) polypeptides, useful as
PT detecting ligands, and for modulating tumor growth, metastasis and
PT immunity, such as separating resting from stimulated immune cells.

PS Disclosure; SEQ ID NO 19; 132pp; English.

| | |
|----|---|
| CC | The invention provides novel tumor necrosis factor receptor (TNFR) |
| CC | znfr14 polynucleotides ADZ67753 and polypeptides ADZ67754, expression |

CC vectors and antibodies. znfnr14 polynucleotides are used in claimed
CC methods for detecting a genetic abnormality in a patient and for
CC detecting a cancer in a patient. Recombinant znfnr14 polypeptide,
CC optionally conjugated to a toxin, is used in a claimed method of killing
CC cancer cells. znfnr14 polypeptides can be used to detect ligands,
CC agonists and antagonists. The polypeptides, polynucleotides and
CC antibodies may also be used in methods that modulate tumor growth,
CC metastasis, and immunity such as separating reeling from stimulated
CC immune cells. The present sequence is that of human TNFR TAC1. This
CC sequence was compared with that of znfnr14 in the identification of
CC znfnr14 as a member of the TNFR family.

SQ Sequence 292 AA;

| | | | | |
|-----------------------|----------------|---------------|----------|------------|
| Query Match | 23.9% | Score 67.5 | DB 9 | Length 292 |
| Best Local Similarity | 30.6% | Pred. No. 12 | | |
| Matches 11 | Conservative 9 | Mismatches 15 | Indels 1 | Gaps 1. |

```

QY      8 CSQNEYFDLSLHACIPQLRCSSNTPPLTQRYCNA 43
      | : : | : : | : : | : : | : : |
Db     34 CPREYWDPLLTGTCMSCKTINHQ-SQRTCAFCRS 66

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| | |
|-----------|------------------------------------|
| RESULT 80 | |
| AAW75783 | |
| ID | AAW75783 standard; protein; 293 AA |

| | |
|----|---------------------------|
| AC | AAW75783; |
| XX | |
| DT | 18-JAN-1999 (first entry) |

Human lymphocyte surface receptor TACI.

KM TAC1; transmembrane activator and CAML-interactor;
KM calcium signal-modulating cyclophilin ligand; human;
KM lymphocyte surface receptor; human; B-cell; B lymphocyte; infection;
KM cancer; rheumatoid arthritis; autoimmune disease; glomerulonephritis
KM immunosuppressive; graft versus host disease; transplant rejection;
KM therapy.

OS Homo sapiens

| Key | Location/Qualifiers |
|-----|------------------------------|
| FH | 1. .166 |
| FT | /label= Extracellular_domain |
| FT | . |

| FT | Peptide | 34. .71 |
|----|---------|---------|
| | | |

| FT | Domain | 167. | .186 |
|----|--------|------|------|
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|----|--------|------|------|
| FT | Domain | 187. | .294 |
|----|--------|------|------|

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FT /note= "Claim 6"
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PN WO9839361-A1

PD 11-SEP-1998

PF 03-MAR-1998; 98WO-US004270.

PR 03-MAR-1997; 97US-00810572.

PA (SJD-) ST JUDE CHILDREN'S RES HOSPITAL.
YY

PI Bram RJ, Von Bulow G;
VY

DR WPI; 1998-506346/43.
DR N-PEND; 1998-506346/43.

DR N-PSDB; AAV57328.

PT New isolated transmembrane activator protein - used to develop products
PT for treating e.g. infections, cancers, autoimmune and inflammatory
PT conditions, transplant rejection or graft-versus-host disease.

XX Disclosure; Page 136-137; 154pp; English.

CC The present invention describes a human tumour necrosis factor receptor
XX designated Znfir2 (I). (I) has cytostatic, immunosuppressive,
CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
CC antineumatic, antiarthritic, antiashtmatic, nephrotropic and hypotensive
CC activities, can be used in gene therapy. (I) can be used for
CC inhibiting, in a mammal, the activity of a ligand that binds Znfir2
CC (e.g. ZTNF4), for treating disorders and diseases associated with B
CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
CC inhibiting the proliferation of tumour cells. (I) is useful for treating
CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
CC leukaemia, nephritis, and pyelonephritis, and for treating renal
CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
CC amyloidosis, hypertension, large vessel diseases, graft-versus host
CC disease, graft rejection and Crohn's disease. (I) is useful for
CC modulating the immune system, for regulating B cell responses and
CC development, for modulating development of other cells, antibody
CC production and cytokine production, and for modulating T and B cell
CC communication. The present sequence represents a protein which is given
CC in the exemplification of the present invention

XX XX

SQ Sequence 293 AA;

Query Match 23.9%; Score 67.5; DB 5; Length 293;
Best Local Similarity 30.6%; Pred. No. 12;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1

QY 8 CSONEYPDSLHACIPCOLRCSSNTPPTCORCYNA 43
ID :|::|||::|::|::|::|:
Db 34 CPREGWMDPLGTGMSCKTICNHQS-QRTCAAFCS 68

RESULT 87
AAU99512
ID AAU99512 standard; protein; 293 AA.
XX
XX AAU99512;
DT 07-OCT-2002 (first entry)
XX
XX Human TACI-IgG Fc fusion protein.
DE
KW Human, tumour necrosis factor; TNF delta; pulmonary system disorder;
KW immunoglobulin production; B-cell proliferation; immune system disorder;
KW autoimmune disease; cancer; lymphoproliferative disorder; pain;
KW microbial infection; parasitic infection; bone disease; atherosclerosis;
KW cardiovascular disorder; neurodegenerative disease; wound healing;
KW graft versus host disease; haematopoietic cell disorder; nephritis;
KW transmembrane activator and CAML-interactor; TACI; TNF epsilon; IgG;
KW immunoglobulin G; Fc portion.
XX
OS Homo sapiens.
XX
XX AAU99512
XX US2002064829-A1.
PD
XX 30-MAY-2002.
PE
PF 14-JUN-2001; 2001US-00879919.
XX
PR 14-MAR-1996; 96US-0016812P.
PR 12-MAR-1997; 97US-00815783.
PR 15-JUN-2000; 2000US-0211537P.
PR 23-OCT-2000; 2000US-0241952P.
PR 13-DEC-2000; 2000US-0254875P.
PR 16-MAR-2001; 2001US-0276248P.
PR 23-MAR-2001; 2001US-0279787P.
PR 25-MAY-2001; 2001US-0293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.

[illegible]

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PD 29-AUG-2002.
PE 06-FEB-2002; 2002MO-US003500.
XX
XX
XX 20-FEB-2001; 2001US-0270274P.
PR 12-APR-2001; 2001US-0283447P.
XX
XX (ZYMO ) ZYMOGENETICS INC.
PA
XX Kindsvogel W;
PI WPI; 2002-723183/78.
XX DR N-PSDB; AAD46411.
XX
XX B-cell maturation antigen and transmembrane activator and calcium-
PT modulator and cyclophilin ligand-interactor, useful for treating
PT disorders e.g. inflammation or lymphoma.
XX
XX Claim 9; Page 66; 67pp; English.
XX
XX The invention relates to the manufacture of a composition for inhibiting
XX the proliferation of tumour cells. The method involves using an antibody
XX component that binds both the B-cell maturation antigen (BCMA) and the
XX transmembrane activator and calcium-modulator and cyclophilin ligand-
XX interactor (TACI). BCMA and TACI binding antibody compositions are useful
XX for inhibiting proliferation of tumour cells, particularly inhibiting
XX ZMYTA activity in a mammal associated with increased endogenous antibody
XX production or a disorder consisting of neoplasm, chronic lymphocytic
XX leukaemia, multiple myeloma, non-Hodgkin's lymphoma, post-transplantation
XX lymphoproliferative disease or light chain gammopathy or inflammation
XX e.g. asthma. The invention is also useful in gene therapy. The present is
XX human TACI protein
XX
XX Sequence 293 AA;
SQ
Query Match 23.9%; Score 67.5; DB 5; Length 293;
Best Local Similarity 30.6%; Pred. No. 12;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
OY 8 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYCNA 43
DB 34 CPBEQYWPDLGTGTCMSCKTICNHQS-QRTCAAFCS 68
RESULT 89
ID AAU75408 standard; protein; 293 AA.
AC AAU75408;
XX
XX 09-APR-2002 (first entry)
DT
XX
XX Tumour necrosis factor (TNF) receptor TACI-Fc fusion.
DE
XX
XX Tumour necrosis factor; TNF; cytostatic; arteriosclerosis; analgesic;
KM cerebrioprotective; neurotrophic; neuroprotective; hepatotropic;
KM immunoglobulin production; B cell proliferation; immunosuppressive; HIV;
KM human immunodeficiency virus; autoimmune disease; immunodeficiency;
KM Sjogren's syndrome; systemic lupus erythematosus; Hodgkin's disease;
KM common variable immunodeficiency; CVID; non-Hodgkin's lymphoma; AIDS;
KM acquired immunodeficiency virus; cancer; multiple myeloma; CLL;
KM chronic lymphocytic leukaemia; lymphoproliferative disorder;
KM bacterial infection; viral infection; osteoporosis; atherosclerosis;
KM pain; cardiovascular disorder; stroke; allergy; Alzheimer's disease;
KM neurodegenerative disease; inflammation; liver disease; cirrhosis;
KM cardiomyopathy; diabetes; asthma; psoriasis; glomerulonephritis;
KM ulcerative colitis; angiogenesis; septic shock; wound healing;
KM tumour necrosis factor receptor; TACI; immunoglobulin; IgG.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
XX WO200196528-A2.
```

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XX
XX 20-DEC-2001.
XX
XX
XX 14-JUN-2001; 2001MO-US019026.
XX
XX 15-JUN-2000; 2000US-0211537P.
XX PR 23-OCT-2000; 2000US-0241952P.
XX PR 13-DEC-2000; 2000US-0254875P.
XX PR 16-MAR-2001; 2001US-0276248P.
XX PR 23-MAR-2001; 2001US-0277978P.
XX PR 25-MAY-2001; 2001US-0293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Yu G, Ni J, Gentz RL, Dillon PJ, Hilbert D;
PI WPI; 2002-130727/17.
XX DR N-PSDB; ABR13415.
XX
XX Novel multimeric human tumor necrosis factor delta or epsilon protein
PT useful for treating cancer, immune system disorders, infection,
PT cardiovascular disorders, liver disease, cardiomyopathy, diabetes and
PT psoriasis.
XX
XX Example 29; Page 341-342; 344pp; English.
XX
XX The invention describes a multimeric human tumour necrosis factor (TNF)
XX delta or epsilon protein (I). (I) or a composition containing them (II)
XX are useful for modulating immunoglobulin production or proliferation of B
XX cells. (I) or (II) is useful for treating a disease or disorder of the
XX immune system, preferably an autoimmune disease (e.g. Sjogren's syndrome,
XX systemic lupus erythematosus or common variable immunodeficiency (CVID));
XX an immunodeficiency e.g. acquired immunodeficiency syndrome (AIDS);
XX cancer of the immune system (e.g. Hodgkin's disease, non-Hodgkin's
XX lymphoma, multiple myeloma and chronic lymphocytic leukaemia (CLL)); in
XX the diagnosis and treatment or prevention of cancer, lymphoproliferative
XX disorder, bacterial and viral infections, osteoporosis, arteriosclerosis,
XX pain, cardiovascular disorders (e.g. stroke), allergy, inflammation,
XX neurodegenerative disease (e.g. Alzheimer's disease), liver disease (e.g.
XX cirrhosis), cardiomyopathy, diabetes, asthma, psoriasis, septic shock,
XX glomerulonephritis, ulcerative colitis, arteriosclerosis, for promoting
XX angiogenesis and wound healing, as a diagnostic research reagent, as an
XX agent to target and kill cells expressing a TNFdelta and/or TNFepsilon
XX receptor; in apoptosis of transformed cell lines; mediation of cell
XX activation and proliferation; and as an immunogen to produce (II). (II)
XX is useful to purify, detect and target (I), for measuring levels of (I)
XX in biological samples, for immunophenotyping samples, and to treat,
XX inhibit or prevent diseases and disorders associated with aberrant
XX expression and/or activity of (I). This is the amino acid sequence of a
XX fusion protein of tumour necrosis factor receptor TACI and immunoglobulin
XX G (IgG) crystallisation fragment, described in the method of the
XX invention
XX
XX Sequence 293 AA;
SQ
Query Match 23.9%; Score 67.5; DB 5; Length 293;
Best Local Similarity 30.6%; Pred. No. 12;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
OY 8 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYCNA 43
DB 34 CPBEQYWPDLGTGTCMSCKTICNHQS-QRTCAAFCS 68
RESULT 90
ID AAU09900 standard; protein; 293 AA.
AC AAU09900;
XX
XX 12-MAR-2002 (first entry)
DT
XX
XX Human AGP-3 related protein receptor.
XX
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| | |
|----|---|
| XX | Human; AGP-3; antiinflammatory; antiarthritic; immunosuppressive; |
| KW | dermatological; neuroprotective; nootropic; immunomodulator; metabolic; |
| KW | antidiabetic; analgesic; nephrotropic; osteopathic; cytostatic; fever; |
| KM | antiParkinsonian; antipoxiatic; vasotropic; antibacterial; asthma; |
| KM | AGP-3 receptor; tumor necrosis factor ligand family; AGP-3 receptor; |
| KM | mesenteric lymph node; AGP-3R; inflammatory disease; immune disorder; |
| KM | rheumatoid arthritis; graft-versus-host disease; Crohn's disease; |
| KM | pancreatitis; amyotrophic lateral sclerosis; ALS; Alzheimer's disease; |
| KM | diabetes; glomerulonephritis; inflammatory bowel disease; ischaemia; |
| KM | multiple sclerosis; Parkinson's disease; transgenic animal. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| PN | WO200185782-A2. |
| XX | |
| PD | 15-NOV-2001. |
| XX | |
| PF | 12-FEB-2001; 2001WO-US004568. |
| XX | |
| PR | 11-FEB-2000; 2000US-0181800P. |
| XX | |
| PA | (AMGE-) AMGEN INC. |
| XX | |
| XX | |
| PI | Boyle WJ, Hsu H; |
| XX | |
| DR | WPI: 2002-049441/06. |
| XX | |
| DR | N-PSDB; AAS18558. |
| XX | |
| PT | Composition, useful for identifying modulator of receptor for treating |
| PT | asthma and glomerulonephritis, comprises AGP-3 (tumor necrosis factor |
| PT | ligand family member) receptor and encoding nucleic acids. |
| XX | |
| XX | Disclosure: Page 117-119; 1240; English. |

The invention relates to a composition (I) comprising AGP-3 receptor (tumour necrosis factor ligand family member)-related protein (II) attached to a vehicle protein. (I) is useful for modulating AGP-3-related activity in mesenteric lymph nodes (MLN) of a mammal. (II) is useful in assays to identify cells and tissues that express AGP-3R or proteins related to AGP-3R-related protein and for identifying compounds (agonists or antagonists) that interact with AGP-3 proteins. (II) is also useful for identifying intracellular proteins that interact with the respective cytoplasmic domains by yeast two-hybrid screening process. (II) is involved in B cell growth, survival and activation particularly in lymph node, spleen, and Peyer's patches. AGP-3R agonists and antagonists identified using (II) are used for modulating B cell response and are used to treat diseases characterised by inflammatory processes or deregulated immune response such as rheumatoid arthritis, graft-versus-host disease, Crohn's disease, lupus, etc. (II) is also useful in the production of hybridoma cells which are derived from B cells, which involves treating the hybridoma cells with (II). (II) is useful in the treatment of inflammatory conditions of joints, e.g., rheumatoid arthritis, osteoarthritis, etc. (II), its agonists or antagonists are useful for treating acute pancreatitis, amyotrophic lateral sclerosis (ALS), Alzheimer's disease, asthma, atherosclerosis, cachexia/anorexia, diabetes, fever, glomerulonephritis, inflammatory bowel disease, ischaemic injury including cerebral ischaemia, multiple myeloma, multiple sclerosis, osteoporosis, Parkinson's disease, pain, reperfusion injury, septic shock, etc. The nucleic acids are also useful for developing transgenic animals expressing (II), which are useful for producing the polypeptides and for the study of in vivo biological activity. The present sequence represents the amino acid sequence of human AGF-3 related protein receptor

Sequence 293 AA;

| | | | | |
|--------------------------|-------|---------------|----------|------------|
| Query Match | 23.9% | Score 67.5 | DB 5 | Length 293 |
| Best Local Similarity | 30.6% | Pred. No. 12 | | |
| Matches 11, Conservative | 9 | Mismatches 15 | Indels 1 | Gaps 1 |

| | | | |
|-----------|---|--------------------------------------|----|
| D6 | | 34 CPBQWYDPLGTGMSCKTICNHQS-QRTCAACRS | 68 |
| RESULT 91 | | | |
| ID | AAE15493 | | |
| XX | AAE15493 | standard; protein: 293 AA. | |
| XX | AAE15493; | | |
| DT | 12-MAR-2002 | (first entry) | |
| DE | Human transmembrane activator and intracellular CAML interactor protein. | | |
| XX | | | |
| KM | Human; transmembrane activator and intracellular CAML interactor; TACI; | | |
| KM | Cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; | | |
| KM | Lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; | | |
| KM | prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; | | |
| KM | drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; | | |
| KM | Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; | | |
| KM | human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; | | |
| XX | rheumatoid arthritis; atherosclerosis. | | |
| OS | Homo sapiens. | | |
| XX | | | |
| FT | Key | Location/Qualifiers | |
| FT | Region | 34..66 | |
| FT | /note="Cysteine-rich consensus region" | | |
| FT | Region | 71..104 | |
| FT | /note="Cysteine-rich consensus region" | | |
| FT | Domain | 167..186 | |
| FT | /label=Transmembrane_domain | | |
| XX | | | |
| PN | WO200187979-A2. | | |
| XX | | | |
| PD | 22-NOV-2001. | | |
| XP | 14-MAY-2001; 2001MO-USO15567. | | |
| XX | | | |
| PR | 12-MAY-2000; 2000US-0204039P. | | |
| PR | 27-JUN-2000; 2000US-0214591P. | | |
| PR | 14-MAY-2001; 2001US-00214591. | | |
| XX | | | |
| PA | (AMGE-) AMGEN INC. | | |
| XX | | | |
| P1 | Theill LE, Yu G; | | |
| XX | | | |
| DR | WPI; 2002-066666/09. | | |
| PT | Inhibiting activity of B cell maturation protein and/or transmembrane | | |
| PT | activator and intracellular cyclophilin ligand interactor, by | | |
| PT | administering a binding partner for APRIL, a tumor necrosis factor family | | |
| PT | ligand. | | |
| XX | | | |
| PS | Disclosure; Fig 12A, 94pp; English. | | |
| XX | | | |
| CC | The invention relates to a method for inhibiting TACI (transmembrane | | |
| CC | activator and intracellular CAML interactor) and/or B cell maturation | | |
| CC | protein (BCMA) activity in a mammal. The method comprises administering a | | |
| CC | specific binding partner for APRIL (G70, a tumour necrosis factor-TNF | | |
| CC | family ligand), having the consensus region of TACI, BCMA, or the TACI/ | | |
| CC | BCMA extracellular consensus sequence, but not the extracellular region | | |
| CC | of TACI or BCMA. The method is useful for inhibiting activity of TACI | | |
| CC | and/or BCMA in a mammal which is useful for treating B-cell or T-cell | | |
| CC | lymphoproliferative disorders, one or more solid tumours such as lung, | | |
| CC | gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI | | |
| CC | antagonists are useful for treating inflammation and immune function | | |
| CC | diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic | | |
| CC | dermatitis, respiratory allergic disease (asthma, hypersensitivity lung | | |
| CC | disease), drug and insect sting allergy, inflammatory bowel disease | | |
| CC | (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple | | |
| CC | sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, | | |
| CC | bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer | | |
| CC | with leucocyte infiltration of the skin or organs. The present sequence | | |

CC is human TACI protein
XX
SQ Sequence 293 AA;

Query Match 23.9%; Score 67.5; DB 5; Length 293;
Best Local Similarity 30.6%; Pred. No. 12;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
QY 8 CSQNEYFDSLHACTPCQLRCSSTNPPLTCGRYCNA 43
DB 34 CPBEQYWDPLLTGTCWSCKTCICNHQS-QRTCAAFCKS 68

RESULT 92
ABG71496
ID ABG71496 standard; protein; 293 AA.
XX
AC ABG71496;
XX
DT 11-MAR-2003 (first entry)
XX
DE Human tumour necrosis factor (TNF) receptor TR17 polypeptide.
XX
KW Human; tumour necrosis factor receptor; TNF; TR17; receptor; cancer;
KW immunodeficiency; autoimmune condition; haemolytic anaemia; dermatitis;
KW myocarditis; glomerulonephritis; allergic encephalomyelitis; vitiligo;
KW rheumatic heart disease; polyendocrinopathy; diabetes mellitus; neuritis;
KW autoimmune pulmonary inflammation; multiple sclerosis; asthma; hepatitis;
KW cirrhosis; Sjogren's syndrome; rheumatoid arthritis; restenosis; AIDS;
KW autoimmune thyroiditis; reticular dysgenesis; ataxia-telangiectasia;
KW systemic lupus erythematosus; B cell lymphoproliferative disorder;
KW kappa chain deficiency; short limbed dwarfism; Crohn's disease; sepsis;
KW bronchitis; otitis media; meningitis; ulcerative colitis.
XX
OS Homo sapiens.
XX
PN US2002106736-A1.
XX
PD 08-AUG-2002.
XX
PF 25-SEP-2001; 2001US-00961376.
XX
PR 10-MAR-2000; 2000US-0188208P.
PR 24-MAR-2000; 2000US-00533822.
PR 26-SEP-2000; 2000US-0235991P.
PR 13-DEC-2000; 2000US-0254874P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Baker KP;
XX
DR WPI: 2002-690756/74.
DR N-PSDB; ABX14552.
XX
PT Tumour necrosis factor receptor polypeptide, useful e.g. for creating
PT immunodeficiency, comprises a specific amino acid sequence, and
PT optionally a heterologous polypeptide sequence.
XX
PS Claim 1; Fig 1; 134pp; English.
XX
CC The invention relates to a tumour necrosis factor (TNF) receptor
CC polypeptide, TR17, and the polynucleotide encoding it. The polypeptide
CC and polynucleotide are used for treating an immunodeficiency or an
CC autoimmune condition. The disorders include haemolytic anaemia,
CC dermatitis, myocarditis, glomerulonephritis, allergic encephalomyelitis,
CC rheumatic heart disease, polyendocrinopathies, autoimmune pulmonary
CC inflammation, multiple sclerosis, diabetes mellitus, asthma, vitiligo,
CC hepatitis, cirrhosis, Sjogren's syndrome, rheumatoid arthritis,
CC autoimmune thyroiditis, reticular dysgenesis, ataxia-telangiectasia,
CC systemic lupus erythematosus, B cell lymphoproliferative disorder, kappa
CC chain deficiency, neuritis, restenosis and short limbed dwarfism, cancer,
CC Crohn's disease, bronchitis, otitis media, sepsis, meningitis, ulcerative
CC colitis and AIDS. The polypeptide is also useful for increasing or

CC inhibiting B-cell proliferation and immunoglobulin production and for
CC killing a cell that expresses the TR17 polypeptide on its cell surface.
CC This sequence represents the human TR17 polypeptide
XX
SQ Sequence 293 AA;

Query Match 23.9%; Score 67.5; DB 5; Length 293;
Best Local Similarity 30.6%; Pred. No. 12;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
QY 8 CSQNEYFDSLHACTPCQLRCSSTNPPLTCGRYCNA 43
DB 34 CPBEQYWDPLLTGTCWSCKTCICNHQS-QRTCAAFCKS 68

RESULT 93
AAE35211
ID AAE35211 standard; protein; 293 AA.
XX
AC AAE35211;
XX
DT 28-MAY-2003 (first entry)
XX
DE Human TACI protein.
XX
KW Transmembrane activator; calcium modulator; nephrotoxic; antibacterial;
KW TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;
KW anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive;
KW glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;
KW dermatological; neuroprotective; cyclophilin ligand-interactor; human;
KW autoimmune disease; systemic lupus erythematosus; multiple sclerosis;
KW diabetes mellitus; rheumatoid arthritis; renal disease; inflammation.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
XX
FT Region 34..104
FT /note= "Cysteine rich pseudo repeat"
FT Region 105..166
FT /note= "Stalk region"
FT Domain 167..186
FT /note= "Transmembrane domain"
XX
PN WO200294852-A2.
XX
PD 28-NOV-2002.
XX
PP 20-MAY-2002; 2002MO-US015910.
XX
PR 24-MAY-2001; 2001US-0293343P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Rixon MW, Gross JA;
XX
DR WPI: 2003-148455/14.
DR N-PSDB; AAD53734.
XX
PT Transmembrane activator and calcium modulator and cyclophilin ligand-
PT interactor (TACI)-immunoglobulin fusion protein, for treating cancer or
PT diabetes, comprises a TACI receptor group and an immunoglobulin group.
XX
PS Claim 17; Col 87-88; 71pp; English.
XX
CC The invention relates to fusion proteins comprising transmembrane
CC activator and calcium modulator and cyclophilin ligand-interactor (TACI)
CC receptor group that binds tumour necrosis factor-like protein (ZTNF2 or
CC ZTNF4; and an immunoglobulin group comprising a constant region of an
CC immunoglobulin. The invention is used to manufacture a medicament for
CC inhibiting the proliferation of tumour cells in a mammalian subject. The
CC composition comprising the fusion protein may also be used in treating
CC autoimmune diseases (e.g. systemic lupus erythematosus, multiple
CC sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal

CC diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft
 CC rejection, anaemia and septic shock. The fusion proteins are also used in
 CC gene therapy. The present sequence is human TACI protein
 CC

XX Sequence 293 AA;

Query Match 23.9%; Score 67.5; DB 6; Length 293;
 Best Local Similarity 30.6%; Pred. No. 12;
 Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 8 CSQNEYFDSLHACIPCOLRCSSNTPTLTCQRYCNA 43
 Db 34 CPBQYWDPLGTGTCMSCKTICNHQS-QRTCAAFCRS 68

RESULT 94
 ABP60551
 ID ABP60551 standard; protein; 293 AA.

XX ABP60551;

DT 28-MAR-2003 (first entry)

XX Human tumour necrosis factor TACI.

XX APRIL; scFv; immunospecific; tumour necrosis factor delta; TNF-delta;
 KW dermatological; immunosuppressive; antiinflammatory; antirheumatic;
 KW antiallergic; cytosolic; antinaemic; antiallergic; antidiabetic;
 KW neuroprotective; ophthalmological; tuberculostatic; antidiabetic;
 KW antiproliferative; anti-HIV; antiatherosclerotic; vasotropic; thyromimetic;
 KW haemostatic; cancer; autoimmune disease; graft versus host disease; GVHD;
 KW inflammatory disorder; proliferative disorder; single chain antibody;
 KW antibody; human; TACI; tumour necrosis factor.

XX Homo sapiens.

XX WO200294192-A2.

XX 28-NOV-2002.

XX 22-MAY-2002; 2002WO-US016106.

XX 24-MAY-2001; 2001US-0293100P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM;

XX WPI; 2003-156740/15.

XX Novel isolated antibody that immunospecifically binds tumor necrosis
 PT factor delta, useful for treating, preventing or ameliorating Non-
 PT Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's
 PT syndrome.

XX Disclosure; Page 220-221; 225pp; English.

XX The invention relates to a novel antibody or its fragment, which
 CC immunospecifically binds tumour necrosis factor Delta (TNF-delta/APRIL).
 CC The antibody of the invention has dermatological, immunosuppressive,
 CC antiinflammatory, antirheumatic, antiallergic, cytosolic, antinaemic,
 CC antiallergic, antidiabetic, neuroprotective, ophthalmological,
 CC tuberculostatic, antiproliferative, anti-HIV,
 CC antiatherosclerotic, vasotropic, thyromimetic, and haemostatic activity.
 CC The antibody or its fragment are useful for treating, preventing or
 CC ameliorating cancer such as Non-Hodgkin's lymphoma or multiple myeloma in
 CC human, disease or disorder such as autoimmune disease, and graft versus
 CC host disease (GVHD). The autoimmune disease is systemic lupus
 CC erythematosus, rheumatoid arthritis or Sjogren's syndrome. The antibody
 CC is useful for detecting, diagnosing, prognosing, treating, preventing or
 CC ameliorating a disease or disorder associated with aberrant APRIL or
 CC APRIL receptor expression or aberrant function of APRIL or APRIL
 CC receptor. The disease or disorders includes autoimmune and inflammatory

CC disorders such as autoimmune neutropenia, hemolytic anaemia, dermatitis,
 CC asthma, allergic encephalomyelitis, myocarditis, multiple sclerosis,
 CC uveitis, tuberculosis, diabetes mellitus, psoriasis, cancer of the immune
 CC system, particularly B cell cancers, immune disorders such as myasthenia
 CC gravis, Hashimoto's disease, immunodeficiency syndrome, Bruton's disease,
 CC infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS)), and
 CC proliferative disorders (e.g. leukemia). The present sequence represents
 CC the tumour necrosis factor TACI

XX Sequence 293 AA;

Query Match 23.9%; Score 67.5; DB 6; Length 293;
 Best Local Similarity 30.6%; Pred. No. 12;
 Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 8 CSQNEYFDSLHACIPCOLRCSSNTPTLTCQRYCNA 43
 Db 34 CPBQYWDPLGTGTCMSCKTICNHQS-QRTCAAFCRS 68

RESULT 95
 ABP97716
 ID ABP97716 standard; protein; 293 AA.

XX ABP97716;

DT 28-MAY-2003 (first entry)

XX Amino acid sequence of human TACI receptor.

XX Human; TACI; BR3; receptor; tumour necrosis factor ligand; TNF ligand;
 KW TALL-1; April; systemic lupus erythematosus.

XX Homo sapiens.

XX WO2003014294-A2.

XX 20-FEB-2003.

XX 24-JUL-2002; 2002WO-US023487.

XX 03-AUG-2001; 2001US-0310114P.

XX 30-APR-2002; 2002US-0377171P.

XX (GETH) GENENTECH INC.

XX Dixie V, Grewal I, Ridgway J, Yan M;

XX WPI; 2003-256560/25.

XX N-PSDB; AB268870.

XX New nucleic acid encoding a TACIs or BR3 polypeptide, useful for
 PT preparing a composition for treating systemic lupus erythematosus.

XX Disclosure; Fig 1A-B; 153pp; English.

XX The present sequence represents a human TACI polypeptide. The
 CC specification also describes BR3 polypeptides. TACI and BR3 are
 CC receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and April
 CC bind to the TACI receptor, while TNF family ligands TALL-1 also binds to
 CC BR3 receptor. The TACI and BR3 receptor nucleic acid is useful for
 CC preparing a composition for treating systemic lupus erythematosus

XX Sequence 293 AA;

Query Match 23.9%; Score 67.5; DB 6; Length 293;
 Best Local Similarity 30.6%; Pred. No. 12;
 Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 8 CSQNEYFDSLHACIPCOLRCSSNTPTLTCQRYCNA 43
 Db 34 CPBQYWDPLGTGTCMSCKTICNHQS-QRTCAAFCRS 68

| | | |
|----------|---|--|
| ID | AAO29592 | standard; protein; 293 AA. |
| AC | AAO29592; | |
| XX | | |
| XX | | |
| DT | 27-AUG-2003 | (first entry) |
| DE | | Human DITACIN protein. |
| XX | | |
| KM | | Metabolic disorder; DITACIN; obesity-related disease; hyperlipidaemia; antidepressant; chronic inflammatory disease; cachexia; immunomodulator; glucose uptake; insulin sensitivity; anorexia; cerebroprotective; AIDS; atherosclerosis; insulin resistance; diabetes; stroke; hypertension; cancer; weight loss; human. |
| XX | | |
| OS | Homo sapiens. | |
| XX | | |
| FH | Key | Location/Qualifiers |
| FT | Domain | 1..159 |
| FT | | /note="Extracellular domain" |
| FT | Domain | 160..182 |
| FT | | /note="intracellular domain" |
| FT | Domain | 183..293 |
| FT | | /note="Transmembrane domain" |
| PN | WO2003041730-A1. | |
| PD | 22-MAY-2003. | |
| PF | 03-OCT-2002; 2002WO-IB004582. | |
| PR | 16-NOV-2001; 2001US-0332361P. | |
| PA | (GEST) GENSET SA. | |
| PI | Lucas J, Briggs K, Dialynas D, Scalia A; | |
| DR | WPI; 2003-468587/44. | |
| N-PDB: | AAL60089. | |
| PT | New agonist and antagonist of DITACIN activity, useful for preventing or treating obesity-related diseases (e.g. hyperlipidaemia or stroke), or increasing body mass (e.g. by treating excessive weight loss, cachexia), respectively. | |
| PS | Disclosure; Page 33-34; 37pp; English. | |
| XX | | |
| CC | The invention relates to agonist or antagonist of DITACIN useful in the treatment of metabolic disorders. The antagonist or agonist of DITACIN or the composition comprising the agonist or antagonist, is useful for treating or preventing obesity-related diseases, e.g. hyperlipidaemia, atherosclerosis, insulin resistance, diabetes, stroke or hypertension. The agonist is useful for reducing body mass and maintaining weight loss by: lowering circulating levels or concentrations of free fatty acids, glucose and/or triglycerides; stimulating muscle lipid or free fatty acid oxidation; increasing leptin uptake in a liver cell; reducing the postprandial increase in plasma free fatty acids or triglycerides, particularly following a high fat meal; reducing or eliminating ketone body production, particularly following a high fat meal; increasing glucose uptake in skeletal muscle cells, adipose cells, neuronal cells, red blood cells or brain; reducing or preventing the postprandial increase in plasma glucose following a high carbohydrate meal; or improving insulin sensitivity. The antagonist of DITACIN activity is useful for increasing body mass, or for treating or preventing disorders associated with excessive weight loss, e.g. cachexia, cancer-related weight loss, AIDS-related weight loss, chronic inflammatory disease- related weight loss, or anorexia. The present sequence is human DITACIN protein | |
| Sequence | 293 AA; | |

| Query Match | Similarity | 23.9% | Score 67.5 | DB 6 | Length 293 |
|-------------|---|---------------|--------------|---------|------------|
| Best Local | Similarity | 30.6% | Pred. No. 12 | | |
| Matches | 11; Conservative | 9; Mismatches | 15; Indels | 1; Gaps | 1 |
| Qy | 8 CSQNEYPDSLHACIPCOLRCSSNTPLTCGRYCN A 43 | | | | |
| Db | 34 CPBERQWBDPLGTGCMSCRTICNHQS-QRTCAFCRS 68 | | | | |
| RESULT 97 | | | | | |
| ADFF72628 | | | | | |
| ID | ADFF72628 standard; protein; 293 AA. | | | | |
| XX | | | | | |
| XX | ADFF72628; | | | | |
| XX | | | | | |
| DT | 12-FEB-2004 (first entry) | | | | |
| XX | | | | | |
| DE | Human tumour necrosis factor (TNF)-related polypeptide. | | | | |
| XX | | | | | |
| KW | Human; tumour necrosis factor; TNF; septic shock; inflammation; cancer; | | | | |
| KW | cerebral malaria; HIV; bone resorption; rheumatoid arthritis; cachexia; | | | | |
| KW | Grave's disease; diabetes; hepatitis; asthma; cardiovascular disorders; | | | | |
| KW | infection; allergy; Alzheimer's disease; Parkinson's disease; nephritis. | | | | |
| XX | | | | | |
| OS | Homo sapiens. | | | | |
| XX | | | | | |
| PN | US2003168664-A1. | | | | |
| XX | | | | | |
| PD | 04-SEP-2003. | | | | |
| XX | | | | | |
| PF | 11-OCT-2002; 2002US-00268951. | | | | |
| XX | | | | | |
| PR | 14-MAR-1996; 96US-0016812P. | | | | |
| PR | 12-MAR-1997; 97US-00815783. | | | | |
| PR | 15-JUN-2000; 2000US-0211537P. | | | | |
| PR | 23-OCT-2000; 2000US-0241952P. | | | | |
| PR | 13-DEC-2000; 2000US-0254875P. | | | | |
| PR | 16-MAR-2001; 2001US-0276248P. | | | | |
| PR | 23-MAR-2001; 2001US-0277978P. | | | | |
| PR | 25-MAY-2001; 2001US-0293499P. | | | | |
| PR | 14-JUN-2001; 2001US-00879919. | | | | |
| PR | 12-OCT-2001; 2001US-0328401P. | | | | |
| PR | 26-FEB-2002; 2002US-00082260. | | | | |
| XX | | | | | |
| PA | (YDGG/) YU G. | | | | |
| PA | (NIJY/) NI J. | | | | |
| PA | (GENTZ/) GENTZ R. | | | | |
| XX | | | | | |
| PI | YU G, NI J, Gentz R; | | | | |
| XX | | | | | |
| DR | WPI; 2003-896107/82. | | | | |
| DR | N-PSDB; ADF72627. | | | | |
| XX | | | | | |
| PT | New human tumor necrosis factor (TNF) delta and epsilon, useful for | | | | |
| PT | diagnosing, preventing or treating dysfunctions or diseases associated | | | | |
| PT | with aberrant activity of TNF delta or epsilon, e.g. septic shock, | | | | |
| PT | inflammation or cancer. | | | | |
| XX | | | | | |
| PS | Example 30; SEQ ID NO 22; 155pp; English. | | | | |
| XX | | | | | |
| CC | The invention relates to human tumour necrosis factor (TNF) polypeptides | | | | |
| CC | and the polynucleotides encoding them. The sequences of the invention are | | | | |
| CC | useful in research, biological, clinical and therapeutic purposes. In | | | | |
| CC | particular, these are used in diagnosing, preventing, treating or | | | | |
| CC | ameliorating dysfunctions or diseases associated with aberrant endogenous | | | | |
| CC | activity of TNF delta or epsilon, such as septic shock, inflammation, | | | | |
| CC | cancer, cerebral malaria, activation of HIV virus, bone resorption, | | | | |
| CC | rheumatoid arthritis, cachexia, Grave's disease, diabetes, hepatitis, | | | | |
| CC | asthma, cardiovascular disorders, infections, allergies, Alzheimer's | | | | |
| CC | disease, Parkinson's disease and nephritis. The sequences may also be | | | | |
| CC | used for chromosome identification or genetic mapping. This sequence | | | | |
| CC | represents a human TNF-related polypeptide of the invention. | | | | |
| XX | | | | | |

